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17. ANIMAL GENETICS & BREEDING

Unit 1: Overview of Genetics

Mendelism and its deviations. Chromosomes and heredity. Sex in relation to chromosomes and genes. Linkage and crossing over. Artificial transmutation of genes. Penetrance and expressivity. Multiple factor inheritance. Gene modifiers. Non-chromosomal genes and their inheritance, Chromosomal aberrations and Genetic disorders. Cytogenetics & Immunogenetics of farm animals. Immune response. Antigen-antibody response. MHC, BoLA, BuLA. Toll like receptors, Interleukins. Hybridoma and its significance.

Unit 2: Advanced Genetics

Fine structure of chromosomes and chromosomal banding. Gene and mechanism of gene action. DNA replication. Genetic code. Recombinant DNA technology. Development of clones in relation to animal productivity and maintaining biodiversity. Production of transgenic animals. Gene mixing for useful functions. Gene expression and its control. Concept of genomics and proteomics. DNA sequencing, Genome Sequencing. Next generation sequencing, GWAS. Epigenetic control. Genomic selection.

Unit 3: Overview of Breeding

Brief history of domestication of livestock. Important breeds of livestock and poultry with special reference to economic characters. Evolution of genetic systems. Isolating mechanisms and origin of species/sub-species, their adaptation. Mating systems for different livestock and poultry. Genetic and phenotypic consequences and applications of inbreeding and out- breeding. Genetic basis of heterosis and its use. Diallele and polyallele crossing. Reciprocal and reciprocal-recurrent-selection. Combining ability. Developments in population and production of livestock and poultry in India. Status of Animal Genetic Resources in India.

Unit 4: Genetic Properties of Population

Population Vs individual. Inheritance and continuity of population. Effective population size. Description of animal population. Value and means; Average effect of gene and gene substitution. Components of total phenotypic variance of a population. Resemblances between relatives. Concept of heritability, repeatability; & phenotypic, genetic and environmental correlations. Methods of estimation, uses, possible biases and precision of estimates. Biodiversity. Genetic diversity assessment. Population structure. Genetic Admixture. Breed signature.

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Unit 5: Population Genetics

Gene and genotypic frequencies and factors affecting them. Hardy Weinberg Law and consequences of it. Prediction of selection response by different methods. Selection for threshold characters. Indirect selection and correlated response. Theoretical basis of change of population mean and variance on inbreeding and cross breeding. Genotype-environment interaction. Metric characters under natural selection. Quantitative trait loci and their applications. Marker-assisted selection. Candidate gene approach.

Unit 6: Genetic Strategies

Purpose-wise breeding strategies for livestock and poultry under different agro- climatic zones of India. Evaluation of past genetic improvement programmes for livestock and poultry in India. Bottlenecks in implementation of livestock breeding programmes in India. Evaluation and characterization of various indigenous breeds of livestock and poultry. *Ex-situ* and *In-situ* conservation of animal and poultry genetic resources. Development of new breeds/ strains for better productivity in animals. Open nucleus breeding system in livestock improvement in India. Bio-technology and its role in improving animals and poultry production. Role of artificial insemination / frozen semen / embryo transfer / ONBS / MOE technology in animal breeding. Formulation of breeding programmes: Purpose wise, breed- wise, region-wise for different species of livestock and poultry. Programmes for genetic improvement of non- descript livestock population of different species. Evaluation and recommendations of breeding programmes of cattle, buffalo, sheep, goat, swine, camel and equine in India.

Unit 7: Selection & Selection Experiments

Basis and methods of selection. Construction of selection indices. Different methods of sire evaluation. Selection differential and intensity of selection. Prediction of response. Improvement of response. Effect of selection on variance. Realized heritability. Long term and short-term objectives of selections. Selection experiments in livestock and poultry. Role of control population in selection experiments. Selection for disease resistance and development of general and specific disease

resistant strains / breeds. Purpose based selection and breeding of domestic animals and poultry. Genetic- slippage. Estimation of genetic divergence and its implications in livestock improvement programmes. Selection for better feed conversion efficiency in meat animals and poultry.

Unit 8: Genetic Laboratory Techniques

Gene sequencing. Karyotyping and chromosomal mapping. Concept of recombinant DNA techniques cloning and gene mapping. Nucleic acid hybridization. Development of breed descriptors at molecular level for different livestock and poultry breeds. Collection and storage of samples for DNA fingerprinting; isolation and quantification of DNA from blood and semen; Restricted enzyme digestion of genome DNA, Analysis and transfer of DNA from agarose electrophoresis; Nucleic acid hybridization; Analysis of DNA fingerprinting, PCR-RFLP assay. Cloning. Cryogenic preservation of animal germplasm. ELISA. FISH chromosome painting and PRINS; SCH and RH panel mapping.

Unit 9: Research Techniques for Quantitative Animal Genetics

Estimation of variances and covariances. ANOVA. Maximum likelihood. REML. MINQUE. Bayesian approach. Development of statistical models for analyses of breed data and to quantify environmental variance. BLUP animal model, sire model and repeatability model. Estimation of inbreeding and relationship. Estimation of inbreeding rate in a closed herd / flock. Estimation and interpretation of genetic and phenotypic parameters. Estimation of genetic gains. Designing field-based progeny testing programmes. Development of efficient methods and traits for genetic evaluation of males under indigenous conditions. Data bank concept. Genetic distance and phylogeny analysis. Whole genome analysis. Bioinformatics tools for sequence analysis. Concept and application of Multiple linear regression, Discriminant function, Cluster analysis, Least squares analysis, Principal component analysis, Multiple dimension scaling and Random regression models.

Unit 10: Laboratory Animal Breeding

Laboratory animal species *viz.,* mice, rat, guinea pig, rabbit, dog and monkey - Their chromosome numbers -genome size major genes. Physiological, nutritional, reproduction parameters, maintenance protocol pedigree recording, planned mating. Selection and Mating methods /systems-monogamous, polygamous and others. Genetic control and monitoring- Record keeping-Ethics and legislation for management and use of laboratory animals. Nomenclature for different strains, inbred lines (SPF line, Knockout mice, etc.) - Animal model for human disease. Specific utility of different laboratory species for different requirements

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CHAPTER 01
Overview of Genetics

2013

1. Which of the following defines the Mendelian law of segregation as applied to livestock breeding?
(A) Genes for different traits assort independently of one another during the formation of gametes
(B) Allele pairs separate during gametogenesis so that each gamete receives only one allele for a given trait
(C) Multiple genes cumulatively contribute to the expression of a single quantitative trait
(D) Dominant alleles mask the phenotypic expression of recessive alleles in a heterozygous state

2003

2. A dairy farmer crosses a purebred polled bull with horned cows. If the F1 offspring are all polled, what type of cross can be used to determine if an F1 individual is heterozygous?
(A) A reciprocal cross with another F1 polled individual
(B) A topcross with an unrelated purebred polled individual
(C) An outcross with a genetically distinct horned individual
(D) A testcross with a homozygous recessive horned individual

2021

3. In poultry, what is the primary purpose of conducting a reciprocal cross when investigating a newly identified plumage trait?
(A) To evaluate the influence of maternal effects or sex-linked inheritance on the trait
(B) To determine the recombination frequency between two linked genes
(C) To measure the degree of incomplete dominance in heterozygous birds
(D) To eliminate the effect of lethal alleles in the breeding population

2017

4. All of the following statements regarding backcrosses in animal genetics are correct EXCEPT:
(A) A backcross involves crossing an F1 hybrid with one of its parents or an individual genetically similar to its parents
(B) All testcrosses are considered backcrosses
(C) All backcrosses are considered testcrosses
(D) Backcrossing is frequently used for introgression of a specific trait into an elite breed

2021

5. Which statement correctly identifies the relationship between testcrosses and expected Mendelian ratios in farm animals?
(A) A dihybrid testcross yields a 1:1:1:1 phenotypic ratio under independent assortment
(B) A monohybrid testcross yields a 3:1 phenotypic ratio even in the absence of linkage
(C) A trihybrid testcross results in a 9:3:3:1 phenotypic ratio in all diploid animals
(D) Testcross ratios are fundamentally unaffected by genetic linkage or recombination

2015

6. If a trait in swine exhibits complete dominance, what is the direct effect of selfing or intermating F1 individuals?
(A) The F2 generation will exclusively show the dominant phenotype
(B) The F2 generation will exhibit a 1:2:1 phenotypic ratio
(C) The F2 generation will show continuous variation
(D) The F2 generation will yield a 3:1 phenotypic ratio

2017

7. The classic Mendelian dihybrid cross ratio of 9:3:3:1 in an F2 generation is fundamentally dependent on which cellular event?
(A) Sister chromatid exchange during mitosis between homologous pairs in somatic tissues
(B) Independent alignment of non-homologous chromosomes during metaphase I of meiosis
(C) Non-disjunction of homologous chromosomes during anaphase II in the germline cells
(D) Random fertilization of gametes carrying

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linked genes located on the same chromosome

2022

8. Which pair correctly matches the Mendelian principle with its underlying cytological basis?
(A) Law of Independent Assortment - Sister chromatids separate during Anaphase II stages
(B) Law of Dominance - Crossing over occurs during the Prophase I stage of meiotic division
(C) Law of Segregation - Homologous chromosomes separate during Anaphase I of meiosis
(D) Particulate Inheritance - DNA replication occurs during the S phase of the cell cycle

2005

9. Which genetic scenario would most reliably eliminate independent assortment as the mechanism governing two traits in sheep?
(A) Both traits are determined by polygenes located at multiple loci throughout the genome
(B) The traits are controlled by genes located on distinct, non-homologous chromosomes
(C) The genes exhibit incomplete dominance or codominance in the heterozygous offspring
(D) A dihybrid testcross yields parental combinations at frequencies significantly above 50%

2021

10. Which statement regarding the application of Mendelian principles to farm animal genetics is INCORRECT?
(A) Milk yield and other complex economic traits follow simple monohybrid Mendelian ratios
(B) Mendelian principles apply to qualitative traits like coat color in major cattle breeds
(C) The inheritance of horns in cattle follows basic rules of Mendelian dominance interaction
(D) Understanding Mendelian genetics is foundational for managing inherited monogenic disorders

2008

11. Which term most appropriately describes an allele that expresses its full phenotype only when present in two copies?
(A) Co-dominant
(B) Recessive
(C) Incompletely dominant
(D) Epistatic

2011

12. Based on Mendelian inheritance, what can be inferred if two phenotypically normal pigs produce an offspring affected by a rare genetic disorder?
(A) The disorder is caused by a dominant allele expressed in both the sire and the dam
(B) Both parents are heterozygous carriers of an underlying autosomal recessive allele
(C) The disorder is strictly governed by a sex-linked dominant gene on the X-chromosome
(D) A spontaneous mutation occurred in somatic cells during the early embryonic stages

2015

13. Which category of genetic inheritance best characterizes traits that show discrete, distinguishable phenotypes without intermediates?
(A) Qualitative inheritance
(B) Polygenic inheritance
(C) Quantitative inheritance
(D) Transgressive inheritance

2008

14. Which definition accurately distinguishes codominance from incomplete dominance in animal genetics?
(A) In codominance, the heterozygote displays a phenotype intermediate between both homozygotes
(B) In incomplete dominance, both alleles are simultaneously and fully expressed in the hybrid
(C) In codominance, both alleles independently express their gene products in the heterozygote
(D) In incomplete dominance, one allele completely masks the other at a specific genetic locus

2012

15. Consider the following statements regarding overdominance in livestock:
I. It occurs when the heterozygote exhibits a phenotypic value outside the range of both homozygous parents.
II. It is entirely synonymous with incomplete dominance.
III. It is frequently associated with fitness traits and hybrid vigor.
Which of the above statements are correct?
(A) I and II

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(B) I and III
(C) II and III
(D) I, II and III

2012

16. The Roan coat color in Shorthorn cattle, where both red and white hairs are present simultaneously, is a classic example of which gene interaction?
(A) Incomplete dominance
(B) Overdominance
(C) Codominance
(D) Multiple allelism

2002

17. Which of the following identifies the correct consequence of an autosomal recessive lethal gene in an inbred sheep population?
(A) It causes lethality only in the heterozygous state when specific environmental factors occur
(B) It shifts the phenotypic ratio of surviving offspring from a heterozygous cross to 2:1
(C) It enhances the survival rate of the herd due to natural selection and fitness advantages
(D) It results in a 1:2:1 ratio among living adult animals regardless of the breeding scheme

2002

18. All of the following traits are typically governed by multiple alleles EXCEPT:
(A) Complex blood group systems commonly identified across multiple major cattle populations
(B) Coat color series in rabbits typically governed by a hierarchy of distinct allelic states
(C) Major histocompatibility complex (MHC) polymorphism in swine populations and other species
(D) Presence or absence of horns (polled vs. horned) in European cattle breeds

2007

19. A farmer breeds two heterozygous creeper chickens. What phenotypic ratio of creeper to normal offspring is expected among the live progeny, assuming the homozygous creeper genotype is lethal during embryonic development?
(A) 2:1
(B) 3:1
(C) 1:2
(D) 1:1

2021

20. Which statement INCORRECTLY characterizes the phenomenon of multiple allelism?
(A) An individual diploid animal can possess a maximum of two different alleles for a given locus
(B) Multiple alleles are studied at the population level rather than in a single diploid animal
(C) Recombination occurs between different alleles of the same multiple allelic series
(D) The ABO blood group system and comparable animal systems are governed by multiple alleles

2022

21. Which pair accurately matches the allelic interaction with its corresponding F2 phenotypic ratio from a monohybrid cross?
(A) Lethal allele (recessive) - 2:1 ratio among the viable offspring
(B) Complete dominance - 1:2:1 ratio among the resulting F2 generation
(C) Incomplete dominance - 3:1 ratio among the resulting F2 generation
(D) Codominance - 9:3:3:1 ratio among the resulting F2 generation

2011

22. In Andalusian fowls, crossing a black bird with a white splash bird produces slate-blue F1 offspring. This intermediate phenotype indicates which type of gene action?
(A) Codominance
(B) Epistasis
(C) Overdominance
(D) Incomplete dominance

2012

23. What is the fundamental cause of the phenotypic manifestation of a dominant lethal allele that allows it to persist in a livestock population?
(A) The allele only affects homozygous individuals within a highly inbred livestock population
(B) The onset of lethality occurs after the animal has reached its peak reproductive age
(C) The allele mutates back to a normal state during the process of germline gametogenesis
(D) Dominant lethals are protected by epistatic interactions with other loci in the genome

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2023

24. Which of the following is the most appropriate description of how multiple alleles arise at a specific genetic locus in an animal population?
(A) Through the fusion of two completely non-homologous chromosomes during the meiotic cycle

(B) Through the physical exchange of genetic material between two entirely different species
(C) Through sequential, distinct mutations of a single wild-type gene over a period of time
(D) Through the suppression of crossing over in heterochromatic regions of the chromosome

2005

25. Consider the following statements regarding allelic interactions:
I. Codominant alleles both produce functional products.
II. Incomplete dominance results from haploinsufficiency of the functional allele.
III. Overdominance always reduces the overall fitness of the population.
IV. Lethal genes can be either dominant or recessive in their lethal effect.
Which of the above statements are correct?
(A) I, II and IV
(B) II, III and IV
(C) I, III and IV
(D) I and II

2003

26. Based on principles of multiple allelism, if a genetic locus in a cattle population has 4 distinct alleles, how many different diploid genotypes are possible in that population?
(A) 4
(B) 6
(C) 10
(D) 16

2004

27. Which definition accurately characterizes epistasis in animal genetics?
(A) The specific interaction between two distinct alleles located at the same genetic locus
(B) The masking of the phenotypic expression of one gene by a gene at a different locus
(C) The physical linkage of two distinct genes located on the same homologous chromosome
(D) The additive effect of multiple minor genes acting on a single continuous trait value

2015

28. In poultry, the inheritance of comb shape involves two independently assorting loci. The F2 cross of walnut comb chickens yields a 9 Walnut : 3 Rose : 3 Pea : 1 Single ratio. This is an example of what type of interaction?
(A) Dominant epistasis resulting in the suppression of one locus by the other dominant gene
(B) Novel phenotypes due to non-epistatic non-allelic gene interaction between two loci
(C) Recessive epistasis where the homozygous recessive state at one locus masks the other
(D) Duplicate recessive epistasis requiring two recessive pairs for the same phenotype

2005

29. A researcher identifies an F2 phenotypic ratio of 9:7 in an animal model. What type of epistasis is being demonstrated?
(A) Duplicate recessive epistasis (Complementary gene action)
(B) Duplicate dominant epistasis within a single genetic system
(C) Dominant epistasis observed in standard Mendelian dihybrids
(D) Recessive epistasis observed in standard Mendelian dihybrids

2017

30. Which condition best excludes the presence of duplicate dominant epistasis in a genetic cross?
(A) The presence of a 15:1 phenotypic ratio in the F2 generation of a dihybrid cross
(B) Either dominant allele from two different loci produces the same phenotypic effect
(C) The presence of a 9:3:4 phenotypic ratio in the resulting F2 generation of the cross
(D) Two distinct gene pairs interact to control a single qualitative trait in a population

2006

31. Identify the correct statement regarding recessive epistasis.
(A) A dominant allele at one locus masks the expression of alleles at a second locus in the cell
(B) The expected F2 phenotypic ratio from a dihybrid cross is 12:3:1 in standard populations
(C) Both loci must be homozygous recessive to produce the masking effect on the final phenotype
(D) Homozygosity for a recessive allele at one locus masks the expression of a second locus

2006

32. In mice, coat color is regulated by an agouti locus and an epistatic albino locus. The albino locus exhibits recessive epistasis. What phenotypic ratio is observed in the F2 progeny of a dihybrid cross?
(A) 9:3:3:1

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(B) 13:3
(C) 9:3:4
(D) 9:7

2002

33. All of the following represent modified dihybrid epistatic F2 ratios EXCEPT:
(A) 12:3:1
(B) 1:2:1
(C) 9:7
(D) 15:1

2011

34. Which pair of epistasis type and its characteristic F2 ratio is INCORRECTLY matched?
(A) Dominant epistasis - 12:3:1
(B) Duplicate recessive epistasis - 9:7
(C) Dominant and recessive epistasis - 13:3
(D) Recessive epistasis - 15:1

2014

35. Consider the following statements about non-allelic interactions:
I. Epistasis alters the standard Mendelian 9:3:3:1 genotypic ratio.
II. In dominant epistasis, a single copy of the epistatic allele is sufficient for masking.
III. The 13:3 ratio occurs when a dominant allele at one locus and a recessive allele at another produce the same phenotype.
IV. Polymeric gene interaction typically yields a 9:6:1 ratio.
V. Complementary genes require at least one dominant allele at each of two loci to express a specific phenotype.
Which of the above statements are INCORRECT?
(A) I and III
(B) II, IV and V
(C) I and IV
(D) III, IV and V

2018

36. An F2 generation ratio of 15:1 is observed in a livestock trait. What inference can be made about the underlying gene interaction?
(A) The trait requires homozygous recessive alleles at both loci to manifest the phenotype
(B) One gene locus inhibits the expression of another completely independent genetic locus
(C) Dominant alleles at either of two independent loci result in the same phenotype
(D) The trait is determined by a single locus with multiple alleles in the population

2022

37. Which term is most appropriate for describing the genetic interaction where a dominant allele at one locus completely suppresses the phenotypic expression of alleles at another locus, resulting in a 12:3:1 ratio?
(A) Dominant epistasis
(B) Recessive epistasis
(C) Duplicate dominant epistasis
(D) Duplicate recessive epistasis

2012

38. How does complementary gene action biologically manifest at the molecular level?
(A) One gene produces an inhibitor that prevents the transcription of a separate gene in the nucleus
(B) A structural protein forms an aggregate only if the other gene is mutated within the same cell
(C) Two identical enzymes are produced by two unlinked loci to catalyze the same specific reaction
(D) Two enzymes from separate genes act sequentially in a pathway to produce a final product

2012

39. Which genetic interaction is structurally based on both dominant and recessive epistatic mechanisms acting on the same trait, leading to a 13:3 phenotypic segregation?
(A) Polymeric gene action
(B) Inhibitory gene action
(C) Supplementary gene action
(D) Additive gene action

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2023

40. What is the fundamental unit of chromatin packaging that consists of DNA wound around a histone octamer?
(A) Solenoid
(B) Centromere
(C) Nucleosome
(D) Telomere

2005

41. What is the primary composition of the core histone octamer in eukaryotic nucleosomes?
(A) Two molecules each of H1, H2A, H2B, and H3
(B) Four molecules each of H3 and H4
(C) One molecule each of H1, H2A, H2B, H3, H4, H5, H6, and H7
(D) Two molecules each of H2A, H2B, H3, and H4

2019

42. Identify the correct statement regarding euchromatin and heterochromatin.
(A) Constitutive heterochromatin remains condensed throughout the entire cell cycle
(B) Euchromatin is highly condensed during the interphase stage of the cell cycle
(C) Heterochromatin is generally gene-rich and remains transcriptionally active
(D) Facultative heterochromatin cannot transition into euchromatin in any cell type

2002

43. Which of the following conditions is an exception to the rule that heterochromatin is transcriptionally inert?
(A) Barr body formation in female mammals to achieve X-chromosome dosage compensation
(B) Expression of genes for centromere function and RNAs for heterochromatin stability
(C) Transposable elements embedded deep within centromeric regions of the chromosome
(D) Methylation of CpG islands in the promoters of various essential housekeeping genes

2009

44. A cytogeneticist observes a standard karyotype of a major farm animal with a diploid chromosome number of $2n = 60$, consisting of 29 pairs of acrocentric autosomes and submetacentric sex chromosomes. What animal is being examined?
(A) Sheep (Ovis aries)
(B) Cattle (Bos taurus)
(C) Horse (Equus caballus)
(D) Pig (Sus scrofa)

2023

45. Read the following Assertion (A) and Reason (R) and select the correct option.
Assertion (A): The linker histone H1 is not part of the core nucleosome octamer.
Reason (R): Histone H1 binds to the entry and exit sites of DNA on the nucleosome, facilitating higher-order chromatin folding.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2001

46. Which pair correctly matches the farm animal with its normal diploid chromosome number ($2n$)?
(A) Goat - 54
(B) Sheep - 60
(C) Pig - 38
(D) Dog - 64

2017

47. Based on the higher-order structure of chromosomes, what causes the 10-nm "beads-on-a-string" fiber to coil into the 30-nm solenoid structure?
(A) The removal of all histone proteins from the DNA backbone by proteolytic enzymes
(B) The enzymatic activity of DNA polymerase during the S phase of the mitotic cycle
(C) The binding of non-histone scaffold proteins to the chromatin fiber exclusively
(D) Interactions mediated by H1 histone and the N-terminal tails of core histones

2005

48. Identify the INCORRECT statement regarding the ultrastructure of a metaphase chromosome.
(A) It contains two identical sister chromatids
(B) The centromere represents the primary constriction
(C) The kinetochore assembles directly on the telomeric regions
(D) Scaffold proteins like topoisomerase II are integral to maintaining its shape

2002

49. What is the most relevant physiological advantage of organizing DNA into euchromatin and heterochromatin domains?
(A) It prevents the occurrence of crossing over during the meiotic stages of division
(B) It provides a mechanism for regulation of gene expression and genome stability
(C) It eliminates the requirement for DNA replication enzymes during the cell cycle
(D) It increases the total amount of DNA a cell can synthesize during the S phase

2015

50. If a chromosome exhibits a centromere located precisely at the midpoint, creating two arms of equal length, how is it classified?
(A) Acrocentric
(B) Telocentric
(C) Submetacentric
(D) Metacentric

2023

51. Which factor contributes most to the dark staining of heterochromatin with standard DNA dyes like DAPI or Giemsa?
(A) High degree of structural compaction and

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DNA concentration
(B) High density of actively transcribing RNA polymerases
(C) Exclusively composed of RNA sequences
(D) Complete absence of histone proteins

2013

52. What inference can be made about a region of an animal's genome that exhibits a high frequency of histone acetylation?
(A) The region is likely organized as constitutive heterochromatin in the cell
(B) The region contains tightly packed, inactive nucleosomes in the nucleus
(C) The region corresponds to euchromatin and is transcriptionally permissive
(D) The region is preparing for immediate apoptosis through DNA fragmentation

2002

53. Which mechanism primarily governs sex determination in mammalian farm animals such as cattle and sheep?
(A) Presence of a dominant Y chromosome carrying the SRY gene
(B) Environmental temperature during the embryonic development stages
(C) The ratio of X chromosomes to full sets of autosomes in the cell
(D) Haplo-diploidy involving unfertilized and fertilized egg cells

2007

54. According to Lyon's hypothesis, what is the primary purpose of X-chromosome inactivation in mammalian females?
(A) To initiate the formation of primary oocytes in the developing female fetus
(B) To promote recombination between the X and Y chromosomes during meiosis
(C) To suppress the manifestation of dominant mutations in the female phenotype
(D) To ensure dosage compensation of X-linked genes between females and males

2017

55. Match the following sex determination systems with the corresponding animal taxa.
List I: (Sex Determination System)
P. XX/XY system
Q. ZZ/ZW system
R. Haplodiploidy
S. Temperature-dependent
List II: (Animal Taxa)
1. Honeybees
2. Crocodiles
3. Bovines
4. Poultry
(A) P-3, Q-4, R-1, S-2
(B) P-3, Q-2, R-1, S-4
(C) P-4, Q-3, R-2, S-1
(D) P-2, Q-4, R-3, S-1

2017

56. Which of the following best describes "sex chromatin" (Barr body)?
(A) An inactivated, condensed Y chromosome found exclusively in the male phenotype
(B) An active X chromosome found in the somatic cells of the male animal species
(C) An inactivated, condensed X chromosome in female somatic cells of mammals
(D) The pseudoautosomal region of the sex chromosomes found in both animal sexes

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2011

57. Identify the correct statement regarding the Sex-determining Region Y (SRY) gene.
(A) It is highly conserved on the X chromosome across all major mammalian species
(B) It acts primarily by suppressing the production of testosterone in the animal
(C) It requires two functional copies for proper phenotypic expression in males
(D) It encodes a transcription factor initiating male sex differentiation

2019

58. All of the following statements about dosage compensation in mammals are true EXCEPT:
(A) In marsupials, X-inactivation randomly targets either the maternal or paternal X
(B) Inactivation of either X chromosome is random in placental mammalian species
(C) Once an X is inactivated, all its clonal descendants will have the same X inactive
(D) It occurs during the early stages of embryonic development in the mammal host

2023

59. What is the phenotypic consequence of random X-chromosome inactivation in a female cat heterozygous for an X-linked coat color gene?
(A) A uniform, blended coat color
(B) A mosaic or tortoiseshell coat pattern
(C) Complete absence of pigmentation
(D) A uniform color corresponding to the dominant allele

2007

60. How does the ZZ/ZW system of sex determination in birds genetically differ from the XX/XY system in mammals?
(A) In birds, the male is the heterogametic sex (ZW) instead of the mammalian male
(B) In birds, the female is the heterogametic sex (ZW) and the male is homogametic
(C) The W chromosome is substantially larger and more gene-rich than the Z chromosome
(D) Birds rely solely on environmental factors for the process of sex determination

2017

61. Which pair accurately matches the chromosomal complement with its corresponding sex phenotype under standard mammalian mechanisms?
(A) XXY - Sterile male (Klinefelter-like syndrome)
(B) XXY - Normal female
(C) XO - Normal male
(D) XXX - Sterile male

2006

62. Which of the following components is primarily responsible for initiating X-chromosome inactivation from the X-inactivation center (Xic)?
(A) SRY protein
(B) DNA polymerase gamma
(C) XIST long non-coding RNA
(D) Caspase 9

2012

63. A cytologist examines squamous epithelial cells from the buccal mucosa of a normal stallion (male horse). How many Barr bodies should be visible in each cell nucleus?
(A) One
(B) Two
(C) Three
(D) Zero

2017

64. What happens to the pseudoautosomal regions (PARs) during X-chromosome inactivation in female mammals?
(A) They are heavily methylated and permanently silenced during the embryonic phase
(B) They detach from the X chromosome and move into the nucleolus of the cell nucleus
(C) They escape inactivation to ensure dosage of genes shared with the Y chromosome
(D) They are specifically targeted by XIST RNA to initiate the condensation process

2017

65. Arrange the following key molecular events in the establishment of X-chromosome inactivation in a female mammalian embryo in the correct sequence:
I. Coating of the chromosome by XIST RNA
II. Upregulation of XIST expression on the future inactive X
III. Chromatin modifications (e.g., DNA methylation, histone deacetylation)
IV. Condensation into a Barr body
(A) I, II, III, IV
(B) II, I, III, IV
(C) III, I, IV, II
(D) II, III, I, IV

2003

66. Which definition accurately distinguishes a sex-influenced trait from a sex-limited trait in livestock?
(A) Sex-influenced traits are on sex chromosomes; sex-limited traits are on autosomes
(B) Sex-influenced traits only appear in males; sex-limited traits only in females
(C) Sex-influenced traits are affected by environment; sex-limited traits are not
(D) Dominance in sex-influenced traits varies by sex; sex-limited traits are mono-sex

2007

67. The presence of horns in some sheep breeds (e.g., Dorset) is governed by an allele that behaves as dominant in males and recessive in females. What type of inheritance does this represent?
(A) Sex-influenced
(B) Sex-linked recessive
(C) Sex-linked dominant
(D) Sex-limited

2004

68. Identify the correct statement regarding sex-limited traits in farm animals.
(A) Genes for sex-limited traits are exclusively located on the Y chromosome
(B) Sex-limited traits exhibit varying degrees of dominance between males and females
(C) Milk yield in dairy cattle is a classic example of a sex-limited trait
(D) Only the heterogametic sex can carry the alleles for sex-limited traits

2010

69. Which condition serves as an exception to the rule that sons inherit their X-linked traits solely from their mothers in mammals?
(A) A son possessing an XXY karyotype due to

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non-disjunction in the paternal parent
(B) A son inheriting an X-linked recessive lethal mutation from the maternal parent
(C) A son expressing a sex-influenced trait derived from a specific autosomal locus
(D) A son displaying an X-linked dominant trait inherited from the maternal parent

2025

70. If a sex-linked recessive lethal gene arises in a poultry flock (ZZ/ZW system), which sex will disproportionately suffer from the lethal effect first?
(A) Males (ZZ), because they are homogametic
(B) Both sexes equally, as the gene is recessive
(C) Neither sex, because recessive lethals are rapidly eliminated
(D) Females (ZW), because they possess only one Z chromosome

2021

71. A breeder observes that a specific feather pattern in chickens is visible only in males, regardless of the genotype, but females with the same genotype never show the trait. This is caused by:
(A) Sex-influenced inheritance
(B) Sex-limited inheritance
(C) Sex-linked recessive inheritance
(D) Y-linked inheritance

2006

72. Which pair of trait and inheritance pattern in livestock is INCORRECT?
(A) Milk production in cattle - Sex-limited
(B) Egg production in poultry - Sex-limited
(C) Horns in sheep - Sex-linked dominant
(D) Haemophilia A in dogs - Sex-linked recessive

2002

73. What is the fundamental basis that typically underlies the differential phenotypic expression of sex-influenced traits?
(A) Variations in growth hormone levels within the circulating blood of the animal
(B) The presence or absence of XIST RNA within the nuclei of the somatic cell line
(C) Deficiencies in insulin production within the pancreatic tissues of the animal
(D) Different circulating levels of androgens and estrogens between the two sexes

2012

74. In a flock of sheep, a breeder crosses a heterozygous horned male with a heterozygous hornless female (assuming the horn trait is sex-influenced, allele H for horns, h for hornless). What fraction of the female progeny will be horned?
(A) 25%
(B) 0%
(C) 50%
(D) 75%

NODIA

2024

75. Arrange the following steps sequentially for validating whether a newly observed trait in a mammalian herd is sex-linked recessive:
I. Perform a reciprocal cross between affected and unaffected lines.
II. Identify the trait predominantly in males within the pedigree.
III. Observe criss-cross inheritance (affected males producing carrier daughters).
IV. Confirm the absence of male-to-male transmission.
Which of the following is the logically correct order of validation?
(A) II, IV, III, I
(B) I, II, III, IV
(C) II, I, IV, III
(D) III, II, I, IV

2004

76. Which characteristic strongly implies that a gene is located on the non-homologous portion of the Y chromosome (holandric inheritance)?
(A) The trait skips generations
(B) The trait is passed from an affected father to all of his sons
(C) Affected mothers pass the trait to all their sons
(D) The trait is expressed only in females

2005

77. A rare condition in horses is found to be X-linked dominant. If an affected stallion is crossed with a normal mare, what will be the phenotypic outcome in the offspring?
(A) All colts will be normal, but all fillies will be affected
(B) All colts (males) and fillies (females) will be affected
(C) All colts will be affected, but all fillies will be normal
(D) Half the colts and half the fillies will be affected

2014

78. What conclusion can be drawn if a quantitative trait locus (QTL) mapped for meat quality is found on an autosome but demonstrates a

significantly higher penetrance in boars than in sows?
(A) The trait is X-linked
(B) The trait is exclusively mitochondrial
(C) The trait exhibits sex-influenced penetrance
(D) The trait is definitively sex-limited

2001

79. Genetic linkage violates which Mendelian principles?
(A) Law of Segregation
(B) Law of Dominance
(C) Concept of Unit Characters
(D) Law of Independent Assortment

2001

80. Match the following terms associated with linkage to their correct definitions.
List I: (Linkage Term)
P. Cis (Coupling) phase
Q. Trans (Repulsion) phase
R. Linkage group
S. Map unit (Centimorgan)
List II: (Definition)
1. One dominant and one recessive allele on each homologous chromosome
2. All genes residing on a single chromosome
3. Distance equivalent to a 1% recombination frequency
4. Both dominant alleles on one chromosome and both recessive alleles on the homologous chromosome
(A) P-1, Q-4, R-2, S-3
(B) P-4, Q-1, R-2, S-3
(C) P-4, Q-1, R-3, S-2
(D) P-2, Q-1, R-4, S-3

2009

81. In a two-point test cross involving two linked genes, what determines the frequency of recombinant offspring?
(A) The specific ploidy level of the animal organism used in the genetic experiment
(B) The physical distance between the two loci located on the homologous chromosome
(C) The degree of dominance of the wild-type alleles at the loci under investigation
(D) The physical size of the sex chromosomes compared to the autosomes of the cell

2001

82. Identify the correct statement regarding linkage groups in an animal.
(A) The number of linkage groups equals the total diploid number of the chromosomes
(B) Linkage groups are only present in female animals due to X-inactivation events
(C) Linkage groups refer to genes that assort independently during the meiotic cycle
(D) Linkage groups strictly correspond to the haploid number of the chromosomes

2013

83. All of the following are requirements for accurately conducting a three-point test cross EXCEPT:
(A) The other parent must be homozygous dominant for all three loci
(B) The heterozygous parent must be heterozygous at all three loci
(C) A sufficient number of offspring must be produced to detect rare double crossover events
(D) The alleles must have clear, distinguishable phenotypes

2003

84. In mapping genetic distance, what specific crossover event is usually underestimated when the distance between two genes is large (e.g., > 20 cM)?
(A) Single crossovers occurring within the distance between the two genetic markers
(B) Sister chromatid exchanges occurring during the early stages of meiotic division
(C) Double crossovers occurring between the two genes located on the same chromosome
(D) Non-disjunction events occurring during the first or second anaphase of meiosis

2011

85. If a test cross yields 80% parental phenotypes and 20% recombinant phenotypes, what is the map distance between the two linked genes?
(A) 20 Centimorgans
(B) 80 Centimorgans
(C) 40 Centimorgans
(D) 10 Centimorgans

NODIA

2001

86. Which phase is represented if an individual with genotype AaBb inherited the 'A' and 'b' alleles from the sire and the 'a' and 'B' alleles from the dam?
(A) Coupling phase
(B) Independent assortment phase
(C) Synteny phase
(D) Repulsion phase

2003

87. What is the fundamental outcome when two linked genes are extremely close to one another on a chromosome (i.e., complete linkage)?
(A) Only recombinant gametes are formed
(B) Only parental gametes are formed
(C) The recombination frequency reaches exactly 50%
(D) Crossing over occurs between them at every meiosis

2003

88. A researcher identifies three linked genes A, B, and C. The recombination frequency between A-B is 5%, between B-C is 15%, and between A-C is 10%. What is the most likely gene order?
(A) A - B - C
(B) B - C - A
(C) B - A - C
(D) The order cannot be determined

2005

89. Which pair correctly matches the mapping parameter with its maximum theoretical limit?
(A) Recombination frequency - 100%
(B) Map units on a single chromosome - 50 cM
(C) Interference - 2.0
(D) Recombination frequency - 50%

2010

90. Read the following Assertion (A) and Reason (R) and select the correct option.
Assertion (A): The genetic map distance and the physical DNA base-pair distance along a chromosome are not strictly proportional across all regions.
Reason (R): Recombination hotspots and coldspots (like centromeres) exist, causing variation in crossover frequencies per physical length of DNA.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2024

91. What causes the discrepancy between expected double crossovers and observed double crossovers in a three-point cross?
(A) Codominance
(B) Chiasma interference
(C) Epistasis
(D) Transposable elements

2017

92. Which cellular process directly constitutes the molecular basis of crossing over during meiosis?
(A) The phosphorylation of histone H3 within the chromatin of the animal cell nucleus
(B) Formation of the synaptonemal complex and subsequent homologous recombination
(C) The degradation of cohesin proteins at the centromere during the Anaphase I stage
(D) Random spindle fiber attachment during the metaphase stage of the meiotic cycle

2010

93. How is the coefficient of coincidence (CC) mathematically derived from a three-point genetic map?
(A) Observed double crossovers divided by the Expected double crossover frequency
(B) Expected double crossovers divided by the Observed double crossover frequency
(C) 1 minus the total Interference value calculated from the three-point cross data
(D) The sum of single crossovers minus the double crossovers within the gene region

2016

94. Identify the INCORRECT statement regarding chiasmata and crossing over.
(A) Chiasmata are the visible cytological manifestations of the crossing over event
(B) Crossing over occurs at the four-strand (tetrad) stage during the meiotic cycle
(C) Crossing over occurs between sister chromatids to generate genetic diversity
(D) Creighton and McClintock provided early cytological proof of the crossover event

2023

95. Read the following Assertion (A) and Reason (R) and select the correct option.
Assertion (A): If the coefficient of coincidence is 1, chiasma interference is completely absent.
Reason (R): Interference is calculated as 1 minus the Coefficient of Coincidence.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2016

96. In a genetic mapping experiment, if interference is measured as 1.0 (or 100%), what is the physiological implication?
(A) Double crossovers occur at a rate equal to

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the expectation of the genetic model
(B) Double crossovers occur more frequently than expected by the calculated product
(C) One crossover inhibits a second crossover in the adjacent chromosomal region
(D) Single crossovers do not occur in any region of the chromosome during the process

2016

97. Which classic experiment provided the definitive cytological proof that genetic recombination is accompanied by a physical exchange of chromosomal segments?
(A) Avery, MacLeod, and McCarty's transformation experiment using bacterial models
(B) Creighton and McClintock's study using morphologically distinct chromosomes
(C) Meselson and Stahl's replication experiment using heavy and light nitrogen isotopes
(D) Hershey and Chase's bacteriophage experiment using radioactive phosphorus and sulfur

2015

98. What is the effect of crossing over occurring outside the region between two genetic markers being mapped?
(A) It increases the calculated recombination frequency between the two gene markers
(B) It decreases the calculated recombination frequency between the two gene markers
(C) It has no effect on the observed recombination frequency between the markers
(D) It reverses the linkage phase from cis to trans within the parental generations

2018

99. Which of the following best explains why the maximum observable recombination frequency between two loci is 50%?
(A) Multiple crossovers randomize alleles, mimicking independent assortment outcomes
(B) The synaptonemal complex restricts crossing over to only 50% of the tetrad strands
(C) Homologous chromosomes only pair during 50% of the meiotic divisions in the cell
(D) DNA ligase fails to repair more than half of the double-strand breaks in the DNA

2011

100. Consider the following statements about crossing over:
I. It takes place during the pachytene stage of prophase I.
II. It involves the exchange of segments between non-sister chromatids of homologous chromosomes.
III. It results in the creation of new alleles not previously existing in the population.
Which of the above statements are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I, II and III

2019

101. Which pair accurately reflects a linkage concept and its mathematical representation?
(A) Expected DCOF requency = Product of individual single crosso verfrequencies
(B) Interference (I) = Coefficient of Coincidence measured in the three-point cross
(C) Map Distance $= \frac{\text{Number of Parentals}}{\text{Total Progeny}} \times 100$ in the test cross data
(D) Coefficient of Coincidence $= 1 + I$ according to the standard genetic formulas

2006

2012

102. If a geneticist observes negative interference ($I < 0$) during mapping, what biological phenomenon is occurring?
(A) A crossover in one region suppresses crossovers in adjacent regions of the cell
(B) Sister chromatid exchanges are mistaken for non-sister crossovers in the data
(C) The chromosomes have undergone a paracentric inversion in the germline tissues
(D) A crossover in one region increases crossover likelihood in adjacent regions

2023

103. What is the fundamental requirement for using crossing over frequency to accurately construct a linear genetic map?
(A) The genes must be epistatic to each other within the metabolic pathway of the cell
(B) Crossover probability is generally uniform across the length of the chromosome
(C) The organism must be highly inbred to ensure homozygosity at all the other loci
(D) The traits must exhibit polygenic inheritance involving multiple additive alleles

2014

104. Which structural complex physically mediates the close pairing and subsequent crossing over between homologous chromosomes?

NODIA

(A) Spliceosome
(B) Kinetochore
(C) Synaptonemal complex
(D) Centrosome

2012

105. Match the following mutagens with their specific mechanisms of action.
List I: (Mutagen)
P. Ultraviolet (UV) light
Q. 5-Bromouracil
R. Nitrous acid
S. Ethidium bromide
List II: (Mechanism of Action)
1. Base analog that induces transition mutations
2. Intercalating agent causing frameshift mutations
3. Deaminates cytosine, adenine, and guanine
4. Induces pyrimidine (thymine) dimers
(A) P-4, Q-1, R-3, S-2
(B) P-4, Q-2, R-3, S-1
(C) P-3, Q-1, R-4, S-2
(D) P-1, Q-4, R-2, S-3

2009

106. Which of the following defines a physical mutagen frequently used for artificial transmutation of genes in agricultural research?
(A) Gamma rays
(B) Ethyl methanesulfonate (EMS)
(C) Sodium azide
(D) Acridine orange

2016

107. Identify the correct statement regarding chemical mutagens.
(A) Alkylating agents predominantly cause frameshift mutations by inserting into DNA
(B) Base analogs are incorporated into DNA during replication and cause mispairing
(C) Intercalating agents specifically cause the formation of thymine dimers in DNA
(D) Nitrous acid primarily acts by breaking the phosphodiester backbone of the DNA

2002

108. All of the following are consequences of ionizing radiation (such as X-rays) acting as a mutagen EXCEPT:
(A) Generation of reactive oxygen species (ROS)
(B) Double-strand DNA breaks
(C) Chromosomal translocations and deletions
(D) Formation of cyclobutane pyrimidine dimers

2021

109. What is the primary genetic consequence of an intercalating agent slipping between stacked base pairs of the DNA double helix?
(A) Frameshift mutations via the addition or deletion of a single base pair in DNA
(B) Nonsense mutations due to premature stop codons appearing in the coding sequence
(C) Transition mutations from A-T to G-C base pairs within the chromosomal sequence
(D) Extensive chromosomal aneuploidy resulting from errors in the meiotic divisions

2002

110. Which condition makes artificial transmutation of genes highly unpredictable in animal breeding programs?
(A) Mutagens typically target only redundant, non-coding DNA sequences in the cell
(B) Physical mutagens exclusively cause dominant lethal mutations in all animals
(C) Mutations are random events occurring throughout the entire chromosomal genome
(D) The induced mutation rate is lower than the spontaneous rate in animal models

2002

111. Which pair accurately matches a chemical mutagen category with an example?
(A) Intercalating agent - 2-Aminopurine
(B) Base analog - Proflavine
(C) Deaminating agent - Mustard gas
(D) Alkylating agent - Ethyl methanesulfonate (EMS)

2014

112. Why is UV radiation generally considered non-ionizing despite being a physical mutagen?
(A) It has sufficient energy to break phosphodiester bonds within the DNA backbone
(B) It creates ions directly in the cellular fluid surrounding the nuclear envelope
(C) It lacks energy to eject electrons but excites them to cause covalent bonds
(D) It solely affects the RNA polymerase enzyme rather than the DNA template itself

2022

113. What molecular mechanism allows 5-Bromouracil to induce genetic mutations?
(A) It specifically cleaves the DNA backbone at pyrimidine sites in the animal cell
(B) It replaces thymine during DNA replication and mispairs with guanine in the enol
(C) It prevents the unwinding of DNA helicase

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during the synthesis phase of division
(D) It methylates the promoter regions of various tumor suppressor genes in the cell

2015

114. Which statement INCORRECTLY evaluates the utility of induced mutations in livestock improvement compared to crop improvement?
(A) Induced mutations are less used in livestock due to ethical and welfare constraints
(B) The generation interval in livestock is longer, slowing the screening of mutants
(C) The cost of maintaining mutant animals for screening is prohibitively high today
(D) Induced mutations in livestock are the primary source of modern genetic gains

2019

115. Consider the following statements on mutation types:
I. A transition mutation substitutes a purine for a purine.
II. A transversion mutation substitutes a purine for a pyrimidine.
III. Frameshift mutations only occur when multiples of three bases are inserted.
IV. Missense mutations result in a different amino acid sequence.
Which of the above statements are correct?
(A) I, II and IV
(B) I, II and III
(C) II, III and IV
(D) I and IV

2002

116. How does the artificial transmutation of genes primarily benefit fundamental genetic research?
(A) By immediately creating superior livestock breeds for use in commercial farming
(B) By increasing the hybrid vigor of outbred populations in a controlled environment
(C) By using reverse genetics to determine gene function via knockout phenotypes
(D) By definitively curing monogenic recessive disorders within a single generation

2017

117. Which term describes a mutation where a normal codon is altered to become a premature termination signal?
(A) Nonsense mutation
(B) Missense mutation
(C) Silent mutation
(D) Suppressor mutation

2016

118. What defines the term "penetrance" in population genetics?
(A) The degree or intensity to which a genotype is expressed phenotypically in a cell
(B) The interaction of multiple genes affecting a single quantitative trait in animals
(C) A single gene affecting multiple, seemingly unrelated phenotypic traits in a herd
(D) The proportion of individuals with a genotype exhibiting the expected phenotype

2006

119. If 100 dairy cows possess the genotype for a specific dominant trait, but only 85 of them express the phenotype, what is the penetrance of this trait?
(A) 15%
(B) 85%
(C) 50%
(D) 100%

2025

120. Identify the correct statement distinguishing penetrance from expressivity.
(A) Expressivity measures the percentage of individuals expressing a specific trait
(B) Penetrance only applies to recessive traits, while expressivity is for dominants
(C) Penetrance is all-or-none, whereas expressivity measures the phenotypic severity
(D) Penetrance and expressivity are identical concepts caused by environmental factors

NODIA

2006

121. All of the following are classic examples of pleiotropy EXCEPT:
(A) The Creeper mutation in chickens causing both short legs in heterozygotes and embryonic lethality in homozygotes
(B) The Merle gene in dogs causing a specific coat pattern as well as deafness and eye abnormalities in homozygotes
(C) The Frizzle gene in poultry affecting feather shape, body temperature regulation, and heart rate
(D) Multiple alleles determining the ABO blood groups

2001

122. How do modifier genes primarily function in a genetic system?
(A) They suppress or enhance the phenotypic expression of a gene at a separate locus
(B) They act as the primary locus dictating the

core phenotype of the animal species
(C) They cause gross chromosomal rearrangements within the genome of the population
(D) They physically mutate the DNA sequence of linked genes during meiotic division

2005

123. A breeder notices that a herd of cattle carrying the same dominant allele for a spotting pattern shows widely varying amounts of white spots. This variation is an example of:
(A) Incomplete penetrance
(B) Variable expressivity
(C) Complete penetrance
(D) Codominance

2016

124. Which pair correctly matches the genetic concept with its definition?
(A) Pleiotropy - Multiple genes controlling a single qualitative trait in a population
(B) Incomplete penetrance - A genotype failing to produce the expected phenotype
(C) Polygenic inheritance - A single gene affecting multiple distinct phenotypic traits
(D) Expressivity - The masking of one gene by another non-allelic gene in the nucleus

2014

125. Consider the following factors that can influence the penetrance and expressivity of a genotype:
I. Environmental conditions (e.g., temperature)
II. The age of the organism
III. The genetic background (presence of modifier genes)
IV. The ploidy level of the species
Which of the above factors typically modulate expression?
(A) I and II
(B) I, II and III
(C) II, III and IV
(D) I, II, III and IV

2011

126. What inference can be made if a monogenic disease exhibits 100% penetrance but variable expressivity in a sheep flock?
(A) Every animal with the mutant genotype is unaffected by the phenotypic condition
(B) Only a fraction of the animals with the mutant genotype show the disease symptoms
(C) Every animal shows the disease, but symptoms range from mild to severe levels
(D) The disease is definitively caused by polygenic inheritance across several loci

2018

127. Which condition serves as an evolutionary advantage of pleiotropy in an organism?
(A) It strictly isolates metabolic pathways from one another in the animal's cells
(B) It guarantees that all mutations are beneficial within the breeding population
(C) It prevents genetic linkage between chromosomes during the meiotic cell stages
(D) It allows a regulatory change to coordinately alter multiple processes in a cell

2009

128. What is the molecular basis often responsible for pleiotropic effects?
(A) Multiple genes are accidentally transcribed into a single mRNA molecule in a cell
(B) Ribosomes translate introns into functional proteins in the cytoplasm of the cell
(C) A single gene encodes a protein that functions in diverse biochemical pathways
(D) Chromosomes completely fail to disjoin during the second anaphase stage of meiosis

2013

129. Which genetic phenomenon is most likely responsible for masking the phenotypic expression of a completely penetrant dominant gene, assuming no environmental variation?
(A) Codominance
(B) Modifier genes acting epistatically
(C) Multiple allelism
(D) Sister chromatid exchange

2008

130. A mutation in the gene encoding the structural protein fibrillin leads to defects in the skeletal, cardiovascular, and ocular systems. This best exemplifies:
(A) Polygenic inheritance
(B) Overdominance
(C) Epigenetics
(D) Pleiotropy

2012

131. Which defining characteristic best separates polygenic (quantitative) traits from qualitative Mendelian traits in livestock?
(A) Polygenic traits exhibit continuous variation and have heavy environmental influence
(B) Polygenic traits exhibit discrete, distinctly recognizable phenotypic animal classes
(C) Polygenic traits are determined by a single major gene with multiple allelic states

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(D) Polygenic traits strictly follow a 3:1 inheritance ratio in a standard population

2025

132. The Multiple Factor Hypothesis, which explains quantitative inheritance, was originally proposed based on studies of grain color in wheat by which scientist?
(A) Gregor Mendel
(B) Thomas Hunt Morgan
(C) Herman Nilsson-Ehle
(D) Barbara McClintock

2018

133. Identify the correct statement concerning the additive gene action seen in polygenic inheritance.
(A) Each contributing allele adds a small, cumulative amount to the phenotypic value
(B) A single dominant allele masks all recessive alleles across all polygenic loci
(C) The total phenotypic variance is determined by environmental factors exclusively
(D) Dominance variance is the only component of genetic variance in polygenic traits

2005

134. All of the following livestock traits are considered classic examples of polygenic inheritance EXCEPT:
(A) Milk yield in Holstein cattle
(B) Body weight at weaning in pigs
(C) Fleece weight in Merino sheep
(D) The presence or absence of the BLAD disorder in cattle

2005

135. Consider the following statements about transgressive segregation:
I. It occurs when F2 offspring exhibit phenotypes extreme beyond either original parental line.
II. It is caused by the sudden appearance of novel, uninherited mutations in the F2 generation.
III. It results from the recombination of additive alleles that were dispersed between the two parents.
IV. It frequently occurs in the inheritance of complex, quantitative traits.
V. It proves that Mendelian segregation does not apply to polygenes.
Which of the above statements are INCORRECT?
(A) I and III
(B) II and V
(C) III and IV
(D) I, IV and V

2011

136. If a quantitative trait in poultry is controlled by 3 unlinked polygenic loci with additive alleles, what is the expected frequency of an offspring displaying the extreme phenotype (e.g., possessing all 6 contributing alleles) in an F2 cross between two heterozygous parents?
(A) $\left(\frac{1}{2}\right)^3$ or $\frac{1}{8}$
(B) $\frac{1}{16}$
(C) $\left(\frac{1}{4}\right)^3$ or $\frac{1}{64}$
(D) $\frac{1}{256}$

2013

137. Which mathematical distribution curve best describes the phenotypic variation of a highly polygenic trait within a large outbred herd?
(A) Bimodal distribution
(B) Poisson distribution
(C) Exponential distribution
(D) Normal (Gaussian) distribution

2023

138. What is the fundamental mechanism that leads to transgressive segregation in an F2 plant or animal population?
(A) Recombination of complementary sets of additive plus (+) and minus (-) alleles
(B) High rates of localized mutagenesis occurring during the process of gametogenesis
(C) Complete loss of environmental variance in the offspring of the parental cross
(D) Complete dominance at all contributing loci affecting the qualitative phenotype

2023

139. Which pair correctly matches a quantitative genetics parameter with its definition?
(A) Heritability (Broad-sense) - The ratio of additive variance to phenotypic variance
(B) Heritability (Narrow-sense) - The ratio of additive to phenotypic variance
(C) Environmental variance - The variance resulting from non-additive gene interactions
(D) Genotypic variance - The variance directly measured from observable animal traits

2007

140. Read the following Assertion (A) and Reason (R) and select the correct option.

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Assertion (A): The principles of independent assortment and segregation apply strictly to polygenes, just as they do to major genes.
Reason (R): The continuous variation observed in polygenic traits is a result of Mendelian segregation of multiple loci combined with environmental effects.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2006

141. How does environmental variance affect the phenotypic expression of a polygenic trait?
(A) It blurs genotypic classes, creating a smooth, continuous phenotypic distribution
(B) It permanently alters the DNA sequence of the polygenes in the animal's somatic cells
(C) It ensures that the trait follows a perfect Mendelian ratio in the F2 generation
(D) It restricts expression exclusively to the heterogametic sex in the population

2005

142. If a farmer wants to improve a polygenic trait like daily weight gain in swine, which genetic metric is most crucial for determining the potential success of a selective breeding program?
(A) Dominance variance
(B) Epistatic variance
(C) Narrow-sense heritability
(D) The number of chromosomes

2019

143. What is the expected outcome if two true-breeding parental lines (AABBCC and aabbcc) for a polygenic trait are crossed, and the F1 generation is raised in completely uniform environmental conditions?
(A) The F1 will show continuous, normal distribution spanning the parental phenotypes
(B) The F1 will be uniform and possess a phenotype intermediate between the parents
(C) The F1 will exhibit transgressive segregation beyond the parental phenotypic range
(D) The F1 will strictly match the dominant parental line AABBCC in the resulting cross

2005

144. Which definition accurately describes cytoplasmic inheritance?
(A) The transmission of genetic material located on the sex chromosomes of the species
(B) The inheritance of traits modified by cytoplasmic RNA stored in the sperm cells
(C) The transmission of traits governed by genetic material found in organelles
(D) The influence of maternal environment on the development of the fetus in utero

2008

145. Read the following Assertion (A) and Reason (R) and select the correct option.
Assertion (A): Mitochondrial DNA (mtDNA) is inherited almost exclusively from the maternal parent in most domestic animals.
Reason (R): Spermatozoa contribute negligible cytoplasm and their mitochondria are typically actively degraded in the zygote after fertilization.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2001

146. Identify the correct statement distinguishing a maternal effect from true cytoplasmic inheritance.
(A) Maternal effects are permanent genetic changes transmitted to subsequent generations
(B) Cytoplasmic inheritance is determined by the mother's environment and health
(C) Both terms refer to exactly the same genetic phenomenon within the animal cell
(D) Maternal effects arise from the mother's nuclear genotype, not her mitochondrial DNA

2009

147. All of the following are characteristic features of the mammalian mitochondrial genome EXCEPT:
(A) It contains multiple large introns and extensive non-coding regions
(B) It is typically a closed circular, double-stranded DNA molecule
(C) It exhibits a high mutation rate compared to nuclear DNA
(D) It strictly relies on nuclear genes for many of its structural proteins and polymerases

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2013

148. Why is mitochondrial DNA analysis widely used for tracing maternal lineages in livestock domestication studies?
(A) Because it undergoes frequent homologous recombination during the meiotic cycle
(B) Because it is paternally inherited and highly conserved in all animal breeds
(C) Because it lacks recombination and mutates at a predictable rate for tracing
(D) Because it is present in only a single copy per cell in the somatic tissues

2014

149. The classic example of shell coiling in the snail Limnaea peregra, where the direction of coiling is determined strictly by the mother's nuclear genotype, is an example of:
(A) Maternal effect
(B) Sex-linked inheritance
(C) Cytoplasmic inheritance
(D) Genomic imprinting

2013

150. Which genetic condition must be met for a trait governed by true cytoplasmic inheritance to be passed on?
(A) The sire must carry the dominant allele
(B) The trait must be present on the maternal X chromosome
(C) Both parents must contribute a recessive allele
(D) The trait must be present in the mitochondrial genome of the dam

2005

151. What phenotypic pattern is expected in a reciprocal cross involving a trait governed by true cytoplasmic inheritance?
(A) The F1 offspring will show identical phenotypes regardless of the cross direction
(B) The F1 offspring will exhibit the phenotype of the maternal parent in each cross
(C) Male offspring take the mother's phenotype, and females take the father's phenotype
(D) The F1 offspring will show a 3:1 segregation ratio in the resulting generations

2013

152. Which pair accurately reflects an organelle and a well-known example of a trait it controls via extranuclear inheritance?
(A) Ribosome - Antibiotic resistance in mammals
(B) Lysosome - Tay-Sachs disease
(C) Chloroplast - Leaf variegation in Mirabilis jalapa
(D) Golgi apparatus - Freemartinism

2001

153. What is the fundamental difference between homoplasmy and heteroplasmy in the context of mitochondrial genetics?
(A) Homoplasmy refers to identical nuclear genes; heteroplasmy to different nuclear genes
(B) Homoplasmy occurs in females; heteroplasmy occurs in males within the population
(C) Homoplasmy means the mtDNA is circular; heteroplasmy means it is linear in form
(D) Homoplasmy means identical mtDNA; heteroplasmy means a mixture of mutant and normal

2010

154. How does maternal lineage tracing via mtDNA assist in animal conservation genetics?
(A) It maps evolutionary matrilines and helps preserve endangered animal populations
(B) It identifies the best sires for increasing meat yield in commercial operations
(C) It determines the exact number of nuclear chromosomes in an extinct animal species
(D) It completely eradicates sex-linked genetic disorders in the breeding population

2008

155. Match the following terms regarding non-nuclear phenomena with their proper definitions.
List I: (Genetic Phenomenon)
P. Genomic Imprinting
Q. Maternal Effect
R. Maternal Inheritance
S. Heteroplasmy
List II: (Definition)
1. Transmission of traits exclusively via the mother's organellar DNA
2. Presence of more than one type of organellar genome within a cell
3. Phenotype determined by the mother's nuclear genotype prior to fertilization
4. Differential expression of an allele depending on its parent of origin
(A) P-4, Q-3, R-1, S-2
(B) P-3, Q-4, R-2, S-1
(C) P-4, Q-1, R-3, S-2
(D) P-1, Q-3, R-4, S-2

2021

156. If a heteroplasmic dairy cow possessing a mixture of normal and deleterious mitochondrial genomes

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produces calves, what determines the severity of the mitochondrial disease in her offspring?
(A) The random segregation and ratio of mutant mitochondria passed into each oocyte
(B) The specific allele inherited from the bull during the process of fertilization
(C) Complete recombination between mutant and normal mtDNA in the germline tissues
(D) The presence of a dominant modifier gene on the Y chromosome of the sire used

2007

157. Which structural chromosomal aberration involves the loss of a chromosomal segment and is generally lethal in a homozygous state?
(A) Deletion
(B) Duplication
(C) Inversion
(D) Translocation

2004

158. The 1/29 translocation is one of the most thoroughly studied chromosomal abnormalities in livestock. Which species does it primarily affect, and what type of translocation is it?
(A) Sheep; Reciprocal translocation
(B) Pig; Tandem translocation
(C) Cattle; Robertsonian translocation
(D) Horse; Non-homologous insertional translocation

2012

159. Identify the correct statement regarding Robertsonian translocations.
(A) They involve the exchange of segments between the middle of two chromosomes in a cell
(B) They result in a net increase in the total diploid chromosome number of the species
(C) They always cause severe physical deformities in the carrier animal in the herd
(D) Centric fusion of non-homologous acrocentric chromosomes forms one bi-armed pair

2013

160. All of the following are potential consequences of chromosomal inversions EXCEPT:
(A) Suppression of crossing over within the inverted region during meiosis
(B) Formation of dicentric and acentric chromatids if crossing over occurs within a paracentric inversion
(C) An increase in the overall amount of genetic material in the nucleus
(D) Reduced fertility in heterozygotes due to the production of unbalanced gametes

2019

161. What distinguishes a pericentric inversion from a paracentric inversion?
(A) A pericentric inversion involves the telomeres; a paracentric inversion does not
(B) A pericentric inversion includes the centromere; a paracentric inversion does not
(C) A pericentric inversion leads to lethality; a paracentric inversion is benign
(D) A pericentric inversion only occurs in sex chromosomes of the mammalian species

2002

162. How does a heterozygous reciprocal translocation typically manifest in a herd of breeding pigs?
(A) Increased litter size due to hybrid vigor and heterosis in the breeding population
(B) Complete sterility in all affected males and females within the breeding herd
(C) Increased incidence of polyploidy occurring during the early embryonic stages
(D) Semi-sterility due to adjacent segregation producing unbalanced gamete cells

2016

163. Which pair accurately maps a structural aberration to its characteristic meiotic pairing configuration in heterozygotes?
(A) Reciprocal Translocation - Cross-shaped (quadrivalent) configuration
(B) Deletion - Cross-shaped (quadrivalent) configuration
(C) Inversion - Deletion loop
(D) Duplication - Trivalent configuration

NODIA

2004

164. What is the primary evolutionary and phenotypic impact of gene duplications?
(A) Immediate organismal lethality occurring during the process of embryonic growth
(B) They cause chromosomes to shatter during the mitotic cycle of the somatic cells
(C) Surplus genetic material can mutate freely to acquire new metabolic functions
(D) They exclusively lead to the formation of pseudogenes in the animal's genome

2024

165. Consider a situation where a bull is identified as a heterozygous carrier of the 1/29 Robertsonian translocation. What will be the observed chromosome number $(2n)$ in the somatic cells of this bull, given that the normal bovine karyotype is $2n = 60$?

(A) 59
(B) 58
(C) 60
(D) 61

2014

166. Which cellular mechanism is predominantly responsible for creating a chromosomal deletion or duplication during meiosis?
(A) Normal, perfectly aligned homologous crossing over
(B) Premature activation of the spindle fibers
(C) Non-disjunction at Anaphase II
(D) Unequal crossing over between misaligned homologous sequences

2009

167. A geneticist evaluates an acentric fragment and a dicentric bridge during Anaphase I of meiosis in an animal. This observation is diagnostic for an individual heterozygous for which structural aberration?
(A) Reciprocal translocation
(B) Paracentric inversion
(C) Pericentric inversion
(D) Interstitial deletion

2003

168. What is the phenotypic consequence of "pseudodominance" caused by a chromosomal deletion?
(A) A dominant allele mutates into a recessive one due to environmental mutagenic stress
(B) Overexpression of a gene due to copy number variation within the somatic cell line
(C) Normal recessive alleles are expressed because the dominant allele was deleted
(D) Complete suppression of the X chromosome during the process of dosage compensation

2004

169. Which class of chromosomal aberration strictly alters the physical position of genes without adding or removing any genetic material from the genome?
(A) Terminal Deletion
(B) Tandem Duplication
(C) Isochromosome formation
(D) Inversion

2016

170. Which term correctly defines an organism whose chromosome number is not an exact multiple of the haploid base number?
(A) Aneuploid
(B) Euploid
(C) Polyploid
(D) Autopolyploid

2003

171. What is the primary cellular error that generates aneuploid gametes?
(A) Premature activation of DNA polymerase during the synthesis phase of the cycle
(B) Non-disjunction of homologous chromosomes or sister chromatids during meiosis
(C) Exposure strictly to non-ionizing radiation in the natural animal environment
(D) Homologous recombination occurring within the somatic cell lines of the body

2004

172. Identify the correct statement regarding polyploidy in domestic animals.
(A) Autopolyploidy is common and used for meat yield in all major mammalian species
(B) Polyploidy generally results in early embryonic lethality in mammals and birds
(C) Allopolyploidy is induced in dairy cattle to increase milk production levels
(D) Polyploid mammals are entirely viable and fertile in the breeding population

2001

173. All of the following are recognized types of aneuploidy EXCEPT:
(A) Triploidy $(3n)$
(B) Nullisomy $(2n-2)$
(C) Monosomy $(2n-1)$
(D) Trisomy $(2n+1)$

2011

174. Which specific aneuploidy is often observed as the karyotypic basis for Turner-like syndrome (e.g., ovarian hypoplasia) in mares?
(A) 65, XXY (Trisomy)
(B) 64, XXX
(C) 63, XO (Monosomy X)
(D) 62, YO

2003

175. Why are autosomal monosomies almost universally lethal in early embryonic development in livestock, whereas some sex-chromosome monosomies are viable?
(A) Autosomes lack genes essential for early development in the animal species used
(B) Sex chromosomes are significantly larger than all autosomes in the animal cell
(C) Monosomy completely prevents cleavage of the zygote during the first divisions
(D) Autosomal monosomy unmasks lethals and

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disrupts dosage, unlike sex chromosomes

2001

176. Which pair correctly matches the numerical aberration term with its chromosomal formula?
(A) Trisomy - $2n+2$
(B) Monoploidy - $n-1$
(C) Tetrasomy - $2n+2$
(D) Hexaploidy - $4n$

2007

177. What is the fundamental difference between autopolyploidy and allopolyploidy?
(A) Autopolyploidy involves multiple sets of chromosomes from a single species; allopolyploidy involves chromosome sets from two or more distinct species
(B) Autopolyploidy involves one species; allopolyploidy involves two or more species
(C) Autopolyploidy occurs in animals; allopolyploidy occurs exclusively in plants
(D) Autopolyploidy alters ploidy by adding one chromosome; allopolyploidy adds a set

2004

178. A genetically engineered triploid ($3n$) fish (e.g., trout or salmon) is highly desirable in aquaculture for which primary reason?
(A) They possess enhanced disease resistance against all known viruses in the water
(B) They can reproduce asexually within a controlled aquaculture environment today
(C) They possess highly complex, patterned scales prized by the commercial market
(D) They are sterile, redirecting energy from reproduction to somatic growth rates

2015

179. Which mechanism can be utilized artificially to induce polyploidy (e.g., triploidy) in fish or amphibian embryos?
(A) Using shocks after fertilization to prevent extrusion of the second polar body
(B) Administering a vaccine during the first trimester to the female parent fish
(C) Inserting transgenes via electroporation into the nucleus of the fertilized egg
(D) Depriving the embryo of oxygen for 24 hours to induce chromosomal doubling

2005

180. Match the following karyotypic designations with their descriptive terms.
List I: (Karyotype Formula)
P. $2n+1$
Q. $2n-1$
R. $2n-2$
S. $3n$
List II: (Descriptive Term)
1. Triploidy
2. Monosomy
3. Nullisomy
4. Trisomy
(A) P-4, Q-2, R-3, S-1
(B) P-4, Q-3, R-2, S-1
(C) P-1, Q-2, R-4, S-3
(D) P-2, Q-4, R-3, S-1

2016

181. What cytological phenomenon causes the occurrence of a mosaic animal possessing both normal diploid cells and aneuploid cells (e.g., $2n/2n+1$)?
(A) Mitotic non-disjunction during the early embryonic cleavage divisions
(B) Meiotic non-disjunction occurring in the germline of the paternal parent
(C) Fertilization of an egg by two separate sperm during the conception phase
(D) Incomplete penetrance of a dominant gene inherited from the parental lines

2001

182. A geneticist attempts to breed an interspecific hybrid between a horse ($2n=64$) and a donkey ($2n=62$). The resulting mule has 63 chromosomes. Why is the mule typically sterile?
(A) It completely lacks sex chromosomes within the somatic and germline tissues
(B) The mule's chromosomes suffer immediate telomere shortening after conception
(C) The Y chromosome of the donkey suppresses spermatogenesis in the hybrid male
(D) Mismatched chromosomes cannot pair in Prophase I, causing gametogenesis failure

NODIA

2006

183. Which of the following best describes Bovine Leukocyte Adhesion Deficiency (BLAD)?
(A) Autoimmune disorder where antibodies attack red blood cells in the animal host
(B) Recessive mutation in the CD18 gene, impairing neutrophil immune function
(C) A structural chromosomal aberration leading to dwarfism in various cattle breeds
(D) A sex-linked dominant trait causing excessive leukocyte proliferation in herds

2015

184. DUMPS (Deficiency of Uridine Monophosphate Synthase) is an inherited disorder in Holstein

cattle. What is its primary physiological consequence?
(A) Excessive accumulation of uric acid in the joints of the adult dairy cattle
(B) Complete failure of the immune system to recognize antigens in the environment
(C) Embryonic mortality at 40 days of gestation due to impaired pyrimidine synthesis
(D) Rapid neurological degeneration in adult cattle within the breeding population

2006

185. Identify the correct statement regarding Bovine Citrullinemia.
(A) It is caused by a dominant mutation in the ASS gene in all major beef breeds
(B) It primarily affects adult beef cattle and causes severe muscle wasting issues
(C) It is an X-linked recessive disorder exclusive to the Jersey breed of cattle
(D) It leads to lethal ammonia toxicity in newborn calves due to a urea cycle defect

2021

186. All of the following are true about Complex Vertebral Malformation (CVM) in cattle EXCEPT:
(A) It causes misshapen vertebrae and congenital joint contractures
(B) It is an autosomal recessive inherited disorder
(C) It is caused by a missense mutation in the SLC35A3 gene
(D) Calves homozygous for the mutation are usually healthy and physically robust

2012

187. What causes Freemartinism, a classic developmental disorder in cattle?
(A) An autosomal recessive lethal mutation inherited from the parental generations
(B) Blood exchange between opposite-sex twins leading to female fetus sterility
(C) A point mutation in the SRY gene located on the Y chromosome of the male twin
(D) A specific trisomy of the sex chromosomes (XXY) found in the female twin cells

2001

188. Which pair correctly matches the genetic disorder with the gene responsible for the defect?
(A) BLAD - SLC35A3 gene
(B) DUMPS - UMPS gene
(C) Citrullinemia - CD18 gene
(D) Syndactyly - PRNP gene

2013

189. How does bovine syndactyly (Mule foot) manifest phenotypically?
(A) The two digits of the hoof are fused into a single digit
(B) Calves are born with missing hooves
(C) The animal develops an extra digit on each limb (polydactyly)
(D) The hoof grows continuously without normal shedding

2006

190. Read the following Assertion (A) and Reason (R) and select the correct option.
Assertion (A): The genetic test for DUMPS is highly recommended for Holstein sires used in artificial insemination.
Reason (R): DUMPS is an autosomal recessive condition that causes early embryonic loss, which masquerades as poor conception rates and leads to economic losses.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2005

191. If a herd has a high prevalence of calves dying shortly after birth with severe infections and drastically elevated leukocyte counts, which genetic disorder should the veterinarian suspect?
(A) CVM
(B) DUMPS
(C) Freemartinism
(D) BLAD

2004

192. What is the fundamental basis for the diagnosis of Freemartinism using cytogenetic techniques?
(A) Detecting a pericentric inversion in chromosome 1 of the bovine somatic cells
(B) Detecting the absence of an X chromosome (XO karyotype) in the female twin
(C) Identifying leukocyte chimerism (XX and XY cells) in the female twin's blood
(D) Visualizing a reciprocal translocation in the germline tissues of the animal

2005

193. Which intervention is the most reliable method to eliminate recessive genetic disorders like BLAD and DUMPS from a modern dairy cattle population?
(A) Vaccinating all newborn calves against the

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primary pathogens in the environment
(B) Genotyping prospective AI sires and strictly excluding the carrier animals
(C) Routine culling of animals showing the clinical disease in the breeding herd
(D) Administering antibiotics to pregnant cows to prevent the onset of symptoms

2002

194. Which of the following best describes the inheritance pattern of bovine syndactyly?
(A) Autosomal dominant with incomplete penetrance
(B) Sex-linked dominant
(C) Mitochondrial inheritance
(D) Autosomal recessive with variable expressivity

2010

195. Read the following Assertion (A) and Reason (R) and select the correct option.
Assertion (A): A Freemartin heifer typically cannot be used as a replacement breeding female.
Reason (R): The transfer of anti-Mullerian hormone and androgens from the male twin via the fused chorionic circulation inhibits the normal development of the female reproductive tract.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2014

196. What is the primary purpose of G-banding in animal cytogenetics?
(A) To strictly identify heterochromatin at the centromeres of the animal chromosomes
(B) To measure the exact sequence of DNA nucleotides within the chromosomal structure
(C) To generate a pattern of light and dark bands for chromosome identification
(D) To detect specific mRNA transcripts in the cytoplasm of the somatic cell line

2013

197. Which specific dye combination is typically used to produce Q-bands on metaphase chromosomes?
(A) Quinacrine mustard, viewed under a fluorescence microscope
(B) Giemsa stain after trypsin digestion
(C) Silver nitrate staining
(D) Acridine orange after heat denaturation

NODIA

2016

198. Identify the correct statement regarding C-banding.
(A) C-banding stains the transcriptionally active euchromatic regions of the genome
(B) C-banding specifically identifies the telomeric sequences at the chromosome ends
(C) C-banding stains constitutive heterochromatin located near the centromeres
(D) C-banding requires the use of fluorescent DNA probes in the hybridization step

2019

199. All of the following are advantages of Fluorescent In Situ Hybridization (FISH) EXCEPT:
(A) It allows mapping of specific genes or DNA sequences to highly precise locations on chromosomes
(B) It can detect microdeletions that are invisible in standard G-banded karyotypes
(C) It can be utilized in both metaphase spreads and interphase nuclei
(D) It provides a higher resolution than standard light microscopy for certain applications

2025

200. What is the physical basis for the dark G-bands formed during Giemsa banding?
(A) Regions rich in G-C base pairs that denature easily during the banding process
(B) Regions containing actively transcribing RNA polymerases in the animal nucleus
(C) Regions rich in A-T base pairs that are condensed and relatively gene-poor
(D) Regions specifically composed of telomerase at the ends of the chromosomal arms

2025

201. Which pair accurately matches the banding technique with its target or characteristic?
(A) R-banding - Produces a banding pattern identical to G-banding
(B) G-banding - Requires treatment with Quinacrine
(C) C-banding - Highlights actively expressed genes
(D) Sister Chromatid Exchange (SCE) - Utilizes BrdU incorporation to detect DNA damage and repair

2002

202. How does R-banding differ structurally from G-banding?

(A) R-banding produces a reverse pattern; dark bands correspond to gene-dense regions
(B) R-banding selectively stains RNA rather than DNA within the animal somatic cells
(C) R-banding only works on plant chromosomes rather than mammalian cell karyotypes
(D) R-banding strictly identifies centromeres within the chromatin of the animal

2015

203. A researcher intends to evaluate the mutagenic effect of a new pesticide on livestock by observing the frequency of DNA breaks and repair events. Which cytogenetic assay is most appropriate?
(A) Standard C-banding
(B) Sister Chromatid Exchange (SCE) assay
(C) Nuclear Organizer Region (NOR) silver staining
(D) Mitochondrial DNA sequencing

2019

204. Which definition best describes the fundamental principle of the FISH technique?
(A) Utilizing a single restriction enzyme to digest the entire genome into fragments
(B) Using a fluorescent DNA or RNA probe to bind to its complementary target sequence
(C) Fusing two distinct animal cells to create a hybridoma for antibody production
(D) Electrophoresing whole chromosomes on an agarose gel in the laboratory setting

2021

205. Match the following cytogenetic techniques with their primary applications.
List I: (Banding/Staining Technique)
P. FISH
Q. G-banding
R. C-banding
S. SCE assay
List II: (Primary Application)
1. Routine identification of homologous chromosome pairs
2. Evaluating genotoxicity and DNA repair
3. Mapping specific gene loci
4. Identifying constitutive heterochromatin polymorphism
(A) P-3, Q-1, R-4, S-2
(B) P-4, Q-1, R-3, S-2
(C) P-3, Q-4, R-1, S-2
(D) P-1, Q-2, R-4, S-3

2017

206. In Sister Chromatid Exchange (SCE) staining, why does one chromatid stain darker than the other?
(A) Because one chromatid completely lacks histones within its chromatin structure
(B) Because one chromatid contains strictly RNA in the nuclei of the somatic cells
(C) Cells are grown in BrdU, leading to differential substitution in the chromatids
(D) Because telomerase preferentially elongates only one chromatid during synthesis

2005

207. What specific structural aberration is FISH uniquely capable of detecting that routine G-banding might miss?
(A) Whole chromosome trisomy
(B) Massive Robertsonian translocations
(C) Complete triploidy
(D) Microdeletions smaller than 3-5 Megabases

2025

208. Which component is strictly necessary for visualizing standard Q-bands?
(A) Bright-field microscope
(B) Electron microscope
(C) Ultraviolet (UV) fluorescence microscope
(D) Phase-contrast microscope

2002

209. Which class of molecules provides the foundational structure for the humoral immune response in domestic animals?
(A) T-cell receptors
(B) Immunoglobulins (Antibodies)
(C) Major Histocompatibility Complex proteins
(D) Toll-like receptors

2016

210. What is the fundamental difference between cell-mediated and humoral immunity?
(A) Humoral immunity is innate, while cell-mediated immunity is adaptive in nature
(B) Humoral immunity targets viruses, while cell-mediated immunity targets bacteria
(C) Humoral immunity operates only in mucosal tissues of the livestock animal host
(D) Humoral immunity relies on B-cells; cell-mediated immunity relies on T-cells

2012

211. Identify the correct statement regarding the structural composition of a typical monomeric immunoglobulin (IgG) molecule.
(A) Two identical heavy chains and two light

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chains held by disulfide bonds
(B) One heavy chain and two light chains forming the core of the immunoglobulin
(C) Four identical heavy chains forming a complex receptor on the cell membrane
(D) Two alpha helices and two beta pleated sheets forming a core receptor system

2007

212. All of the following are primary functions of antibodies in domestic animals EXCEPT:
(A) Opsonization of pathogens for phagocytosis
(B) Activation of the classical complement pathway
(C) Direct, enzymatic degradation of viral DNA
(D) Neutralization of bacterial toxins

2022

213. Which immunoglobulin class is the predominant antibody found in the mucosal secretions (e.g., saliva, tears, colostrum) of livestock?
(A) IgA
(B) IgM
(C) IgG
(D) IgE

2006

214. Which functional characteristic is strictly associated with IgM in the bovine immune response?
(A) It is the principal immunoglobulin mediating allergic responses in the animal
(B) It provides the majority of passive immunity through the placenta in ungulates
(C) It is a monomer uniquely specialized to bind helminth parasites in the host
(D) It is the first isotype secreted in a primary response, existing as a pentamer

2015

215. Consider the following statements regarding immunoglobulins in farm animals:
I. IgE plays a critical role in immunity against parasitic helminths.
II. IgG is the most abundant immunoglobulin in circulating plasma.
III. Newborn ruminants acquire passive immunity transplacentally before birth.
IV. The variable (V) regions of the heavy and light chains form the antigen-binding site.
Which of the above statements are correct?
(A) I, II and IV
(B) I, II and III
(C) II, III and IV
(D) I, III and IV

NODIA

2016

216. How does the transfer of passive humoral immunity in ungulates (cattle, horses, pigs) differ fundamentally from that in humans?
(A) Ungulates transfer immunity entirely via the yolk sac during the fetal stage
(B) Ungulate calves synthesize their own full complement of IgG in utero normally
(C) Ungulates lack transplacental IgG; calves rely on colostrum ingestion at birth
(D) Ungulates transfer immunity strictly via IgD in the maternal blood circulation

2003

217. Which pair correctly identifies the immunoglobulin class and its primary functional role?
(A) IgD - Dominant antibody in milk
(B) IgM - Transplacental transport in cows
(C) IgA - Activation of the alternative complement pathway in blood
(D) IgE - Mediation of Type I hypersensitivity (allergic) reactions

2009

218. What region of the immunoglobulin molecule is responsible for determining its class (isotype) and mediating effector functions such as complement fixation or binding to macrophage receptors?
(A) The constant region of the heavy chain (Fc fragment)
(B) The Fab fragment of the immunoglobulin molecule structure
(C) The hypervariable regions (CDRs) of the antigen-binding site
(D) The variable region of the light chain within the antibody

2019

219. Which cellular component is explicitly responsible for generating a cell-mediated immune response to intracellular pathogens like Brucella abortus in cattle?
(A) Plasma cells
(B) Cytotoxic T lymphocytes (CD8+)
(C) Erythrocytes
(D) Megakaryocytes

2015

220. What is the consequence of enzymatic cleavage of an IgG molecule by papain?
(A) One F(ab')2 fragment and fragmented Fc peptides are produced
(B) Two Fab fragments and one Fc fragment are produced
(C) The heavy chains completely dissociate from

the light chains
(D) The molecule is reduced to free amino acids

2009

221. Which term accurately describes the strength of the non-covalent interactions between a single antigen-binding site on an antibody and a single corresponding epitope?
(A) Affinity
(B) Avidity
(C) Cross-reactivity
(D) Valence

2001

222. How does avidity differ from affinity in antigen-antibody interactions?
(A) Avidity is the strength of a single bond; affinity is the strength of many
(B) Avidity applies only to T-cells; affinity applies to B-cells in the host
(C) Affinity is attraction; avidity is total binding strength to a multivalent antigen
(D) They are synonymous terms used interchangeably in veterinary immunology

2012

223. What phenomenon occurs when an antibody raised against one specific antigen binds to a structurally similar but distinct epitope on a different antigen?
(A) Agglutination
(B) Opsonization
(C) Isotype switching
(D) Cross-reactivity

2005

224. Which condition is the underlying cause for false-positive results in many serological immunodiagnostic assays?
(A) High affinity
(B) High avidity
(C) Cross-reactivity
(D) Monoclonal specificity

2015

225. Consider the following immunodiagnostic assays used in veterinary medicine:
I. Enzyme-Linked Immunosorbent Assay (ELISA)
II. Polymerase Chain Reaction (PCR)
III. Fluorescent Antibody Technique (FAT)
IV. Agar Gel Immunodiffusion (AGID)
V. Western Blotting
Which of the above are strictly based on antigen-antibody interactions?
(A) I, III, IV and V
(B) I, II, III and IV
(C) I, IV and V
(D) II, III and V

2023

226. In an indirect ELISA for detecting Brucellosis in a dairy herd, what is directly conjugated to the reporter enzyme?
(A) The specific Brucella antigen
(B) The primary antibody from the cow's serum
(C) A substrate that changes color
(D) A secondary anti-bovine immunoglobulin antibody

NODIA

2003

227. Which immunodiagnostic assay relies on the principle of antigens and antibodies diffusing toward each other in a semi-solid matrix to form a visible line of precipitation?
(A) Agar Gel Immunodiffusion (AGID)
(B) Flow cytometry
(C) Radioimmunoassay (RIA)
(D) Competitive ELISA

2023

228. What is the fundamental utility of the Western Blotting technique in livestock disease diagnosis?
(A) To strictly quantify the total amount of DNA in a sample from the animal host
(B) To measure the live cell count in a blood sample from the livestock population
(C) To separate proteins by weight, followed by identification using antibodies
(D) To rapidly agglutinate whole bacteria in the blood plasma of the animal host

2021

229. If an IgM pentamer has an individual binding affinity to an antigen that is considered low, why is it highly effective at clearing pathogens like bacteria?
(A) It has 10 identical binding sites, granting it exceedingly high avidity
(B) It quickly mutates to an IgG form through the process of isotype switching
(C) It can enter the host cell nucleus and block the replication of viral DNA
(D) It prevents transcription of bacterial DNA by binding directly to the gene

2011

230. Which specific interaction primarily drives the binding of an epitope to an antibody's paratope?
(A) Covalent bonding between the antigen and the antibody molecule in the host
(B) Peptide bond formation occurring between

the paratope and the epitope site
(C) Disulfide bond formation between the heavy and light chains of the antibody
(D) Non-covalent forces such as hydrogen bonds and van der Waals interactions

2017

231. An agglutination test is frequently used for blood typing in animals. What physical characteristic defines agglutination?
(A) The formation of an insoluble precipitate from soluble antigens and antibodies
(B) Clumping of particulate antigens cross-linked by specific antibody molecules
(C) The emission of light upon antigen binding within the diagnostic assay kit
(D) The cleavage of the antigen by the antibody during the immune response cycle

2002

232. Which format is most appropriate if a veterinarian needs to detect a very small amount of a specific viral antigen in a complex tissue sample using a fluorescently labeled antibody directly applied to the tissue section?
(A) Indirect ELISA
(B) Radial Immunodiffusion
(C) Direct Immunofluorescence (Direct FAT)
(D) Complement Fixation Test

2002

233. What is the primary advantage of a competitive ELISA over a standard direct ELISA?
(A) It requires fewer washing steps and is faster than a standard direct ELISA
(B) It strictly uses radioactive isotopes for detection within the laboratory
(C) It does not rely on antigen-antibody binding for the quantification step
(D) It can quantify antigens in complex samples without species-specific antibodies

2014

234. In the context of the Major Histocompatibility Complex (MHC), what is its primary physiological function?
(A) To present peptide antigens to T-cells, initiating adaptive immune responses
(B) To produce circulating antibodies within the plasma of the livestock host
(C) To directly phagocytize invading bacteria in the tissues of the animal body
(D) To serve as structural proteins in the cell membrane of every animal cell

2023

235. Consider the following statements about MHC classes:
I. Class I molecules are expressed on almost all nucleated cells.
II. Class II molecules are expressed primarily on professional antigen-presenting cells (APCs).
III. Class I molecules present endogenous antigens to CD8+ T cells.
IV. Class III genes code exclusively for T-cell receptors.
V. Class II molecules present exogenous antigens to CD4+ T cells.
Which of the above statements are INCORRECT?
(A) I and II
(B) III and V
(C) IV only
(D) II and IV

2006

236. Which feature characterizes the structure of an MHC Class I molecule?
(A) Two identical alpha chains and two identical beta chains forming the complex
(B) Alpha chain non-covalently associated with smaller beta-2 microglobulin
(C) A single beta chain bound to a light chain in the cellular plasma membrane
(D) Five repeating domains forming a pentameric structure on the cell surface

2015

237. The extraordinary genetic polymorphism observed in MHC genes is primarily concentrated in which region of the MHC molecule?
(A) The peptide-binding groove (cleft)
(B) The transmembrane domain
(C) The cytoplasmic tail
(D) The beta-2 microglobulin binding site

2025

238. Identify the correct statement regarding MHC Class III genes.
(A) They strictly encode molecules involved in antigen presentation to the cell
(B) They are located on a different chromosome from Class I and II animal genes
(C) They encode immune proteins like complement components and various cytokines
(D) They are solely responsible for the rejection of tissue grafts in animals

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2023

239. All of the following are examples of professional antigen-presenting cells (APCs) that express MHC Class II molecules EXCEPT:
(A) Dendritic cells
(B) Macrophages
(C) B-lymphocytes
(D) Erythrocytes

2021

240. What is the fundamental basis for the association between specific MHC alleles and disease resistance in livestock?
(A) Certain MHC alleles produce more immunoglobulins than others in the animal
(B) Certain MHC alleles mutate the pathogen's DNA directly in the host tissues
(C) Specific MHC molecules bind and present peptides more effectively to T-cells
(D) MHC alleles physically block viral entry into the cell of the livestock host

2025

241. Which pair accurately reflects an MHC class and its primary cellular interaction?
(A) MHC Class II - CD8+ Cytotoxic T cells
(B) MHC Class I - CD8+ Cytotoxic T cells
(C) MHC Class I - CD4+ Helper T cells
(D) MHC Class II - Erythrocytes

2006

242. How are MHC genes typically inherited in mammals?
(A) As completely independent, unlinked loci within the genome of the animal
(B) As extranuclear, maternally inherited factors within the mitochondrial DNA
(C) Only via the sex chromosomes of the mammalian species under investigation
(D) As linked haplotype blocks inherited as a single unit from each parent

2022

243. The Major Histocompatibility Complex in cattle is formally known by which acronym?
(A) BoLA
(B) HLA
(C) SLA
(D) BuLA

2011

244. What is the primary evolutionary advantage of the high degree of polymorphism and polygeny found in the MHC complex of outbred animal populations?
(A) It strictly prevents the occurrence of autoimmune diseases in the animal
(B) It ensures all individuals are genetically identical in the breeding herd
(C) It ensures the population can present an array of pathogenic viral peptides
(D) It suppresses the action of Toll-like receptors in the innate immune system

2018

245. Read the following Assertion (A) and Reason (R) and select the correct option.
Assertion (A): The bovine leukocyte antigen (BoLA) system has been extensively studied to improve disease resistance in dairy cattle.
Reason (R): Specific BoLA class II alleles (such as DRB3 exon 2 polymorphisms) have been strongly associated with resistance or susceptibility to Bovine Leukemia Virus (BLV) and mastitis.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2006

246. Which structural component of the BoLA complex restricts the presentation of exogenous peptides derived from bacteria?
(A) BoLA Class I molecules
(B) Beta-2 microglobulin
(C) Complement component C4
(D) BoLA Class II molecules

2009

247. The BuLA system represents the Major Histocompatibility Complex of which domestic animal species?
(A) Sheep (Ovis aries)
(B) Water Buffalo (Bubalus bubalis)
(C) Goat (Capra hircus)
(D) Pig (Sus scrofa)

NODIA

2024

248. Identify the INCORRECT statement regarding the BoLA system in cattle.
(A) It is located on bovine chromosome 23
(B) The BoLA-DRB3 gene is the most highly polymorphic locus in the class II region
(C) Polymorphisms in the BoLA genes are typically identified using PCR-RFLP or DNA sequencing
(D) BoLA genes exhibit complete dominance where only one parental allele is expressed

2003

249. Which mechanism generates the extensive polymorphism seen in the DRB3 locus of the BoLA system?
(A) Artificial introgression of genes from other animal species into the herd
(B) Somatic hypermutation occurring in T-cells during a bacterial infection
(C) Splicing of mRNA transcripts within the nucleus of the somatic cell lines
(D) High rates of point mutations and recombination over evolutionary time

2022

250. How does a heterozygous state at the BoLA loci provide an immunological advantage to a calf?
(A) It allows expression of two MHC sets, broadening the repertoire of antigens
(B) It leads to the complete deletion of viral DNA within the host animal cells
(C) It prevents the calf from developing allergies to various environmental factors
(D) It makes the calf resistant to genetic disorders throughout its entire life

2015

251. Which specific disease has been the most historically significant driver of research into BoLA-disease associations due to its economic impact on dairy herds?
(A) Bovine Spongiform Encephalopathy (BSE)
(B) Enzootic Bovine Leukosis (EBL) caused by BLV
(C) Foot and Mouth Disease (FMD)
(D) Rabies

2009

252. The Swine Leukocyte Antigen (SLA) complex has garnered intense modern research interest primarily for which application?
(A) Improving wool yield
(B) Xenotransplantation (transplanting pig organs into humans)
(C) Increasing litter size directly
(D) Eradicating African Swine Fever

2005

253. What defines the specific molecules recognized by Toll-like Receptors (TLRs) during an innate immune response?
(A) Pathogen-associated molecular patterns highly conserved across microbes
(B) Highly variable, newly mutated viral proteins within the animal host body
(C) Immunoglobulin heavy chains found circulating in the blood of the animal
(D) Host cell nuclear DNA released into the environment during cellular death

2025

254. Which fundamental characteristic distinguishes Toll-like Receptors (TLRs) from T-cell receptors or Immunoglobulins?
(A) TLRs are highly polymorphic and clonally distributed
(B) TLRs undergo V(D)J somatic recombination to generate diversity
(C) TLRs are germline-encoded, non-clonal receptors of the innate immune system
(D) TLRs specifically recognize only endogenous host antigens

2003

255. Match the specific Toll-like Receptors with their primary corresponding PAMP ligands.
List I: (Toll-like Receptor)
P. TLR-4
Q. TLR-5
R. TLR-3
S. TLR-9
List II: (PAMP Ligand)
1. Double-stranded RNA (dsRNA) of viruses
2. Unmethylated CpG DNA motifs from bacteria
3. Lipopolysaccharide (LPS) from Gram-negative bacteria
4. Flagellin from motile bacteria
(A) P-3, Q-4, R-1, S-2
(B) P-4, Q-3, R-2, S-1
(C) P-3, Q-2, R-1, S-4
(D) P-1, Q-4, R-3, S-2

2017

256. Which cellular outcome strictly follows the activation of Toll-like Receptor signaling pathways in livestock macrophages?
(A) Immediate cell lysis within the tissues of the animal body upon infection
(B) Production of immunoglobulins by the B-cells of the adaptive immune system
(C) Translocation of NF-kappaB to the nucleus and production of cytokines
(D) Inhibition of antigen presentation within the professional APCs of the host

2018

257. Identify the correct cellular localization of TLRs 3, 7, 8, and 9.
(A) They are expressed on the outer plasma membrane to detect bacterial species
(B) They are localized in endosomes to detect

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nucleic acids of internal pathogens
(C) They are freely circulating in the blood plasma of the livestock population
(D) They are embedded strictly in the mitochondrial membrane of the animal cell

2012

258. All of the following are recognized consequences of a mutation causing TLR-4 dysfunction in a farm animal EXCEPT:
(A) Reduced susceptibility to septic shock caused by endotoxins
(B) Impaired innate immune response to Gram-negative bacterial infections
(C) Failure to adequately produce cytokines such as TNF-alpha in response to LPS
(D) Complete failure to mount an antibody response against Gram-positive bacteria

2001

259. What is the role of MyD88 in the context of Toll-like Receptor function?
(A) It is a critical adaptor protein used to initiate downstream signal pathways
(B) It is the specific viral ligand that binds to TLR-3 during an infection phase
(C) It is an enzyme that degrades extracellular PAMPs in the animal bloodstream
(D) It is a transcription factor that directly binds DNA in the animal cell nuclei

2002

260. Which pair accurately relates an innate immune receptor to the type of organism it evolved to combat?
(A) TLR-4 - Helminth parasites
(B) TLR-9 - Fungal cell walls
(C) TLR-5 - Flagellated bacteria
(D) TLR-3 - Extracellular protozoa

2009

261. How does the activation of TLRs physically bridge the innate and adaptive immune systems in animals?
(A) TLR signaling induces dendritic cell maturation and upregulates MHC molecules
(B) TLR activation directly mutates the MHC genes in the germline of the animal
(C) TLRs bind physically to B-cell receptors within the secondary lymphoid organs
(D) TLRs convert macrophages into T-cells through a process of transdifferentiation

2024

262. In veterinary immunology, what are interleukins?
(A) A group of structural proteins found in the extracellular matrix of lymph nodes
(B) Antibodies that specifically bind to viruses within the blood of the animal
(C) Enzymes that degrade the bacterial cell wall in the livestock animal host
(D) Cytokines produced by leukocytes to regulate the growth of all immune cells

2021

263. Which specific cytokine is primarily responsible for promoting the clonal expansion and survival of activated T-cells, often acting in an autocrine manner?
(A) Interleukin-1 (IL-1)
(B) Interleukin-2 (IL-2)
(C) Interleukin-10 (IL-10)
(D) Tumor Necrosis Factor-alpha (TNF-alpha)

2018

264. Identify the correct statement characterizing the function of Interleukin-10 (IL-10) in the bovine immune system.
(A) It is a potent pro-inflammatory cytokine that initiates fever in the animal host
(B) It specifically induces the development of Th1 cells in the lymphoid tissues
(C) It acts as an anti-inflammatory cytokine inhibiting macrophage functions
(D) It exclusively stimulates the production of IgE in the bovine immune system

NODIA

2012

265. Arrange the following events in a standard pro-inflammatory immune cascade initiated by a bacterial infection in the correct sequence:
I. Secretion of pro-inflammatory cytokines (IL-1, IL-6, TNF-alpha)
II. Phagocytosis of the pathogen by macrophages
III. Recognition of PAMPs by TLRs
IV. Induction of acute-phase proteins from the liver and onset of fever
Which of the following is the logically correct order of validation?
(A) III, II, I, IV
(B) II, III, I, IV
(C) I, III, II, IV
(D) III, I, II, IV

2018

266. Which cellular subset of Helper T-cells is classically associated with the production of IL-4, IL-5, and IL-13, thereby promoting B-cell class switching to IgE and fighting helminth infections?
(A) Th2 cells

(B) Th1 cells
(C) Th17 cells
(D) Regulatory T cells (Tregs)

2005

267. What is the fundamental role of Interferon-gamma (IFN-gamma) in the ovine immune response?
(A) It is the primary mediator of allergic reactions within the ovine populations
(B) It activates macrophages to kill pathogens and directs a Th1-type response
(C) It acts as a powerful anti-inflammatory agent within the livestock animal host
(D) It primarily stimulates the differentiation of osteoclasts in the bone marrow

2016

268. Which condition defines the phenomenon of cytokine pleiotropy?
(A) One cytokine has the same effect on multiple cell types in the animal tissues
(B) One cytokine exerts different biological effects on different target cells
(C) Multiple cytokines have the exact same functional effect in the immune system
(D) Cytokines inhibit the action of other cytokines within the lymphoid organs

2009

269. A severe systemic release of large quantities of cytokines (a "cytokine storm"), particularly TNF-alpha and IL-1, in response to bacterial endotoxin leads directly to which veterinary emergency?
(A) Endotoxic (septic) shock
(B) Autoimmune hemolytic anemia
(C) Severe Combined Immunodeficiency (SCID)
(D) Acquired tolerance

2013

270. Which pair accurately matches the cytokine with its primary cellular source?
(A) IL-2 - Activated B-cells
(B) IL-4 - Macrophages
(C) IFN-gamma - Natural Killer (NK) cells and Th1 cells
(D) IL-1 - Erythrocytes

2011

271. What is the specific functional consequence of Interleukin-6 (IL-6) action in livestock?
(A) Inducing apoptosis in healthy cells within the somatic tissues of the animal
(B) Directly neutralizing viral particles in the blood of the livestock population
(C) Blocking the transcription of MHC Class I genes in the professional APC lines
(D) Mediating the acute phase response and stimulating liver protein production

2009

272. In sheep, what cytokine strictly directs the differentiation of naive CD4+ T-cells into the Th17 subset, critical for mucosal defense against extracellular bacteria?
(A) IL-2 alone
(B) IL-4 alone
(C) A combination of TGF-beta and IL-6
(D) IFN-gamma alone

2007

273. How do cytokines mediate cellular communication within the immune system?
(A) By freely diffusing through the lipid bilayer into the nucleus of the target cell
(B) By binding to transmembrane receptors, activating internal signal pathways
(C) By direct enzymatic degradation of target cell DNA within the animal tissue
(D) By acting as structural elements connecting cells in the lymphoid tissues

2005

274. What defines hybridoma technology, developed by Köhler and Milstein?
(A) A method for cloning whole animals through somatic cell nuclear transfer
(B) A technique to create transgenic livestock using various viral vector systems
(C) A strategy for directly mutating immunoglobulin genes in the live animal
(D) Fusing a B-cell with a myeloma cell to produce monoclonal antibodies

2006

275. Arrange the following key procedural steps in producing monoclonal antibodies via hybridoma technology in the correct sequence:
I. Fusion of spleen cells with myeloma cells using PEG (Polyethylene glycol)
II. Immunization of a mouse or suitable animal with the target antigen
III. Selection of hybrid cells in HAT medium
IV. Screening of hybridoma clones for specific antibody production
Which of the following is the logically correct order of validation?
(A) I, II, III, IV
(B) II, I, III, IV
(C) II, I, IV, III

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(D) I, III, II, IV

2004

276. Identify the correct function of Aminopterin in the HAT medium used for hybridoma selection.
(A) It provides essential nutrients for the survival of unfused spleen cells
(B) It acts as a fuse-inducing agent, similar to PEG in the hybridization process
(C) It blocks the de novo synthesis pathway, forcing use of the salvage pathway
(D) It directly stimulates the secretion of antibodies by the resulting hybridomas

2024

277. Why do unfused myeloma cells die in HAT medium during hybridoma generation?
(A) They lack the HGPRT enzyme, preventing use of the salvage pathway in the cell
(B) They are inherently short-lived cells when grown in a laboratory environment
(C) The medium contains high concentrations of toxic heavy metals like mercury
(D) They are targeted and killed by the unfused B-cells through cytotoxic action

2006

278. All of the following are characteristic features of monoclonal antibodies (mAbs) compared to polyclonal antibodies EXCEPT:
(A) They recognize a single specific epitope on an antigen in the diagnostic kit
(B) They are homogeneous and can be produced in limitless quantities consistently
(C) They are produced by the descendants of a single cloned B-cell hybridoma line
(D) They exhibit high cross-reactivity and bind to multiple diverse epitopes

2017

279. Which specific reagent is conventionally used to physically promote the fusion of the plasma membranes of B-cells and myeloma cells?
(A) Hypoxanthine
(B) Polyethylene glycol (PEG)
(C) Aminopterin
(D) Trypsin

2011

280. What is the fundamental reason unfused B-lymphocytes (spleen cells) do not survive long-term in the cell culture during hybridoma selection?
(A) They are killed by Aminopterin within the selective medium in the laboratory
(B) They lack the HGPRT enzyme required for the salvage pathway of synthesis
(C) They naturally have a limited lifespan in vitro and undergo senescence
(D) They are destroyed by the myeloma cells within the hybridoma culture vessel

2003

281. Which pair accurately matches the hybridoma component with its specific contribution to the resulting fused cell?
(A) B-lymphocyte - Provides the specific antibody gene to the resulting hybrid
(B) B-lymphocyte - Confers immortality in culture for the resulting cell line
(C) Aminopterin - Provides the HGPRT enzyme for the salvage pathway synthesis
(D) Myeloma cell - Confers the ability to divide indefinitely in cell culture

NODIA

2014

282. How has monoclonal antibody technology most significantly impacted veterinary diagnostics?
(A) By allowing highly specific diagnostic kits with no batch-to-batch variation
(B) By replacing all vaccines used for the prevention of livestock animal diseases
(C) By strictly serving as dietary supplements for newborn calves in the dairy herd
(D) By permanently altering the genome of the infected animal in the breeding farm

2007

283. What genetic modification must be present in the myeloma cell line prior to fusion for the HAT selection system to work?
(A) It must be genetically engineered to produce the target antigen in the cell
(B) It must be entirely devoid of MHC molecules within its plasma membrane structure
(C) It must be a mutant lacking functional genes for the HGPRT or TK enzymes
(D) It must contain an extra copy of chromosome 1 within its nuclear karyotype

2005

284. Which condition represents a major limitation when administering mouse-derived monoclonal antibodies therapeutically to domestic animals like dogs or horses?
(A) The antibodies will degrade instantly in the blood of the recipient animal host
(B) The immune system will recognize mouse antibody as foreign, causing clearance
(C) The antibodies will bind to absolutely every cell in the animal's somatic tissues

(D) They cannot be produced in sufficient quantities for wide therapeutic use today

2018

285. A researcher observes multiple positive clones reacting with the target antigen after the initial hybridoma fusion. What is the critical next step to ensure each cell line is truly producing a monoclonal antibody?
(A) Performing limiting dilution cloning to ensure the culture is from a single cell
(B) Immediately injecting the cells back into a mouse for the purpose of production
(C) Boiling the culture to remove unbound antibodies from the laboratory vessel
(D) Sequencing the entire genome of the cells to check for any potential mutations

2023

286. Which application is NOT a standard use of monoclonal antibodies in modern animal agriculture?
(A) Treatment of specific canine lymphomas (e.g., using anti-CD20 mAbs)
(B) Passive immunization against specific pathogens (e.g., E. coli in calves)
(C) Routine artificial induction of multiple ovulation in dairy cattle
(D) Precise phenotyping of leukocyte subpopulations via flow cytometry

2024

287. What does the 'T' stand for in HAT medium?
(A) Thymine
(B) Tryptophan
(C) Threonine
(D) Thymidine

2007

288. How does the salvage pathway of nucleotide synthesis utilize Hypoxanthine?
(A) It converts hypoxanthine directly into DNA polymerase in the somatic cell nuclei
(B) Hypoxanthine blocks the action of aminopterin during the selection process stage
(C) Hypoxanthine is a precursor converted by HGPRT into purine nucleotides
(D) Hypoxanthine degrades RNA molecules within the cytoplasm of the hybridoma cells

2004

289. Which characteristic makes a monoclonal antibody particularly useful for purifying specific viral antigens from a complex tissue homogenate via affinity chromatography?
(A) Its ability to bind universally to all proteins
(B) Its high specificity and consistent affinity for a single epitope
(C) Its short half-life
(D) Its completely variable heavy chain structure

2008

290. Read the following Assertion (A) and Reason (R) and select the correct option.
Assertion (A): Chimeric or "animalized" (e.g., caninized or felinized) monoclonal antibodies are highly preferred over murine monoclonal antibodies for therapeutic use in pets.
Reason (R): Replacing the mouse constant regions with the corresponding species-specific constant regions significantly reduces the immunogenicity of the therapeutic antibody.
(A) Both A and R are true and R is the correct explanation of A
(B) Both A and R are true but R is not the correct explanation of A
(C) A is true but R is false
(D) A is false but R is true

2019

291. What is the primary purpose of the enzyme Thymidine Kinase (TK) in the context of hybridoma selection?
(A) It is required for salvage pathway synthesis of pyrimidines from thymidine
(B) It cleaves peptide bonds in the myeloma cells during the selection phase process
(C) It inhibits the function of PEG during the fusion of the two animal cell lines
(D) It promotes the secretion of IgM instead of IgG by the resulting hybridoma cell

2014

292. Identify the fundamental distinction between an epitope and a paratope in the context of monoclonal antibody targeting.
(A) An epitope is found only on viruses; a paratope is found only on bacteria lines
(B) An epitope is the entire antigen molecule; the paratope is the whole antibody
(C) An epitope is the antigenic determinant on the antigen; the paratope is the antigen-binding site on the antibody
(D) They represent the exact same physical structure within the diagnostic assay kit

2010

293. Which technique involves producing monoclonal antibodies in vivo by injecting hybridoma cells

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into the peritoneal cavity of a compatible mouse to produce ascites fluid?
(A) Ascites method
(B) In vitro tissue culture
(C) Transgenic plant expression
(D) Phage display

2021

294. Which ethical consideration has driven the transition from the ascites method to high-density in vitro bioreactors for mAb production?
(A) In vitro methods strictly yield polyclonal antibodies in the laboratory setting
(B) Ascites fluid never contains the target antibody required for the diagnosis
(C) Bioreactors require completely live animals to function in the diagnostic center
(D) The ascites method causes pain and distress due to tumor and fluid growth

2004

295. Which pair accurately relates a hybridoma screening method to its core principle?
(A) ELISA - Uses a fluorescent microscope to visually detect binding
(B) Flow Cytometry - Detects fluorescently labeled antibodies bound to single cells suspended in a fluid stream
(C) Western blot - Uses a labeled secondary antibody and an enzyme-substrate reaction in a microtiter plate well
(D) PCR - Measures the exact weight of the antibody protein

2015

296. How is "class switching" occasionally manipulated in hybridoma technology?
(A) By deleting all heavy chain genes from the genome of the hybridoma cell line
(B) By strictly exposing the cells to intense UV radiation in the laboratory culture
(C) By selecting rare subclones that have undergone spontaneous isotype switching
(D) By replacing the entire B-cell genome with viral DNA sequences in the cell nucleus

2004

297. What defines an "isotype control" when using monoclonal antibodies in a diagnostic assay?
(A) An antibody that binds explicitly to the target antigen with maximum affinity
(B) A chemical that dissolves the antigen completely within the diagnostic test kit
(C) The specific antigen used to immunize the mouse during the production phase
(D) An antibody of the same isotype used to measure background non-specific binding

2012

298. In veterinary medicine, Lokivetmab is a well-known monoclonal antibody therapy used in dogs. What specific target does this mAb neutralize to treat atopic dermatitis?
(A) Interleukin-31 (IL-31)
(B) CD20 on B-cells
(C) The rabies virus glycoprotein
(D) Toll-like Receptor 4

2003

299. Which component of the immune system is primarily responsible for the rapid, highly specific recall response upon secondary exposure to an antigen, a principle closely mimicked when generating B-cells for hybridoma fusion?
(A) Neutrophils
(B) Memory B and Memory T lymphocytes
(C) Natural Killer cells
(D) Erythrocytes

2010

300. Consider the overall utility of monoclonal antibodies in modern animal genetics and health. Which application most fundamentally relies on the uniform specificity of mAbs to differentiate between highly similar infectious agents?
(A) Broad-spectrum antibiotic therapy
(B) Strain-specific antigen subtyping (serotyping)
(C) Routine measurement of total blood calcium
(D) Inducing general anesthesia

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ANSWERS

1. (B) Allele pairs separate during gametogenesis so that each gamete receives only one allele for a given trait
The Mendelian law of segregation describes the fundamental process by which alleles for a specific trait are partitioned. During the formation of gametes in livestock, the two alleles at a locus separate so that each resultant sperm or egg cell carries only one allele. This ensures that the offspring inherit a single genetic contribution from each parent.

2. (D) A testcross with a homozygous recessive horned individual
To distinguish a heterozygous individual from a homozygous dominant one, a testcross is the most definitive method. This involves breeding the animal of unknown genotype with an individual that is homozygous recessive for the trait. If any offspring display the recessive phenotype, the parent under investigation is proven to be a carrier of the recessive allele.

3. (A) To evaluate the influence of maternal effects or sex-linked inheritance on the trait
Reciprocal crosses are performed by reversing the sexes of the parents associated with specific phenotypes. This technique is essential for identifying whether a trait is inherited through sex chromosomes or influenced by the maternal cytoplasm. If the phenotypic ratios differ between the two crosses, the inheritance pattern is likely non-autosomal, indicating sex-linkage or maternal inheritance effects.

4. (C) All backcrosses are considered testcrosses
A backcross involves mating a hybrid offspring with one of its original parental genotypes. While a testcross is a specific type of backcross using a homozygous recessive parent, not all backcrosses qualify as testcrosses. Backcrossing is commonly used in livestock breeding to introgress specific desirable traits from a donor line into a superior, elite recurrent parent line.

5. (A) A dihybrid testcross yields a 1:1:1:1 phenotypic ratio under independent assortment
In a dihybrid testcross involving two independently assorting loci, the heterozygous parent produces four types of gametes in equal proportions. When these are combined with the gametes from a homozygous recessive parent, the resulting offspring exhibit a 1:1:1:1 phenotypic ratio. This expected Mendelian ratio confirms that the two genes are located on different chromosomes or are distant.

6. (D) The F_2 generation will yield a 3:1 phenotypic ratio
When F_1 individuals that are heterozygous for a single trait are intermated or self-fertilized, the resulting F_2 generation follows a predictable segregation pattern. Under conditions of complete dominance, three-quarters of the progeny will display the dominant phenotype, while one-quarter will show the recessive phenotype. This 3:1 ratio is a classic hallmark of Mendelian inheritance for monogenic traits.

7. (B) Independent alignment of non-homologous chromosomes during metaphase I of meiosis
The characteristic 9:3:3:1 phenotypic ratio in a dihybrid cross arises from the random orientation of different homologous chromosome pairs during the first meiotic division. This cellular event allows alleles of different genes to distribute into gametes independently of one another. Consequently, all possible combinations of traits are produced, provided the genes are not physically linked on the same chromosome.

8. (C) Law of Segregation - Homologous chromosomes separate during Anaphase I of meiosis
The Law of Segregation is directly explained by the physical separation of homologous chromosomes during the first stage of meiotic anaphase. Since each chromosome in a pair carries one allele for a gene, their migration to opposite poles ensures that each gamete receives only one allele. This cytological process is the biological foundation for Mendel's first law of inheritance.

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9. (D) A dihybrid testcross yields parental combinations at frequencies significantly above 50%
Independent assortment predicts that parental and recombinant phenotypic combinations will appear with equal frequency in a testcross. When the proportion of parental types significantly exceeds fifty percent, it indicates that the genes are physically linked on the same chromosome. Such linkage prevents the random distribution of alleles, causing them to be inherited together more often than expected by chance.

10. (A) Milk yield and other complex economic traits follow simple monohybrid Mendelian ratios
Complex economic traits in livestock, such as milk yield or growth rate, are polygenic and heavily influenced by environmental factors. Unlike qualitative traits that follow simple Mendelian ratios, these quantitative traits exhibit continuous variation. Understanding that these traits result from the cumulative action of many genes is essential for implementing effective selective breeding strategies in modern animal production systems.

11. (B) Recessive
A recessive allele is defined by its inability to manifest a phenotype when paired with a dominant allele in a heterozygous state. Therefore, the characteristic trait is only observable in the phenotype when an individual carries two copies of the allele, making them homozygous recessive. This pattern is common in many inherited disorders and specific qualitative traits in domestic animals.

12. (B) Both parents are heterozygous carriers of an underlying autosomal recessive allele
When phenotypically normal parents produce an affected offspring, it typically indicates that the disorder is governed by an autosomal recessive gene. In this scenario, both the sire and the dam must be asymptomatic heterozygous carriers who each passed the recessive allele to the progeny. This inheritance pattern allows rare genetic defects to persist silently within a breeding population for generations.

13. (A) Qualitative inheritance
Qualitative inheritance involves traits that are governed by one or a few major genes, resulting in discrete phenotypic categories. These traits, such as coat color or the presence of horns, do not show intermediate forms and are usually not significantly affected by environmental factors. This contrasts with quantitative inheritance, where traits show a continuous range of variation across the population.

14. (C) In codominance, both alleles independently express their gene products in the heterozygote
Codominance occurs when both alleles at a locus are fully and simultaneously expressed in a heterozygous individual. This results in a phenotype where the characteristics of both homozygotes are clearly visible, rather than being blended. In contrast, incomplete dominance produces an intermediate phenotype that appears as a mixture of the two parental traits, representing a different form of allelic interaction.

15. (B) I and III
Overdominance is a genetic phenomenon where the phenotypic value of the heterozygote exceeds that of either homozygous parent. This interaction is a significant component of hybrid vigor and is frequently observed in traits related to fitness and overall vigor. It is distinct from incomplete dominance, as it represents a superior phenotypic performance rather than a simple intermediate or blended state.

16. (C) Codominance
The roan coat color in Shorthorn cattle is a classic example of codominance because both red and white hairs are expressed individually. Neither allele masks the other, nor do they blend to create a new color like pink. Instead, the distinct gene products of both alleles are present simultaneously in the heterozygote, resulting in the characteristic mottled or roan appearance.

17. (B) It shifts the phenotypic ratio of surviving offspring from a heterozygous cross to 2:1
An autosomal recessive lethal gene causes the death of individuals who inherit two copies of the mutant allele. In a cross between two heterozygous carriers, the expected Mendelian genotypic ratio is 1:2:1. However, because the homozygous recessive class does not survive to birth or adulthood, the observed ratio among the living progeny is modified to two heterozygotes for every homozygote.

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18. (D) Presence or absence of horns (polled vs. horned) in European cattle breeds
Most major blood group systems and coat color series are governed by multiple alleles, meaning more than two allelic variants exist at a single locus within a population. In contrast, the polled versus horned condition in many European cattle breeds is typically inherited as a simple biallelic trait. In this system, the polled allele is dominant over the horned recessive allele.

19. (A) 2:1
The creeper trait in chickens is caused by a dominant allele that is lethal when homozygous. When two heterozygous creeper birds are mated, one-quarter of the embryos die, one-half are creeper, and one-quarter are normal. Among the surviving hatched chicks, the phenotypic ratio is two creepers to one normal bird, demonstrating a deviation from the standard Mendelian 3:1 ratio.

20. (C) Recombination occurs between different alleles of the same multiple allelic series
Multiple allelism refers to the existence of more than two alleles at a specific locus within a population. While a population may have many alleles, an individual diploid animal can only possess two. Importantly, because these alleles occupy the same exact position on homologous chromosomes, crossing over and recombination cannot occur between them, as they are not located at different loci.

21. (A) Lethal allele (recessive) - 2:1 ratio among the viable offspring
Recessive lethal alleles alter the standard phenotypic ratios because the homozygous recessive individuals fail to survive. In a monohybrid cross of carriers, the typical 3:1 ratio is transformed into a 2:1 ratio among the progeny that reach maturity. This observed shift is a key indicator for researchers and breeders that a lethal genetic mutation is present within the breeding stock.

22. (D) Incomplete dominance
The slate-blue color of Andalusian fowls is an intermediate phenotype resulting from a cross between black and white-splash parents. This occurs through incomplete dominance, where the dominant allele does not completely mask the recessive one, leading to a blended appearance in the heterozygote. In these cases, the phenotypic ratio in the F_2 generation perfectly matches the 1:2:1 genotypic ratio.

23. (B) The onset of lethality occurs after the animal has reached its peak reproductive age
Dominant lethal alleles are usually eliminated quickly because affected individuals die before reproducing. However, if the lethal effect is delayed until after the animal has reached sexual maturity and produced offspring, the allele can persist in the population. This late onset allows the genetic defect to be transmitted to the next generation before the carrier animal succumbs to the condition.

24. (C) Through sequential, distinct mutations of a single wild-type gene over a period of time
Multiple alleles originate from a single ancestral wild-type gene that undergoes different mutations at various points in time. Each unique mutation creates a new allelic variant of the original gene. Over many generations, these diverse alleles accumulate within the population, resulting in a multiple allelic series that can produce a wide range of phenotypic variations for a single trait.

25. (A) I, II and IV
Allelic interactions are diverse; codominant alleles both produce functional proteins, while incomplete dominance often results from a single allele being insufficient to produce the full phenotype. Lethal genes can act in either a dominant or recessive manner regarding their impact on survival. However, overdominance is often associated with increased fitness and heterosis, rather than always reducing the population's overall vigor.

26. (C) 10
For a genetic locus with multiple alleles, the number of possible diploid genotypes is calculated using the formula $\frac{n(n+1)}{2}$, where n represents the number of alleles. With four distinct alleles present in the cattle population, the calculation results in ten unique genotypes. This includes four different homozygous genotypes and six different heterozygous combinations possible among the animals in the herd.

27. (B) The masking of the phenotypic expression of one gene by a gene at a different locus
Epistasis is a form of non-allelic interaction where the genotype at one genetic locus influences or masks the expression of a gene at an entirely

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different locus. This interaction distinguishes it from dominance, which involves alleles at the same locus. Epistatic effects are responsible for many complex color patterns and physiological traits observed in various domestic animal species and breeds.

28. (B) Novel phenotypes due to non-epistatic non-allelic gene interaction between two loci
The inheritance of comb shape in poultry demonstrates how two independent gene pairs can interact to produce entirely new phenotypes. The walnut, rose, pea, and single combs result from specific combinations of dominant and recessive alleles at two loci. This interaction is non-epistatic because neither gene masks the other; instead, they combine their effects to create four distinct phenotypic classes.

29. (A) Duplicate recessive epistasis (Complementary gene action)
A 9:7 phenotypic ratio in the F_2 generation is a hallmark of duplicate recessive epistasis, also known as complementary gene action. This occurs when a dominant allele at both loci is required to produce a specific phenotype. If either locus is homozygous recessive, the biochemical pathway is blocked, resulting in the same alternative phenotype for the remaining seven out of sixteen offspring.

30. (C) The presence of a 9:3:4 phenotypic ratio in the resulting F_2 generation of the cross
Duplicate dominant epistasis is characterized by a 15:1 F_2 ratio, where a dominant allele at either of two loci produces the same phenotype. A 9:3:4 ratio, however, is the specific signature of recessive epistasis, where homozygosity for a recessive allele at one locus masks the expression of the second locus. These distinct ratios allow geneticists to identify specific gene interactions.

31. (D) Homozygosity for a recessive allele at one locus masks the expression of a second locus
Recessive epistasis occurs when the homozygous recessive state of one gene, known as the epistatic gene, prevents the phenotypic expression of another gene, called the hypostatic gene. Regardless of the alleles present at the hypostatic locus, the individual will display the phenotype associated with the epistatic recessive condition. This interaction typically results in a 9:3:4 phenotypic ratio in the F_2 generation.

32. (C) 9:3:4
In mice, the albino locus is epistatic to the agouti locus. When an individual is homozygous recessive for albinism, it cannot produce pigment, masking whatever color is dictated by the agouti gene. This interaction represents classic recessive epistasis. In a dihybrid cross of heterozygotes, the resulting progeny will segregate in a 9:3:4 ratio, representing agouti, black, and albino phenotypes respectively.

33. (B) 1:2:1
Modified dihybrid ratios like 12:3:1, 9:7, and 15:1 result from epistatic interactions between two different genes. These ratios are all variations of the standard 9:3:3:1 Mendelian distribution. In contrast, the 1:2:1 ratio is characteristic of a monohybrid cross involving incomplete dominance or codominance at a single locus. It does not represent an interaction between two separate and independent genetic loci.

34. (D) Recessive epistasis - 15:1
The mapping between epistatic types and their F_2 ratios is precise. Dominant epistasis yields 12:3:1, duplicate recessive epistasis yields 9:7, and dominant-recessive interactions yield 13:3. The 15:1 ratio is actually the result of duplicate dominant epistasis, where a single dominant allele at either locus is sufficient. Recessive epistasis is instead characterized by a 9:3:4 ratio in the resulting progeny.

35. (A) I and III
Epistasis modifies the phenotypic ratios of the F_2 generation but does not alter the underlying 9:3:3:1 Mendelian genotypic segregation. Furthermore, a 13:3 ratio occurs specifically through inhibitory gene action, where a dominant allele at one locus suppresses the expression of a dominant allele at another. The other statements regarding dominant, polymeric, and complementary gene interactions accurately describe their respective mechanisms.

36. (C) Dominant alleles at either of two independent loci result in the same phenotype
An F_2 ratio of 15:1 indicates duplicate dominant epistasis. In this scenario, two different genes control the same trait, and possessing at least one dominant allele at either locus results in the same dominant phenotype. Only the double homozygous recessive genotype, which occurs in one out of sixteen instances, produces the

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alternative recessive phenotype, resulting in the highly skewed observed ratio.

37. (A) Dominant epistasis
Dominant epistasis occurs when a dominant allele at one locus, the epistatic locus, completely masks the phenotypic effects of alleles at a second, hypostatic locus. This results in the 12:3:1 ratio because the twelve individuals carrying the dominant epistatic allele all share the same phenotype, regardless of the other gene. This interaction is common in determining coat colors in various livestock.

38. (D) Two enzymes from separate genes act sequentially in a pathway to produce a final product
Complementary gene action often reflects a multi-step biochemical pathway where each step is catalyzed by an enzyme encoded by a different gene. To produce the final end product and its associated phenotype, a functional dominant allele must be present at every locus in the pathway. If any step is blocked by a homozygous recessive genotype, the final phenotype cannot be expressed by the animal.

39. (B) Inhibitory gene action
Inhibitory gene action, also known as dominant and recessive epistasis, results in a 13:3 ratio. This occurs when a dominant allele at one locus acts as an inhibitor, preventing the expression of a dominant allele at a second locus. The dominant phenotype is only expressed when the inhibitor is absent and the second gene is dominant, which accounts for three out of sixteen offspring.

40. (C) Nucleosome
The nucleosome is the fundamental repeating unit of chromatin in eukaryotic cells. It consists of a segment of DNA, approximately 147 base pairs long, wrapped twice around a core of eight histone proteins. This structure allows for the initial level of DNA compaction within the nucleus. Multiple nucleosomes connected by linker DNA create the "beads-on-a-string" appearance visible under an electron microscope.

41. (D) Two molecules each of H2A, H2B, H3, and H4
The core of a nucleosome is a histone octamer formed by two copies each of four highly conserved histone proteins: H2A, H2B, H3, and H4. These proteins are rich in basic amino acids, allowing them to bind tightly to the negatively charged phosphate backbone of the DNA. This octameric core provides the structural framework around which the genetic material is meticulously organized and packaged.

42. (A) Constitutive heterochromatin remains condensed throughout the entire cell cycle
Chromatin is divided into euchromatin, which is lightly packed and transcriptionally active, and heterochromatin, which is highly condensed and generally silent. Constitutive heterochromatin is a permanent feature of specific chromosomal regions, such as centromeres and telomeres, across all cell types. It remains tightly coiled throughout the cell cycle, playing a vital role in maintaining structural integrity and stabilizing the animal genome.

43. (B) Expression of genes for centromere function and RNAs for heterochromatin stability
While heterochromatin is traditionally viewed as transcriptionally inert, certain regions are active. Genes required for proper centromere function and the production of small regulatory RNAs necessary for heterochromatin maintenance must be transcribed. These specific exceptions are critical for the cell to maintain the stability of its chromosomes and to ensure accurate segregation of the genetic material during the process of cell division.

44. (B) Cattle (Bos taurus)
The description of twenty-nine pairs of acrocentric autosomes and submetacentric sex chromosomes, totaling sixty chromosomes, is the defining karyotype of Bos taurus cattle. While goats also possess sixty chromosomes, their sex chromosomes are typically acrocentric. This detailed chromosomal morphology is a primary tool used by cytogeneticists to identify species and detect large-scale structural abnormalities that might affect health or fertility.

45. (A) Both A and R are true and R is the correct explanation of A
Histone H1 is known as the linker histone because it binds to the DNA outside the core nucleosome particle. By securing the DNA at the entry and exit points of the octamer, H1 stabilizes the nucleosome and facilitates the coiling of chromatin into more compact, higher-order fibers. Thus, H1 is essential for the transition

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from simple packaging to complex chromosomal structures.

46. (C) Pig - 38
Domestic pigs (Sus scrofa) possess a diploid chromosome number of thirty-eight, consisting of nineteen homologous pairs. This is lower than many other major farm animals, such as cattle and goats, which have sixty, or sheep, which have fifty-four. Knowing the correct chromosome number for each species is foundational for performing karyotypic analysis and investigating various congenital defects or reproductive failures in livestock.

47. (D) Interactions mediated by H1 histone and the N-terminal tails of core histones
The folding of the 10-nm nucleosome fiber into the 30-nm solenoid structure is driven by interactions involving the linker histone H1 and the protruding tails of the core histones. These proteins help pull adjacent nucleosomes together, creating a more tightly coiled spiral. This higher-order packaging is necessary to fit the massive amount of genomic DNA into the microscopic volume of the cell nucleus.

48. (C) The kinetochore assembles directly on the telomeric regions
During metaphase, chromosomes are at their most condensed state and consist of two sister chromatids. The centromere, which is the primary constriction, serves as the assembly site for the kinetochore, a protein complex that attaches to spindle fibers. Telomeres, conversely, are specialized structures at the ends of the chromosomes that protect them from degradation and are not involved in spindle attachment.

49. (B) It provides a mechanism for regulation of gene expression and genome stability
Organizing DNA into euchromatin and heterochromatin allows the cell to precisely control which genes are accessible for transcription. Euchromatic regions are open for gene expression, while heterochromatic regions are silenced and protected. This spatial organization is not only vital for tissue-specific gene regulation but also protects the genome from the destabilizing effects of repetitive elements and promotes accurate chromosomal segregation.

50. (D) Metacentric
A metacentric chromosome is defined by having a centromere positioned in the center, resulting in two arms of approximately equal length. When such chromosomes migrate during anaphase, they typically assume a V-shape. In many livestock species, most autosomes are acrocentric, making the presence of metacentric or submetacentric chromosomes a distinctive feature used for identifying specific pairs or detecting certain types of chromosomal translocations.

51. (A) High degree of structural compaction and DNA concentration
Heterochromatin stains intensely with DNA-specific dyes because of its exceptionally high level of coiling and compaction. This dense packaging results in a greater concentration of DNA molecules within a small volume compared to euchromatin. During the staining process, these compact regions absorb and retain more dye, making them appear as dark, prominent bands or blocks under a light or fluorescence microscope.

52. (C) The region corresponds to euchromatin and is transcriptionally permissive
Histone acetylation is a major epigenetic modification that reduces the positive charge on histone proteins, weakening their interaction with negatively charged DNA. This results in a more relaxed and open chromatin structure known as euchromatin. Consequently, regions with high levels of acetylation are typically associated with active transcription, as the DNA becomes accessible to RNA polymerase and various other regulatory transcription factors.

53. (A) Presence of a dominant Y chromosome carrying the SRY gene
In mammalian farm animals, sex is determined by the presence or absence of the Y chromosome. The SRY gene, located on the Y chromosome, acts as a master switch that triggers the development of male gonads from the undifferentiated embryonic tissue. Without the Y chromosome and the SRY gene, the embryo defaults to female development, regardless of the number of X chromosomes present.

54. (D) To ensure dosage compensation of X-linked genes between females and males
Females have two X chromosomes, while males have only one. To prevent females from producing

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twice the amount of X-linked gene products, one X chromosome is randomly inactivated in each female somatic cell. This process, known as dosage compensation or Lyonization, balances the expression of X-linked genes between the sexes, ensuring that both males and females have functionally equivalent levels of these proteins.

55. (A) P-3, Q-4, R-1, S-2
Animals utilize various mechanisms for sex determination; bovines use the XY system common to mammals, while poultry utilize the ZZ/ZW system where females are heterogametic. In contrast, honeybees rely on haplodiploidy, where males develop from unfertilized eggs. Some reptiles, like crocodiles, exhibit temperature-dependent sex determination, where the incubation temperature of the eggs during a critical period dictates the sex of the hatchlings.

56. (C) An inactivated, condensed X chromosome in female somatic cells of mammals
Sex chromatin, or a Barr body, is the cytological manifestation of the inactivated X chromosome in female mammals. It appears as a small, darkly staining mass located against the inner nuclear membrane of somatic cells during interphase. The number of Barr bodies is always one less than the total number of X chromosomes, providing a simple method for screening chromosomal sex and detecting aneuploidies.

57. (D) It encodes a transcription factor initiating male sex differentiation
The SRY gene is the primary sex-determining gene in mammals. It encodes a protein that functions as a transcription factor, which binds to specific DNA sequences and activates a cascade of other genes necessary for testis development. Once the testes form, they produce hormones like testosterone and anti-Mullerian hormone, which further drive the anatomical and physiological differentiation of the male reproductive system.

58. (A) In marsupials, X-inactivation randomly targets either the maternal or paternal X
In placental mammals, X-inactivation is a random process occurring early in embryonic development, where either the maternal or paternal X chromosome is silenced. However, marsupials represent a notable exception where X-inactivation is non-random and specifically targets the paternally derived X chromosome. Once established, this inactive state is stable and inherited by all clonal daughter cells throughout the animal's lifetime.

59. (B) A mosaic or tortoiseshell coat pattern
The tortoiseshell pattern in female cats is a direct phenotypic result of random X-chromosome inactivation. In a cat heterozygous for orange and black alleles, different patches of skin cells will have either the orange-bearing X or the black-bearing X active. This creates a mosaic of colored fur. Since this depends on having two X chromosomes, this characteristic pattern is almost exclusively found in females.

60. (B) In birds, the female is the heterogametic sex (ZW) and the male is homogametic
In the ZZ/ZW sex determination system used by birds, the female is the heterogametic sex, possessing two different sex chromosomes (ZW), while the male is homogametic (ZZ). This is the inverse of the mammalian XX/XY system. This difference is crucial in poultry genetics, as it alters the inheritance patterns of sex-linked traits and the phenotypic consequences of various sex chromosome abnormalities.

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61. (A) XXY - Sterile male (Klinefelter-like syndrome)
In mammals, the Y chromosome is strongly male-determining due to the presence of the SRY gene. An individual with an XXY chromosomal complement will develop as a male phenotype because of the Y chromosome, but the presence of the extra X chromosome typically leads to infertility and abnormal gonad development. This condition is analogous to Klinefelter syndrome in humans and has been documented in various livestock.

62. (C) XIST long non-coding RNA
X-chromosome inactivation is initiated by the expression of the XIST gene, which produces a long non-coding RNA. This RNA molecule does not leave the nucleus; instead, it "coats" the chromosome from which it is transcribed, triggering a series of epigenetic changes that lead to heavy condensation and silencing. XIST is only expressed from the future inactive X, making it the master regulator of dosage compensation.

63. (D) Zero
Barr bodies represent inactivated X chromosomes and are only present when an individual has more than one X chromosome. In a normal

male horse (stallion), the karyotype is 64,XY, meaning there is only a single X chromosome which remains active to provide essential gene products. Consequently, no Barr bodies will be observed in the nuclei of his somatic cells, unlike a normal mare.

64. (C) They escape inactivation to ensure dosage of genes shared with the Y chromosome
Pseudoautosomal regions (PARs) are segments of the X and Y chromosomes that share homologous genes and can undergo recombination during meiosis. Because these genes are present in two copies in both males and females, they do not require dosage compensation. Therefore, the PARs on the inactive X chromosome escape the silencing process and remain transcriptionally active, ensuring balanced gene expression between the two sexes.

65. (B) II, I, III, IV
X-chromosome inactivation follows a precise molecular sequence. First, the XIST gene is upregulated on the chromosome destined to be silenced. The resulting XIST RNA then coats that specific chromosome. This coating recruits proteins that cause chromatin modifications, such as DNA methylation and histone deacetylation. Finally, the chromosome condenses into a dense, inactive Barr body, completing the silencing process for the cell.

66. (D) Dominance in sex-influenced traits varies by sex; sex-limited traits are mono-sex
Sex-influenced traits are governed by autosomal genes where the dominance of an allele depends on the sex of the animal, often due to hormonal differences. Sex-limited traits are also controlled by autosomal genes, but their phenotypic expression is completely restricted to only one sex. Understanding these differences is vital for breeders when selecting for traits like milk production or certain morphological features.

67. (A) Sex-influenced
The inheritance of horns in many sheep breeds is a classic example of a sex-influenced trait. The allele for horns behaves as a dominant trait in males, meaning only one copy is needed for horns to develop. In females, however, the same allele behaves as a recessive trait, requiring two copies for the phenotypic expression of horns. This creates distinct sexual dimorphism for the trait.

68. (C) Milk yield in dairy cattle is a classic example of a sex-limited trait
Milk yield is a sex-limited trait because its phenotypic expression is restricted to females, even though the genes controlling it are located on autosomes and inherited from both parents. Bulls carry and transmit these genes to their daughters, which is why sire selection is critical for improving dairy production. The expression is limited by the anatomical and hormonal requirements for lactation found only in females.

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69. (A) A son possessing an XXY karyotype due to non-disjunction in the paternal parent
Normally, sons receive their only X chromosome from their mother. However, if paternal non-disjunction occurs during meiosis, a sperm cell might carry both an X and a Y chromosome. If this sperm fertilizes a normal egg, the resulting son will have an XXY karyotype. In this rare case, the son has inherited an X chromosome from his father, violating the typical pattern of criss-cross inheritance.

70. (D) Females (ZW), because they possess only one Z chromosome
In poultry, females are the heterogametous sex (ZW), while males are homogametic (ZZ). For an X-linked (or Z-linked) recessive lethal gene, females will be affected by a single copy because they lack a second Z chromosome to carry a dominant normal allele. This makes females more vulnerable to sex-linked recessive defects, as the lethal phenotype is immediately unmasked in the heterogametic sex.

71. (B) Sex-limited inheritance
When a trait is visible in only one sex despite being present in the genotypes of both, it is categorized as sex-limited inheritance. The genes for these traits are typically autosomal, but their expression is entirely dependent on the internal hormonal environment or anatomical structures unique to a specific sex. Examples include cock-feathering in poultry and various reproductive traits in mammals that are critical for breeding programs.

72. (C) Horns in sheep - Sex-linked dominant
The presence of horns in sheep is not a sex-linked trait; rather, it is a sex-influenced trait governed by autosomal genes. The dominance of the horned allele shifts based on the sex of the animal, appearing dominant in males and

recessive in females. In contrast, traits like milk production are sex-limited, and conditions like haemophilia A are truly sex-linked, residing on the X chromosome.

73. (D) Different circulating levels of androgens and estrogens between the two sexes
The differential expression of sex-influenced traits is primarily driven by the endocrine system. Variations in the concentration of sex hormones, such as testosterone and estrogen, alter how specific autosomal genes are expressed or how their products function. These hormonal triggers cause an allele to act as dominant in one sex while appearing recessive in the other, leading to the observed sexual dimorphism in many traits.

74. (A) 25%
In this sex-influenced scenario, females only display horns if they are homozygous for the horn allele (HH). When two heterozygotes (Hh) are crossed, Mendelian segregation results in 25% HH, 50% Hh, and 25% hh genotypes. Among the female offspring, only the 25% that are HH will be horned, as the H allele behaves recessively in females and will not be expressed in heterozygotes.

75. (A) II, IV, III, I
To validate a sex-linked recessive trait, a researcher first notes the trait's higher frequency in males. Next, the absence of father-to-son transmission is confirmed, as males only pass their Y chromosome to sons. Criss-cross inheritance is then observed, where affected males produce carrier daughters. Finally, reciprocal crosses are conducted to provide definitive proof that the inheritance pattern depends on the sex of the affected parent.

76. (B) The trait is passed from an affected father to all of his sons
Holandric inheritance refers to genes located on the non-homologous region of the Y chromosome. Since only males possess a Y chromosome, these traits are transmitted exclusively from fathers to all of their biological sons. Such traits never appear in females and never skip a generation in the male line, providing a very clear and distinct pedigree pattern that is easily identified in livestock populations.

77. (A) All colts will be normal, but all fillies will be affected
In X-linked dominant inheritance, an affected stallion passes his only X chromosome, which carries the dominant trait, to all of his daughters (fillies). Consequently, every daughter will be affected. To his sons (colts), he passes only his Y chromosome. Since the sons must receive their X chromosome from their normal mother, they will all be unaffected by the dominant trait in this cross.

78. (C) The trait exhibits sex-influenced penetrance
If a trait is controlled by an autosomal locus but is expressed more frequently or intensely in one sex, it demonstrates sex-influenced penetrance. This means the genetic background and hormonal environment of the animal affect whether the genotype actually results in the observable phenotype. This differs from sex-limited traits, which are never expressed in one of the sexes regardless of the genotype or environment.

79. (D) Law of Independent Assortment
Genetic linkage occurs when genes are located close to each other on the same chromosome, causing them to be inherited together as a unit. This directly contradicts Mendel's Law of Independent Assortment, which states that alleles of different genes segregate independently. Because linked genes do not distribute randomly during meiosis, the phenotypic ratios in offspring deviate from the standard expected Mendelian proportions for unlinked genes.

80. (B) P-4, Q-1, R-2, S-3
Linkage terminology describes the arrangement of alleles on homologous chromosomes. The cis or coupling phase refers to having both dominant alleles on one chromosome. The trans or repulsion phase describes having one dominant and one recessive allele on each chromosome. A linkage group comprises all genes on a single chromosome, while the map unit measures the distance between genes based on the frequency of recombination events.

81. (B) The physical distance between the two loci located on the homologous chromosome
The frequency of recombinant offspring in a test cross is primarily determined by the physical distance between the two linked genes. The farther apart two genes are on a chromosome, the more likely a crossover event will occur between

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them during meiosis. This relationship allows geneticists to use recombination frequencies to calculate map distances and determine the relative linear order of genes along the chromosome.

82. (D) Linkage groups strictly correspond to the haploid number of the chromosomes
A linkage group consists of all the genes that are physically located on the same chromosome and therefore tend to be inherited together. Consequently, the total number of linkage groups in a species is equal to its haploid chromosome number (n). For example, in cattle with a diploid number of 60, there are 30 distinct linkage groups representing each of the unique chromosomes in the genome.

83. (A) The other parent must be homozygous dominant for all three loci
In a three-point test cross, the heterozygous individual must be crossed with a parent that is homozygous recessive for all three genes. This ensures that the phenotypes of the offspring directly reveal the gametes produced by the heterozygous parent. This method allows for the simultaneous measurement of distances between three genes and the detection of double crossover events, providing a more accurate genetic map.

84. (C) Double crossovers occurring between the two genes located on the same chromosome
When mapping two genes that are far apart, double crossovers can occur between them. Because a second crossover effectively "undoes" the first, the resulting gametes appear as parental rather than recombinant. This lead to an underestimation of the actual genetic distance. Using intermediate markers in a three-point cross helps detect these double crossovers, providing a more precise measurement of the total map distance.

85. (A) 20 Centimorgans
Map distance is defined as the percentage of recombinant offspring produced in a test cross. Since twenty percent of the progeny in this example exhibit recombinant phenotypes, the genetic distance between the two linked loci is exactly twenty centimorgans. This measurement provides a relative estimate of how far apart the genes are on the chromosome, based on the frequency of crossing over events observed.

86. (D) Repulsion phase
The repulsion phase, or trans configuration, occurs when an individual inherits a dominant allele for one gene and a recessive allele for another from each parent. In this case, the linked alleles on one chromosome are 'Ab' and on the other are 'aB'. This arrangement affects which combinations of traits will be most common in the offspring and is a crucial consideration when analyzing linkage in genetic crosses.

87. (B) Only parental gametes are formed
Complete linkage occurs when two genes are located so close together on a chromosome that no crossing over ever happens between them. As a result, the alleles at these loci are always inherited together in their original parental combinations. In this extreme scenario, the heterozygous parent only produces two types of gametes, and the recombination frequency remains at zero percent, regardless of the number of offspring.

88. (C) $B - A - C$
To determine gene order, the distances between all pairs must be compared. Here, the largest distance is fifteen units between B and C, which means these two genes are the furthest apart. Gene A must be located between them because the distance from B to A is five units and from A to C is ten units, which correctly sum to the total $B - C$ distance of fifteen units.

89. (D) Recombination frequency - 50%
The maximum observable recombination frequency between any two genes is fifty percent. At this level, the genes appear to assort independently, even if they are physically located on the same chromosome. This limit exists because multiple crossover events effectively randomize the alleles, making the frequency of recombinant gametes indistinguishable from the frequency expected if the genes were on entirely different chromosomes or very far apart.

90. (A) Both A and R are true and R is the correct explanation of A
Genetic maps are based on recombination frequencies, but the biological rate of crossing over is not uniform throughout the genome. Certain areas, known as hotspots, have high crossover rates, while others, like centromeres, are coldspots. Because of this variation, a centimorgan does not correspond to a fixed

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number of DNA base pairs, making genetic and physical maps slightly different in their relative proportions.

91. (B) Chiasma interference
Chiasma interference is the biological phenomenon where a crossover event in one region of a chromosome reduces the likelihood of a second crossover occurring nearby. This typically results in fewer observed double crossover offspring than would be mathematically expected by chance alone. Geneticists calculate the degree of interference to understand how crossover events are spatially distributed and how they influence the overall recombination patterns.

92. (B) Formation of the synaptonemal complex and subsequent homologous recombination
Crossing over is the physical exchange of genetic material between non-sister chromatids of homologous chromosomes. This process occurs during the pachytene stage of prophase I and is mediated by the synaptonemal complex, which holds the homologs in tight alignment. The molecular mechanism involves the breakage and reciprocal rejoining of DNA strands, resulting in new combinations of alleles that significantly increase the genetic diversity of gametes.

93. (A) Observed double crossovers divided by the Expected double crossover frequency
The coefficient of coincidence is a numerical value that compares the number of double crossovers actually observed in a cross to the number expected based on the product of independent probabilities. A value less than one indicates that interference is occurring, while a value of one means the crossover events are independent. This metric is foundational for quantifying how much one crossover event inhibits another nearby.

94. (C) Crossing over occurs between sister chromatids to generate genetic diversity
Crossing over must occur between non-sister chromatids of homologous chromosomes to produce new allelic combinations and genetic variation. While exchanges can happen between identical sister chromatids, these events do not result in any genetic changes since the sequences are exactly the same. Chiasmata are the visible cross-shaped structures that represent the physical sites where non-sister chromatid exchange has successfully taken place during the meiotic process.

95. (A) Both A and R are true and R is the correct explanation of A
Interference is calculated as one minus the coefficient of coincidence. If the coefficient of coincidence is exactly one, it means that the number of observed double crossovers matches the expected number, resulting in an interference value of zero. This indicates that the occurrence of one crossover had no effect on the likelihood of a second crossover in the adjacent chromosomal segment.

96. (C) One crossover inhibits a second crossover in the adjacent chromosomal region
An interference value of 1.0, or 100 percent, signifies that no double crossovers were observed in the progeny of a cross. This biological state occurs when the formation of a single chiasma completely prevents any other crossing over events from happening in the neighboring parts of the chromosome. In this situation, the coefficient of coincidence is zero, as the observed frequency of double crossovers is non-existent.

97. (B) Creighton and McClintock's study using morphologically distinct chromosomes
In 1931, Harriet Creighton and Barbara McClintock used maize with cytologically distinct chromosomal features, such as knobs and translocated segments, to prove that genetic recombination involves a physical swap of chromosome parts. By tracking these physical markers alongside specific genetic traits, they demonstrated that offspring with recombinant phenotypes also possessed chromosomes with new combinations of physical features, providing the first definitive evidence for the mechanism of crossing over.

98. (C) It has no effect on the observed recombination frequency between the markers
Recombination frequency is only measured by counting crossover events that occur specifically in the interval between the two genetic markers under investigation. Any crossing over that happens outside of this designated region will not alter the combination of alleles at those two loci. Therefore, while such external crossovers contribute to overall genetic diversity, they are irrelevant for calculating the map distance between those two specific markers.

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99. (A) Multiple crossovers randomize alleles, mimicking independent assortment outcomes
Even if genes are located very far apart on the same chromosome, the observable recombination frequency will never exceed fifty percent. This is because multiple crossover events, such as double or triple crossovers, can occur. These complex exchanges effectively randomize the distribution of alleles between the two loci, resulting in a gametic proportion that is identical to what would be produced if the genes were assorting independently on different chromosomes.

100. (A) I and II
Crossing over is a precise biological event that takes place during the pachytene stage of prophase I in meiosis. It involves the physical exchange of chromosomal segments between non-sister chromatids of homologous pairs, which shuffles existing alleles into new combinations. However, it does not create new alleles; allelic diversity is the result of mutations, while crossing over simply reorganizes the alleles already present in the genome.

101. (A) Expected DCO Frequency = Product of individual single crossover frequencies
In genetic mapping, the expected frequency of double crossovers is mathematically predicted by multiplying the frequencies of the two single crossovers in the adjacent intervals. This calculation assumes that each crossover event occurs independently of the other. Comparing this theoretical expectation to the actual observed number of double crossovers allows researchers to calculate the coefficient of coincidence and determine the strength of chromosomal interference in that region.

102. (D) A crossover in one region increases crossover likelihood in adjacent regions
Negative interference occurs when the observed number of double crossovers is higher than the mathematically expected frequency, resulting in an interference value less than zero. This suggests a biological phenomenon where the occurrence of one crossover event actually promotes or facilitates the formation of a second crossover in a nearby region. While rare in most eukaryotes, negative interference is sometimes observed in certain specific genetic contexts or organisms.

103. (B) Crossover probability is generally uniform across the length of the chromosome
The construction of a linear genetic map based on recombination frequencies relies on the assumption that crossing over can occur with equal probability at any point along the chromosome. If this probability is relatively uniform, the frequency of recombination will be directly proportional to the physical distance between genes. However, the existence of hotspots and coldspots means that genetic maps provide a relative rather than an absolute physical scale.

104. (C) Synaptonemal complex
The synaptonemal complex is a specialized protein structure that forms between homologous chromosomes during the prophase of the first meiotic division. It acts as a scaffold that holds the homologs in precise longitudinal alignment, which is absolutely necessary for the process of synapsis and subsequent crossing over. Without this complex, the efficient and accurate exchange of genetic material between non-sister chromatids would not be possible.

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105. (A) P-4, Q-1, R-3, S-2
Mutagens are categorized by their specific molecular actions on DNA. Ultraviolet light causes pyrimidine dimers, while 5-bromouracil is a base analog that induces transition mutations during replication. Nitrous acid acts by deaminating nitrogenous bases, leading to mispairing. Ethidium bromide is an intercalating agent that wedges into the DNA helix, typically resulting in frameshift mutations. Understanding these mechanisms is essential for studying both spontaneous and induced mutations.

106. (A) Gamma rays
Gamma rays are a form of high-energy ionizing radiation that acts as a potent physical mutagen. They possess enough energy to penetrate tissues and cause direct damage to the DNA molecule, such as double-strand breaks and chromosomal rearrangements. In agricultural research, ionizing radiation has been used to artificially induce mutations in order to generate new genetic variation for study or to develop novel traits in plants and animals.

107. (B) Base analogs are incorporated into DNA during replication and cause mispairing
Base analogs are chemical mutagens that structurally resemble the standard nitrogenous

bases found in DNA. Because of this similarity, they are mistakenly incorporated into the growing DNA strand by polymerase enzymes during the synthesis phase. Once integrated, these analogs often undergo tautomeric shifts that cause them to pair with the wrong complementary base, ultimately leading to permanent transition mutations after subsequent rounds of replication.

108. (D) Formation of cyclobutane pyrimidine dimers
Ionizing radiation, such as X-rays and gamma rays, primarily causes damage through the production of reactive oxygen species and the breakage of the DNA phosphodiester backbone. This leads to complex mutations like deletions and translocations. In contrast, the formation of cyclobutane pyrimidine dimers is a characteristic effect of non-ionizing ultraviolet radiation, which lacks the energy to ionize atoms but can cause covalent bonds between adjacent pyrimidines.

109. (A) Frameshift mutations via the addition or deletion of a single base pair in DNA
Intercalating agents are flat, hydrophobic molecules that can slide between the stacked base pairs of the DNA double helix. This insertion distorts the helical structure, which often causes the DNA polymerase to accidentally add or skip a base pair during replication. The resulting insertion or deletion shifts the genetic reading frame, typically leading to a completely non-functional protein and having a significant phenotypic impact.

110. (C) Mutations are random events occurring throughout the entire chromosomal genome
The primary challenge in using artificial mutagens is that they cause random changes throughout the genome rather than targeting specific genes. Most induced mutations are either neutral or deleterious, and the likelihood of producing a beneficial trait is extremely low. Consequently, breeders must screen vast numbers of individuals to identify any useful mutants, making artificial transmutation a highly unpredictable and resource-intensive approach in livestock improvement programs.

111. (D) Alkylating agent - Ethyl methanesulfonate (EMS)
Ethyl methanesulfonate is a well-known alkylating agent that is frequently used in genetic research to induce mutations. It works by adding alkyl groups to the nitrogenous bases of DNA, particularly guanine. This modification alters the base-pairing properties of the guanine, leading to G-C to A-T transition mutations. Other examples include base analogs like 5-bromouracil and intercalating agents such as proflavine or acridine orange.

112. (C) It lacks energy to eject electrons but excites them to cause covalent bonds
Ultraviolet radiation is classified as non-ionizing because it does not possess sufficient energy to remove electrons from atoms. However, it does have enough energy to excite electrons to higher energy states. This excitation can lead to the formation of abnormal covalent bonds between adjacent pyrimidine bases, particularly thymine, on the same DNA strand. These dimers distort the DNA structure and can lead to mutations during repair or replication.

113. (B) It replaces thymine during DNA replication and mispairs with guanine in the enol
5-bromouracil is a base analog of thymine that can exist in two different tautomeric forms. In its common keto form, it pairs correctly with adenine. However, it frequently shifts into an enol form that pairs with guanine. If this mispairing occurs during DNA replication, it results in a transition mutation where an A-T base pair is eventually replaced by a G-C base pair in the daughter DNA.

114. (D) Induced mutations in livestock are the primary source of modern genetic gains
While induced mutations have been successfully used in crop improvement, they are not the primary source of genetic gains in livestock. Modern animal breeding relies mostly on selecting existing natural variation using advanced statistical and genomic tools. The high costs, long generation intervals, and ethical concerns associated with large-scale mutagenesis and screening in animals make this approach far less practical than traditional selection or targeted gene editing technologies.

115. (A) I, II and IV
Point mutations are classified by their effects on the DNA and protein sequences. Transitions involve substituting one purine for another, while transversions replace a pyrimidine with a purine. Missense mutations change the codon so it specifies a different amino acid. Frameshift mutations, however, occur whenever the number

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of inserted or deleted bases is not a multiple of three, as this disrupts the triplet reading frame.

116. (C) By using reverse genetics to determine gene function via knockout phenotypes
Artificial mutation is a vital tool in fundamental research for discovering the function of specific genes. By inducing mutations and observing the resulting phenotypic changes, researchers can infer the normal role of the mutated gene. This reverse genetics approach, including the creation of "knockout" models, has provided profound insights into the molecular basis of development, physiology, and disease in both laboratory and domestic animal species.

117. (A) Nonsense mutation
A nonsense mutation is a type of point mutation that changes a codon specifying an amino acid into one of the three stop codons. This results in the premature termination of protein synthesis during translation, leading to a truncated and usually non-functional protein. Because of their severe impact on protein structure and function, nonsense mutations often cause significant phenotypic defects or inherited genetic disorders in animals.

118. (D) The proportion of individuals with a genotype exhibiting the expected phenotype
Penetrance is a population-level concept that describes the statistical probability that a specific genotype will result in its associated phenotype. If everyone with the genotype shows the trait, it is called complete penetrance. If some individuals remain phenotypically normal despite carrying the gene, it is called incomplete penetrance. This phenomenon is often caused by the influence of modifier genes or environmental factors on the expression of the primary gene.

119. (B) 85%
Penetrance is calculated by dividing the number of individuals who express the expected phenotype by the total number of individuals who possess the corresponding genotype. In this specific case, eighty-five out of one hundred cows show the dominant trait. Therefore, the penetrance is eighty-five percent. This indicates that fifteen percent of the carrier animals do not express the trait, likely due to genetic or environmental suppression.

120. (C) Penetrance is all-or-none, whereas expressivity measures the phenotypic severity
Penetrance and expressivity are related but distinct concepts in genetics. Penetrance is a binary measure of whether a genotype is expressed at all in an individual. Expressivity, on the other hand, describes the range or intensity of the phenotype among those individuals who do show the trait. For example, a disease may be fully penetrant but show variable expressivity, with some animals being mildly affected and others severely.

121. (D) Multiple alleles determining the ABO blood groups
Pleiotropy occurs when a single gene influences multiple, seemingly unrelated phenotypic traits. The creeper mutation in chickens and the merle gene in dogs are classic examples because they affect both physical appearance and survival or health. Multiple alleles at a single locus, like those for the ABO blood groups, represent a different concept where many variants exist for one trait, rather than one gene affecting many traits.

122. (A) They suppress or enhance the phenotypic expression of a gene at a separate locus
Modifier genes are genes that have a secondary effect on the phenotype controlled by a major gene at a different locus. They do not produce a trait on their own but instead alter the expression of the primary gene by making its effect more or less intense. Modifier genes are often responsible for the variable expressivity and incomplete penetrance observed in many qualitative and quantitative traits in livestock.

123. (B) Variable expressivity
When individuals with the same genotype show different degrees of the same phenotype, it is referred to as variable expressivity. In this cattle herd, all animals carry the gene for spotting, but the actual amount of white fur varies from small patches to nearly the whole body. This variation is typically caused by the interaction of the primary spotting gene with various modifier genes and different environmental influences during development.

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124. (B) Incomplete penetrance - A genotype failing to produce the expected phenotype
Incomplete penetrance is the correct term for the situation where an individual carries a specific

allele but does not manifest the corresponding trait. This concept is vital for understanding why some animals can be silent carriers of dominant disorders. In contrast, pleiotropy involves one gene affecting many traits, and polygenic inheritance involves many genes affecting one trait. Expressivity refers to the severity of a trait, not its presence or absence.

125. (B) I, II and III
The phenotypic manifestation of a genotype is frequently modulated by several factors. Environmental conditions like temperature or nutrition can trigger or suppress gene expression. Additionally, some traits only appear as an animal ages or are influenced by the presence of other modifier genes in the individual's genetic background. While ploidy level affects overall gene dosage, it is generally not considered a primary modulator of penetrance and expressivity.

126. (C) Every animal shows the disease, but symptoms range from mild to severe levels
100 percent penetrance means that every single individual with the specific genotype will express the associated phenotype to some degree. However, variable expressivity indicates that the clinical manifestation of the disease will not be uniform across the flock. Some sheep might only show very minor signs of the disorder, while others could be severely incapacitated, reflecting the diverse ways the gene can express itself within different individuals.

127. (D) It allows a regulatory change to coordinately alter multiple processes in a cell
Pleiotropy can be an evolutionary advantage because it allows a single genetic or regulatory change to simultaneously affect several biological pathways. This can lead to rapid and coordinated adaptations to environmental challenges. For example, a mutation that improves a core metabolic enzyme might enhance both growth rate and immune efficiency. However, pleiotropy also means that selection for one desirable trait might inadvertently lead to negative side effects in other systems.

128. (C) A single gene encodes a protein that functions in diverse biochemical pathways
The molecular basis of pleiotropy often lies in the versatile nature of proteins. Many genes encode enzymes or structural proteins that are utilized in multiple different tissues or biochemical processes. For instance, a protein involved in connective tissue formation will affect the heart, skeleton, and eyes. When such a gene is mutated, it inevitably produces a wide array of phenotypic defects across all the systems where that specific protein is required.

129. (B) Modifier genes acting epistatically
Even if a dominant gene has 100 percent penetrance, its phenotypic expression can be completely masked by the action of modifier genes at other loci. This is a form of epistasis where the modifier gene prevents the primary gene from manifesting its trait. Such interactions can complicate pedigree analysis and breeding programs, as an animal may carry a dominant allele for a desirable or undesirable trait without showing any visible signs of it.

130. (D) Pleiotropy
A mutation in a single gene that results in multiple phenotypic defects across different organ systems, such as the skeleton and heart, is a clear example of pleiotropy. Since the gene product, like fibrillin, is a common structural component of many tissues, its absence or dysfunction has widespread consequences. This single-gene effect on multiple traits is distinct from polygenic inheritance, where many genes combine to influence a single phenotypic character.

131. (A) Polygenic traits exhibit continuous variation and have heavy environmental influence
Polygenic traits, also known as quantitative traits, are influenced by many genes at different loci, each having a small additive effect. This leads to a continuous range of phenotypes rather than discrete categories. Furthermore, these traits are highly susceptible to environmental factors like nutrition and management. In contrast, qualitative Mendelian traits are usually determined by one or two genes and show distinct, easily recognizable phenotypic classes.

132. (C) Herman Nilsson-Ehle
The Multiple Factor Hypothesis was established by Herman Nilsson-Ehle in 1909 through his experiments on the inheritance of kernel color in wheat. He demonstrated that the continuous variation in color was actually due to the cumulative effect of several independent genes following Mendelian principles. This work provided the first evidence that quantitative traits are governed by the same genetic laws

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as qualitative traits, laying the foundation for modern quantitative genetics.

133. (A) Each contributing allele adds a small, cumulative amount to the phenotypic value
Additive gene action is the primary mechanism underlying quantitative inheritance. In this model, each "contributing" or "plus" allele at multiple loci adds a specific, incremental amount to the overall phenotypic value of the trait. The total phenotype of the animal is simply the sum of these small individual effects. This additive component is highly predictable and is the most important part of genetic variance for livestock selection and improvement.

134. (D) The presence or absence of the BLAD disorder in cattle
Bovine Leukocyte Adhesion Deficiency is a qualitative trait because it is caused by a single recessive mutation that results in two discrete classes: affected and normal. In contrast, traits like milk yield, weaning weight, and fleece weight are classic polygenic traits. They are influenced by hundreds of genes and show a continuous distribution across the population, making them much more complex to manage and improve through selective breeding.

135. (B) II and V
Transgressive segregation occurs when F_2 offspring show phenotypes more extreme than either parent. This is not due to new mutations but results from the recombination of existing additive alleles from both parents into a single individual. It perfectly follows Mendelian segregation of multiple loci. Incorrectly assuming it involves new mutations or violates Mendelian laws ignores the fundamental additive nature of polygenic inheritance that allows for these novel, extreme phenotypic combinations.

136. (C) $\left(\frac{1}{4}\right)^3$ or $\frac{1}{64}$
For a polygenic trait controlled by n unlinked loci, the probability of an F_2 individual inheriting the extreme phenotype (all dominant or all recessive alleles) is $\frac{1}{4}$ raised to the power of n. In this trihybrid example where n equals three, the frequency is one out of sixty-four. As the number of genes increases, the probability of obtaining these extreme phenotypes decreases exponentially, leading to the characteristic normal distribution of the population.

137. (D) Normal (Gaussian) distribution
Quantitative traits in a large, outbred population typically follow a normal or Gaussian distribution, represented by a bell-shaped curve. This pattern occurs because most individuals possess an average number of contributing alleles, while very few possess either very many or very few. The combined effects of many additive genes and environmental variation naturally lead to this smooth, symmetrical distribution of phenotypes around the population mean.

138. (A) Recombination of complementary sets of additive plus (+) and minus (-) alleles
Transgressive segregation arises because original parental lines may each carry a different set of positive and negative alleles for a polygenic trait. Through crossing and subsequent recombination in the F_2 generation, some offspring can inherit all the positive alleles from both parents. These individuals will exhibit a phenotype that exceeds the range seen in either of the original parental generations, demonstrating the power of recombination in generating new phenotypic extremes.

139. (B) Heritability (Narrow-sense) - The ratio of additive to phenotypic variance
Narrow-sense heritability is one of the most critical parameters in quantitative genetics. it measures the proportion of total phenotypic variation that is due specifically to additive genetic effects. This is the only portion of genetic variation that can be predictably transmitted from parents to offspring. A high narrow-sense heritability indicates that selective breeding will be highly effective for improving that particular trait within the livestock population.

140. (A) Both A and R are true and R is the correct explanation of A
Although quantitative traits show continuous variation, the underlying genes, called polygenes, still follow Mendel's laws of segregation and independent assortment. The appearance of a smooth distribution rather than discrete classes is simply due to the large number of genes involved and the blurring effect of the environment. Therefore, Mendelian principles are the fundamental basis for understanding and calculating the inheritance of both simple and complex traits.

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141. (A) It blurs genotypic classes, creating a smooth, continuous phenotypic distribution
Environmental variance acts on the small phenotypic differences produced by individual polygenes. It adds a layer of non-genetic variation that causes individuals with slightly different genotypes to overlap phenotypically. This "blurring" effect transforms what would be discrete, closely-spaced genotypic classes into a perfectly smooth and continuous bell curve. Without environmental influence, a polygenic trait would show many small, distinct steps rather than a truly continuous range.

142. (C) Narrow-sense heritability
Narrow-sense heritability is the most important metric for a breeder because it determines how much of the parental superiority will actually be passed to the next generation. If heritability is high, selecting the best animals as parents will lead to rapid genetic progress. If it is low, environmental factors dominate, and traditional selection will be slow. In such cases, improved management or crossbreeding might be more effective strategies for improvement.

143. (B) The F_1 will be uniform and possess a phenotype intermediate between the parents
When two true-breeding lines with extreme phenotypes for a polygenic trait are crossed, the F_1 generation is genetically identical, being heterozygous at all contributing loci. In a uniform environment, this results in an F_1 population that is phenotypically uniform and intermediate between the two parents. The continuous variation and extreme phenotypes characteristic of quantitative inheritance only reappear in the F_2 generation through the process of genetic segregation and recombination.

144. (C) The transmission of traits governed by genetic material found in organelles
Cytoplasmic inheritance, also known as extranuclear inheritance, refers to the transmission of traits through DNA located in organelles like mitochondria and chloroplasts. Unlike nuclear DNA, which follows Mendelian patterns, organellar DNA is usually inherited from only one parent, typically the mother. This type of inheritance is essential for understanding certain metabolic disorders and for tracing the maternal evolutionary history of different livestock breeds and species.

145. (A) Both A and R are true and R is the correct explanation of A
In most domestic animals, mitochondrial DNA is strictly maternally inherited. This occurs because the large egg cell contains thousands of mitochondria, while the much smaller sperm cell contributes very few. Furthermore, any paternal mitochondria that do enter the egg during fertilization are usually identified and destroyed by the zygote's cellular machinery. This ensures that the offspring's mitochondrial genome is an exact copy of the mother's.

146. (D) Maternal effects arise from the mother's nuclear genotype, not her mitochondrial DNA
A maternal effect is not true cytoplasmic inheritance; it occurs when the offspring's phenotype is determined by the mother's nuclear genes through her influence on the egg or the uterine environment. In contrast, cytoplasmic inheritance involves the transmission of actual organellar DNA from mother to offspring. This is a crucial distinction, as maternal effects do not persist beyond one generation, whereas cytoplasmic traits are transmitted through the maternal line indefinitely.

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147. (A) It contains multiple large introns and extensive non-coding regions
The mammalian mitochondrial genome is highly efficient and compact. Unlike nuclear DNA, it typically lacks introns and has very little non-coding space between its genes. It exists as a circular molecule and encodes essential components for oxidative phosphorylation and its own translation machinery. However, it still depends on the nuclear genome for many necessary proteins, including DNA and RNA polymerases, illustrating a complex inter-genomic dependency.

148. (C) Because it lacks recombination and mutates at a predictable rate for tracing
Mitochondrial DNA is a powerful tool for evolutionary studies because it is inherited as a single, non-recombining unit through the maternal line. This means that changes in its sequence only occur through mutation. These mutations accumulate over time at a relatively steady rate, acting as a molecular clock. By comparing mtDNA sequences, researchers can reconstruct maternal lineages and identify the geographic origins and domestication patterns of various livestock species.

149. (A) Maternal effect
Shell coiling in Limnaea peregra is a classic example of a maternal effect. The direction of coiling in an individual is not determined by its own genotype, but by the nuclear genotype of its mother. This happens because the mother's gene products in the egg cytoplasm dictate the orientation of the first mitotic divisions of the embryo. This results in a one-generation delay in the expression of the phenotype based on the nuclear genes.

150. (D) The trait must be present in the mitochondrial genome of the dam
For a trait to be passed on via true cytoplasmic inheritance, the genetic information must reside in the organellar DNA of the mother. Because mitochondria are inherited through the egg's cytoplasm, any mutation or variant in the mother's mitochondrial genome will be transmitted to all of her offspring. The father's genotype and nuclear DNA play no role in the transmission of these specific extranuclear traits to the next generation.

151. (B) The F_1 offspring will exhibit the phenotype of the maternal parent in each cross
In traits governed by cytoplasmic inheritance, reciprocal crosses yield different results. The offspring always mirror the phenotype of their mother because they inherit her mitochondrial or chloroplast DNA. This maternal inheritance pattern is a key diagnostic feature used by geneticists to distinguish extranuclear traits from standard autosomal or sex-linked Mendelian traits, where the offspring's phenotype would either be identical or follow specific sex-linked ratios in reciprocal crosses.

152. (C) Chloroplast - Leaf variegation in Mirabilis jalapa
Leaf variegation in Mirabilis jalapa was the first documented case of extranuclear inheritance, discovered by Carl Correns. He showed that the color of the offspring's leaves was determined entirely by the chloroplasts inherited from the female parent's egg. While mitochondria are the primary organelles for cytoplasmic inheritance in animals, this chloroplast example remains the foundational model for understanding how organellar genomes can dictate phenotypic traits independently of the nucleus.

153. (D) Homoplasmy means identical mtDNA; heteroplasmy means a mixture of mutant and normal
Homoplasmy occurs when all the mitochondria within a cell or individual carry the same genetic sequence. Heteroplasmy is a condition where two or more different mitochondrial genotypes, such as normal and mutant versions, coexist within the same cell. The level of heteroplasmy can vary significantly and is a major factor in determining the severity and onset of mitochondrial diseases, as well as the variability of cytoplasmic traits in animal populations.

154. (A) It maps evolutionary matrilines and helps preserve endangered animal populations
Mitochondrial DNA analysis is invaluable in conservation genetics for identifying distinct maternal lineages within a species. By tracing these matrilines, scientists can assess the genetic diversity of endangered populations and avoid inbreeding. This information is critical for designing effective breeding programs and management strategies aimed at preserving the unique genetic heritage and long-term viability of rare or threatened domestic and wild animal species.

155. (A) P-4, Q-3, R-1, S-2
Non-Mendelian inheritance patterns are diverse. Genomic imprinting involves differential allele expression based on the parent of origin. Maternal effects occur when the offspring's phenotype reflects the mother's nuclear genotype. Maternal inheritance refers to the transmission of organellar DNA through the egg. Heteroplasmy describes the presence of different organellar genomes in a single cell. Understanding these distinctions is crucial for correctly interpreting complex inheritance patterns in livestock and other animal species.

156. (A) The random segregation and ratio of mutant mitochondria passed into each oocyte
When a heteroplasmic cow produces eggs, the mitochondria are distributed randomly among the oocytes. This process, known as vegetative segregation, can lead to some eggs having a high proportion of mutant mitochondria and others having very few. Consequently, the calves produced will have different levels of heteroplasmy, which directly determines the severity of any mitochondrial disease symptoms they might exhibit throughout their lives.

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157. (A) Deletion
A chromosomal deletion involves the physical loss of a segment of a chromosome. This results in the removal of multiple genes, which is often severely deleterious. While heterozygotes for a small deletion may survive, homozygous deletions are almost always lethal because they result in the complete absence of essential genes. Deletions are a significant cause of congenital defects and early embryonic loss in many domestic animal breeding programs.

158. (C) Cattle; Robertsonian translocation
The 1/29 translocation is a well-known Robertsonian translocation in cattle, where chromosomes 1 and 29 fuse at their centromeres to form a single submetacentric chromosome. This reduces the total chromosome number from sixty to fifty-nine in heterozygous carriers. Although these animals are phenotypically normal, they often show reduced fertility due to the production of unbalanced gametes, making it a major concern in the commercial cattle industry.

159. (D) Centric fusion of non-homologous acrocentric chromosomes forms one bi-armed pair
A Robertsonian translocation, or centric fusion, occurs when the long arms of two non-homologous acrocentric chromosomes fuse at the centromere. This results in a single large, bi-armed (metacentric or submetacentric) chromosome and the loss of the tiny short arms. This rearrangement reduces the total chromosome count by one but keeps most genetic material intact. It is a common structural variation in various livestock species and can significantly impact their reproductive performance.

160. (C) An increase in the overall amount of genetic material in the nucleus
Chromosomal inversions are balanced rearrangements where a segment of DNA is flipped 180 degrees. Unlike deletions or duplications, inversions do not add or remove any genetic material. However, they can cause significant problems during meiosis, such as the suppression of crossing over and the formation of unbalanced gametes in heterozygotes. This often leads to reduced fertility and increased rates of embryonic mortality in the affected breeding animals.

161. (B) A pericentric inversion includes the centromere; a paracentric inversion does not
The distinction between pericentric and paracentric inversions is based on whether the centromere is included in the inverted segment. Pericentric inversions involve both arms of the chromosome and include the centromere, which can change the relative arm lengths. Paracentric inversions occur within a single chromosome arm and do not involve the centromere. Both types can interfere with normal meiotic pairing and recombination, leading to the production of non-viable gametes.

162. (D) Semi-sterility due to adjacent segregation producing unbalanced gamete cells
In pigs, heterozygous reciprocal translocations cause semi-sterility. During meiosis, the involved chromosomes form a quadrivalent configuration. Depending on how they segregate, many gametes will end up with either missing or extra chromosomal segments. These unbalanced gametes lead to non-viable embryos, which significantly reduces the average litter size. Identifying and culling carriers of such translocations is a common practice to maintain high reproductive efficiency in commercial swine herds.

163. (A) Reciprocal Translocation - Cross-shaped (quadrivalent) configuration
During the prophase of meiosis I, chromosomes heterozygous for a reciprocal translocation must form a cross-shaped quadrivalent to allow all homologous segments to pair. This complex structure is a definitive cytogenetic marker for translocations. In contrast, deletions and duplications form loops, and inversions form characteristic inversion loops. These unique meiotic configurations are essential for identifying the specific type of structural aberration present in the genome of a breeding animal.

164. (C) Surplus genetic material can mutate freely to acquire new metabolic functions
Gene duplication provides an important mechanism for evolutionary innovation. When a gene is duplicated, one copy can maintain its original essential function while the second copy is free to accumulate mutations. Over time, these mutations can lead to the development of new, specialized functions that benefit the organism. Many large gene families in livestock, such as those involved in the immune system and

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metabolism, originated through this process of duplication and divergence.

165. (A) 59
A normal bull has a diploid chromosome number of sixty. A Robertsonian translocation involves the fusion of two individual acrocentric chromosomes into one large bi-armed chromosome. In a heterozygous carrier, this results in the loss of one physical chromosome from the count, although almost all the genetic material is preserved. Therefore, the bull will possess fifty-nine chromosomes in his somatic cells, a diagnostic feature used in karyotype screening.

166. (D) Unequal crossing over between misaligned homologous sequences
Deletions and duplications are frequently caused by unequal crossing over during meiosis. This occurs when homologous chromosomes misalign, often due to the presence of repetitive DNA sequences. When recombination happens between these misaligned regions, one resulting chromatid will have a deletion and the other will have a duplication. This mechanism is responsible for many spontaneous copy number variations that can impact health, fertility, and production traits in farm animals.

167. (B) Paracentric inversion
If a crossover event occurs within a paracentric inversion loop, it results in the formation of a dicentric bridge and an acentric fragment during anaphase I. The dicentric bridge is pulled between the two poles and eventually breaks, while the acentric fragment is lost because it lacks a centromere. This diagnostic meiotic error produces highly unbalanced gametes that are typically non-viable, leading to reduced fertility in animals carrying these specific inversions.

168. (C) Normal recessive alleles are expressed because the dominant allele was deleted
Pseudodominance is a genetic phenomenon that occurs when a recessive allele is phenotypically expressed because the corresponding dominant allele on the homologous chromosome has been deleted. Although the individual only has one copy of the recessive gene, it appears dominant because there is no other allele to mask it. This can be used by geneticists to map the physical location of genes by correlating deletions with the unexpected expression of recessive traits.

169. (D) Inversion
An inversion is a "balanced" structural aberration because it only involves a 180-degree reversal of a chromosomal segment. No DNA is added or removed from the genome; only the linear order and physical position of the genes within that segment are altered. While inversions do not typically cause phenotypic defects in the carrier, they can have significant impacts on fertility and recombination patterns by interfering with normal meiotic chromosome pairing.

170. (A) Aneuploid
Aneuploidy is a condition where an individual has a chromosome number that is not an exact multiple of the haploid set. This usually involves the addition or loss of one or a few individual chromosomes, such as in trisomy or monosomy. Aneuploidy often leads to severe developmental defects and reduced fertility because it disrupts the normal balance of gene expression, which is critical for the proper functioning of complex physiological systems.

171. (B) Non-disjunction of homologous chromosomes or sister chromatids during meiosis
The primary cause of aneuploidy is non-disjunction, which is the failure of chromosomes to separate properly during meiosis. If non-disjunction occurs in meiosis I, a pair of homologous chromosomes goes to one pole. If it occurs in meiosis II, sister chromatids fail to separate. Both errors result in gametes with either an extra chromosome or a missing one, which leads to aneuploid offspring following fertilization with a normal gamete.

172. (B) Polyploidy generally results in early embryonic lethality in mammals and birds
Polyploidy, the possession of three or more complete sets of chromosomes, is extremely rare in domestic mammals and birds because it is almost always lethal during early embryonic development. While common and often beneficial in plants, the complex dosage-sensitive systems in animals cannot tolerate such massive chromosomal imbalances. Consequently, polyploid embryos in livestock typically fail to implant or result in early spontaneous abortions, making it a significant factor in reproductive failure.

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173. (A) Triploidy ($3n$)
Aneuploidy involves the gain or loss of individual chromosomes, resulting in formulas like $2n+1$ or $2n-1$. Triploidy, however, is a form of polyploidy where the individual possesses three entire sets of chromosomes ($3n$). While both are numerical abnormalities, polyploidy affects the entire genome uniformly, whereas aneuploidy creates a specific imbalance for only one or a few chromosome pairs, leading to different biological and phenotypic consequences in the affected organism.

174. (C) 63, XO (Monosomy X)
In horses, a condition analogous to human Turner syndrome is caused by X-chromosome monosomy. Affected mares have sixty-three chromosomes instead of the normal sixty-four and lack a second sex chromosome. Phenotypically, these mares are typically small in stature and suffer from ovarian hypoplasia, which leads to permanent infertility. This is one of the most common and economically significant chromosomal abnormalities identified in the equine industry.

175. (D) Autosomal monosomy unmasks lethals and disrupts dosage, unlike sex chromosomes
Autosomal monosomy is almost always lethal because it results in a fifty percent reduction in the dosage of many essential genes and unmasks any recessive lethal mutations present on the remaining chromosome. Sex chromosome monosomies, like XO, are sometimes viable because mammals already have mechanisms for X-chromosome dosage compensation and the Y chromosome contains relatively few essential genes for basic survival. This allows some sex-chromosome aneuploids to survive, albeit often with significant fertility issues.

176. (C) Tetrasomy - $2n+2$
Numerical chromosomal abnormalities are described by specific formulas based on the diploid number ($2n$). Trisomy is $2n+1$, representing an extra chromosome. Monosomy is $2n-1$, representing a missing chromosome. Tetrasomy is $2n+2$, indicating the presence of an extra pair of homologous chromosomes. Monoploidy and triploidy refer to changes in the number of entire sets of chromosomes, rather than individual ones, and are classified as types of euploidy or polyploidy.

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177. (B) Autopolyploidy involves one species; allopolyploidy involves two or more species
The fundamental distinction between autopolyploidy and allopolyploidy lies in the origin of the extra chromosome sets. Autopolyploidy occurs when multiple chromosome sets are derived from a single species, often through a failure of cell division. Allopolyploidy results from the hybridization of two different species followed by a doubling of the chromosomes. This creates an organism with a complete diploid set from each parent species, which can sometimes lead to fertile new species.

178. (D) They are sterile, redirecting energy from reproduction to somatic growth rates
Triploid fish are highly valued in aquaculture because they are functionally sterile. Since they do not invest energy into developing gonads or producing gametes, they can channel more nutrients into muscle development and somatic growth. This leads to faster growth rates and larger final sizes. Additionally, triploidy prevents escaped farmed fish from interbreeding with wild populations, which is an important environmental safeguard in many aquaculture operations.

179. (A) Using shocks after fertilization to prevent extrusion of the second polar body
Artificial triploidy in fish is often induced by applying a physical shock, such as heat, cold, or high pressure, shortly after fertilization. This shock prevents the egg from extruding the second polar body, which contains a haploid set of maternal chromosomes. When the egg nucleus then fuses with the sperm nucleus, the resulting zygote ends up with three sets of chromosomes (two maternal and one paternal), effectively creating a triploid individual for aquaculture production.

180. (A) P-4, Q-2, R-3, S-1
Geneticists use specific terms to categorize different types of numerical chromosome abnormalities. $2n+1$ is trisomy, $2n-1$ is monosomy, and $2n-2$ is nullisomy, all of which are forms of aneuploidy. $3n$ represents triploidy, which is a type of polyploidy involving three complete sets of chromosomes. Correctly identifying these karyotypic formulas is essential for diagnosing the underlying cause of various developmental and reproductive disorders in livestock and other animals.

181. (A) Mitotic non-disjunction during the early embryonic cleavage divisions
Mosaicism occurs when an individual has two or more genetically different cell lines. This is typically caused by a non-disjunction event during mitosis in the early stages of embryonic development. As the embryo grows, all cells descending from the original mutated cell will carry the aneuploidy, while others remain normal. The resulting phenotypic effect depends on which tissues are affected and what proportion of the cells are aneuploid.

182. (D) Mismatched chromosomes cannot pair in Prophase I, causing gametogenesis failure
A mule is the offspring of a male donkey and a female horse. Because these two species have different chromosome numbers and structures, their chromosomes cannot pair correctly during the prophase of meiosis I in the hybrid mule. This failure of synapsis leads to the production of non-functional gametes and results in the mule's characteristic sterility. This is a classic example of how chromosomal differences act as a barrier to interspecific reproduction.

183. (B) Recessive mutation in the CD18 gene, impairing neutrophil immune function
Bovine Leukocyte Adhesion Deficiency is an autosomal recessive disorder caused by a point mutation in the CD18 gene. This mutation prevents the normal expression of adhesion molecules on the surface of neutrophils, which are essential for these immune cells to migrate to the site of an infection. Affected calves suffer from recurrent bacterial infections and typically die at a young age, making it a critical genetic defect to monitor in Holstein populations.

184. (C) Embryonic mortality at 40 days of gestation due to impaired pyrimidine synthesis
DUMPS is an autosomal recessive disorder in Holstein cattle caused by a deficiency in the enzyme uridine monophosphate synthase. This enzyme is crucial for the de novo synthesis of pyrimidine nucleotides. In homozygous recessive embryos, the inability to produce DNA and RNA precursors leads to early embryonic death, usually around day forty of pregnancy. This often results in a significant economic loss due to reduced reproductive efficiency in the herd.

185. (D) It leads to lethal ammonia toxicity in newborn calves due to a urea cycle defect
Bovine citrullinemia is an autosomal recessive metabolic disorder caused by a mutation in the argininosuccinate synthetase gene. This enzyme is a critical component of the urea cycle, which converts toxic ammonia into urea. In affected calves, ammonia rapidly accumulates in the blood and brain, leading to severe neurological symptoms and death within a few days of birth. Genetic testing of breeding stock is used to prevent the birth of affected calves.

186. (D) Calves homozygous for the mutation are usually healthy and physically robust
Complex Vertebral Malformation is a severe autosomal recessive genetic disorder in Holstein cattle. It is caused by a mutation in the SLC35A3 gene, which affects normal skeletal development. Affected individuals suffer from malformed vertebrae and other physical deformities, and they are almost never healthy or robust. In fact, many CVM-affected calves are either aborted during gestation or are stillborn, leading to significant reproductive losses for dairy farmers.

187. (B) Blood exchange between opposite-sex twins leading to female fetus sterility
Freemartinism is a developmental abnormality in cattle that occurs when a female is born co-twin to a male. Because the placental blood vessels of the twins often fuse, hormones and cells from the male twin enter the circulation of the female. These male factors, particularly anti-Mullerian hormone, inhibit the normal development of the female reproductive tract, resulting in a sterile heifer with masculinized internal organs. This condition is a major cause of infertility in female twins.

188. (B) DUMPS - UMPS gene
Each of these genetic disorders is caused by a specific mutation in a particular gene. DUMPS is caused by a defect in the UMPS gene, which is essential for nucleotide synthesis. Citrullinemia is linked to the ASS gene, and BLAD is caused by mutations in the CD18 gene. Correctly identifying these gene-disorder associations is fundamental for developing molecular diagnostic tests that allow breeders to identify carrier animals and eliminate these deleterious alleles from their livestock populations.

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189. (A) The two digits of the hoof are fused into a single digit
Bovine syndactyly, commonly known as "mule foot," is characterized by the fusion of the two functional digits of the bovine hoof into a single, solid digit. This condition is inherited as an autosomal recessive trait with variable expressivity, meaning the severity and the number of limbs affected can differ between individuals. Affected cattle often suffer from lameness and have reduced production value, making it a trait that breeders actively select against.

190. (A) Both A and R are true and R is the correct explanation of A
DUMPS is a serious economic concern in dairy cattle because it causes early embryonic death, which can be mistaken for poor conception rates. Since heterozygous carriers are phenotypically normal and highly productive, the allele can easily spread through a population if not monitored. Therefore, genetic testing of elite AI sires is essential to ensure they are not carriers, thereby preventing the significant financial losses associated with high rates of early pregnancy failure.

191. (D) BLAD
If calves are dying from persistent infections and show a massive increase in white blood cell counts, Bovine Leukocyte Adhesion Deficiency is the primary suspect. The high leukocyte count occurs because the body produces more white blood cells to fight the infection, but they are unable to leave the bloodstream and enter the tissues to kill the bacteria. This clinical profile is characteristic of the immune dysfunction caused by the CD18 gene mutation.

192. (C) Identifying leukocyte chimerism (XX and XX cells) in the female twin's blood
The standard cytogenetic diagnosis of Freemartinism involves analyzing the chromosomes of the female twin's white blood cells. Because of the blood exchange between the twins in utero, the female will possess both her own XX cells and her male twin's XY cells. This condition, known as leukocyte chimerism, is a definitive indicator of Freemartinism. Detecting the presence of the Y chromosome in the female's blood provides a reliable and cost-effective screening method.

193. (B) Genotyping prospective AI sires and strictly excluding the carrier animals
The most effective way to eliminate recessive disorders like BLAD and DUMPS from a population is through molecular screening and selective breeding. By identifying and excluding heterozygous carrier sires from artificial insemination programs, breeders can quickly reduce the frequency of the deleterious alleles. This proactive approach prevents the birth of affected animals and ensures the long-term genetic health and economic viability of the livestock industry.

194. (D) Autosomal recessive with variable expressivity
Bovine syndactyly is inherited as an autosomal recessive trait. While two copies of the mutant allele are required for the condition to appear, the actual phenotype can vary significantly among affected animals. Some might have only one fused hoof, while others have multiple, and the degree of fusion can also differ. This variable expressivity is likely due to the influence of other genes and environmental factors during fetal limb development.

195. (A) Both A and R are true and R is the correct explanation of A
Freemartinism is a permanent developmental condition that renders the heifer sterile. The male hormones transferred from the co-twin through the shared placental blood supply interfere with the normal formation of the female's internal reproductive organs, such as the uterus and ovaries. Because these structural defects cannot be reversed, Freemartin heifers are unsuitable for breeding and are typically culled or used only for meat production in the livestock industry.

196. (C) To generate a pattern of light and dark bands for chromosome identification
G-banding is a primary cytogenetic technique that uses Giemsa stain to produce a series of reproducible light and dark bands along the length of a chromosome. These bands provide a unique "barcode" that allows cytogeneticists to identify specific homologous pairs and detect structural abnormalities like deletions, duplications, or translocations. This high-resolution mapping is essential for characterizing the karyotypes of various livestock species and investigating inherited genetic disorders.

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197. (A) Quinacrine mustard, viewed under a fluorescence microscope
Q-banding is a fluorescent staining technique that uses quinacrine mustard or similar dyes to produce a banding pattern on chromosomes. When viewed under ultraviolet light, different regions of the chromosome fluoresce with varying intensities, creating a distinct pattern of bright and dull bands. These Q-bands are particularly useful for identifying heteromorphic regions and for analyzing sex chromosomes, providing a complementary approach to standard G-banding methods in animal cytogenetics.

198. (C) C-banding stains constitutive heterochromatin located near the centromeres
C-banding is a specialized staining technique designed to highlight constitutive heterochromatin. This type of chromatin is highly condensed, gene-poor, and typically located around the centromeres of chromosomes. C-banding allows researchers to visualize these structural regions and detect variations or polymorphisms in heterochromatin levels between individuals. This is particularly important for studying chromosome stability and for distinguishing between homologous pairs that might otherwise appear similar using other banding methods.

199. (B) It can detect microdeletions that are invisible in standard G-banded karyotypes
Fluorescent In Situ Hybridization is a powerful molecular cytogenetic tool that uses fluorescently labeled DNA probes to target specific genomic sequences. It can identify the presence or absence of specific genes and map their exact location on chromosomes. However, its resolution for detecting very small microdeletions is limited by the size of the probe and the resolution of the microscope. While it surpasses standard banding in many ways, it is still part of a broader suite of diagnostic tools.

200. (C) Regions rich in A-T base pairs that are condensed and relatively gene-poor
The dark G-bands formed during Giemsa staining correspond to regions of the chromosome that are rich in adenine and thymine (A-T) base pairs. These areas are generally more condensed and contain fewer actively expressed genes than the light-staining regions. This predictable pattern of A-T rich and G-C rich regions provides the basis for the characteristic banding patterns used to identify chromosomes and to precisely locate structural genetic rearrangements in various livestock species.

201. (D) Sister Chromatid Exchange (SCE) - Utilizes BrdU incorporation to detect DNA damage and repair
The Sister Chromatid Exchange assay is a sensitive cytogenetic method used to measure the rate of DNA exchange between sister chromatids. It involves growing cells in the presence of 5-bromodeoxyuridine (BrdU), which is incorporated into the new DNA strands. A high frequency of exchanges is an indicator of DNA damage and increased genomic instability. This assay is frequently used in veterinary toxicology to evaluate the potential mutagenic effects of chemicals and environmental pollutants.

202. (A) R-banding produces a reverse pattern; dark bands correspond to gene-dense regions
R-banding, or reverse banding, produces a pattern that is essentially the opposite of G-banding. In R-banding, the gene-rich, G-C rich regions of the chromosome stain darkly, while the A-T rich regions appear light. This technique is particularly useful for studying the ends of chromosomes (telomeres), which are often gene-dense but may stain poorly with other methods. Using both G and R-banding together provides a more complete and detailed analysis of chromosomal structure.

203. (B) Sister Chromatid Exchange (SCE) assay
To evaluate the genotoxic effects of a chemical like a pesticide, the Sister Chromatid Exchange assay is the most appropriate cytogenetic tool. By measuring the frequency of reciprocal exchanges between sister chromatids, researchers can assess the degree of DNA damage and repair activity within the animal's cells. This provides a direct measure of how the mutagen affects genomic stability, making it an essential assay for environmental monitoring and livestock health assessment.

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204. (B) Using a fluorescent DNA or RNA probe to bind to its complementary target sequence
The fundamental principle of FISH is the hybridization of a fluorescently labeled nucleic acid probe to its complementary DNA sequence within a chromosome. By allowing the probe to find and bind to its specific target, researchers can visually pinpoint the location of a gene or

DNA segment under a fluorescence microscope. This technique bridges molecular biology and cytogenetics, enabling highly precise physical mapping of the genome and the detection of specific chromosomal rearrangements.

205. (A) P-3, Q-1, R-4, S-2
Cytogenetic techniques are tailored for specific goals: G-banding is the standard for pair identification, while FISH is used for high-precision gene mapping. C-banding is specialized for visualizing centromeric heterochromatin polymorphisms, and the SCE assay is the primary tool for assessing DNA damage and genotoxicity. Together, these methods provide a comprehensive toolkit for analyzing the chromosomal health, genetic diversity, and evolutionary relationships of various domestic animal species and breeds.

206. (C) Cells are grown in BrdU, leading to differential substitution in the chromatids
In the SCE assay, cells go through two rounds of replication in a medium containing BrdU. After the first round, each DNA molecule has one original strand and one BrdU-labeled strand. After the second round, one sister chromatid has two BrdU strands, while the other still has only one. This difference in BrdU content causes the chromatids to stain with different intensities, allowing any exchanges between them to be easily visualized.

207. (D) Microdeletions smaller than 3-5 Megabases
While standard G-banding is excellent for detecting large chromosomal changes, its resolution is limited to about 3-5 megabases. FISH can detect much smaller alterations, including microdeletions that remove only a single gene or a few neighboring genes. This makes FISH an essential tool for diagnosing specific genetic syndromes and microdeletion disorders in livestock that might otherwise be missed during a routine karyotypic analysis with standard light microscopy.

208. (C) Ultraviolet (UV) fluorescence microscope
Q-banding relies on the use of fluorescent dyes like quinacrine, which only emit light when excited by specific wavelengths of ultraviolet radiation. Therefore, an ultraviolet fluorescence microscope is absolutely necessary to visualize the resulting banding pattern. This equipment allows researchers to see the distinct bright and dull fluorescent bands that characterize each chromosome pair, providing a high-contrast method for identifying chromosomes and detecting various types of structural and numerical abnormalities.

209. (B) Immunoglobulins (Antibodies)
Immunoglobulins, commonly known as antibodies, are the core components of the humoral immune response. Produced by B-lymphocytes, these proteins circulate in the blood and other body fluids, where they recognize and bind specifically to foreign antigens. This binding initiates several mechanisms for neutralizing or destroying pathogens, such as bacteria and viruses. Antibodies are essential for protecting livestock from infectious diseases and form the basis for most vaccines and diagnostic tests.

210. (D) Humoral immunity relies on B-cells; cell-mediated immunity relies on T-cells
Adaptive immunity in animals is divided into two main branches: humoral and cell-mediated. Humoral immunity is mediated by antibodies produced by B-cells and primarily targets pathogens in the extracellular fluids. Cell-mediated immunity, conversely, is driven by T-cells and is essential for destroying intracellular pathogens and infected host cells. Both systems work together in a highly coordinated manner to provide comprehensive protection against a wide array of infectious agents in domestic animals.

211. (A) Two identical heavy chains and two light chains held by disulfide bonds
A typical IgG molecule, the most common type of antibody, is a Y-shaped structure composed of four polypeptide chains. It consists of two identical heavy chains and two identical light chains, which are linked together by covalent disulfide bonds. This arrangement creates two identical antigen-binding sites at the tips of the "Y" and a constant tail region that mediates effector functions. This basic structure is highly conserved across all mammalian species.

212. (C) Direct, enzymatic degradation of viral DNA
Antibodies protect the host through various effector mechanisms such as neutralizing toxins, opsonizing pathogens for phagocytosis, and activating the complement system. However, antibodies themselves do not possess enzymatic activity and cannot directly degrade the DNA of a virus or bacterium. Instead, they act as "tags" that identify and target pathogens for

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destruction by other components of the immune system, such as specialized phagocytic cells or the complement protein complex.

213. (A) IgA
Immunoglobulin A is the primary antibody class found in mucosal secretions, including colostrum, milk, saliva, and tears. It plays a vital role in protecting the mucosal surfaces of the respiratory, gastrointestinal, and urogenital tracts from infection. In livestock, the high concentration of IgA in colostrum provides essential passive immunity to the newborn calf, protecting its gut from pathogens during the critical early stages of life before its own immune system matures.

214. (D) It is the first isotype secreted in a primary response, existing as a pentamer
Immunoglobulin M is the first antibody isotype produced by the immune system in response to a new antigen. It typically exists as a large pentameric molecule, consisting of five monomeric units held together by a J-chain. Because of its ten antigen-binding sites, IgM is exceptionally efficient at agglutinating pathogens and activating the complement system. This makes it a critical early-stage defense mechanism in the bovine immune response against bacterial and viral infections.

215. (A) I, II and IV
Immunoglobulins serve diverse functions: IgG is the most abundant in plasma, IgE mediates anti-parasitic responses, and the variable regions form the antigen-binding site. A key difference in ruminants is that they do not transfer passive immunity through the placenta; instead, calves must ingest colostrum shortly after birth to acquire maternal antibodies. Understanding these species-specific immune mechanisms is fundamental for managing the health and disease resistance of domestic livestock populations.

216. (C) Ungulates lack transplacental IgG; calves rely on colostrum ingestion at birth
In ungulates like cattle, horses, and pigs, the structure of the placenta prevents the transfer of large immunoglobulin molecules from the mother to the fetus. Consequently, these animals are born without any passive immunity. They must ingest colostrum, which is rich in maternal antibodies, within the first few hours of life. The neonatal gut is specially adapted to absorb these intact antibodies into the bloodstream, providing the calf with essential protection against environmental pathogens.

217. (D) IgE - Mediation of Type I hypersensitivity (allergic) reactions
Each immunoglobulin class has a specialized role in the immune system. IgE is primarily involved in mediating allergic reactions and protecting against parasitic helminth infections. When IgE binds to mast cells or basophils, it triggers the release of inflammatory mediators like histamine. In contrast, IgG is the dominant antibody in blood and provides long-term immunity, while IgA is the key protective antibody in mucosal secretions and milk across various livestock species.

218. (A) The constant region of the heavy chain (Fc fragment)
The constant region of the heavy chain, also known as the Fc fragment, determines the isotype or class of the antibody and dictates its biological effector functions. While the variable regions bind to the antigen, the Fc region interacts with other parts of the immune system, such as complement proteins and Fc receptors on macrophages or natural killer cells. This allows the antibody to trigger the appropriate response needed to eliminate the specific type of pathogen encountered.

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219. (B) Cytotoxic T lymphocytes (CD8+)
Cell-mediated immunity is specifically designed to eliminate intracellular pathogens that are "hidden" from circulating antibodies. CD8+ cytotoxic T lymphocytes play a central role in this process by recognizing and destroying infected host cells. This is essential for controlling chronic infections in cattle, such as Brucellosis. These T-cells identify foreign peptides presented on the surface of the infected cell and release toxins that trigger programmed cell death, thereby halting the spread of the pathogen.

220. (B) Two Fab fragments and one Fc fragment are produced
Papain is a proteolytic enzyme that cleaves the IgG molecule at a specific point above the disulfide bonds that hold the heavy chains together. This enzymatic digestion results in three separate pieces: two identical Fab fragments, which contain the antigen-binding sites, and one Fc fragment, which represents the

tail of the antibody. These fragments have been used extensively in research to study the distinct structural and functional properties of different parts of the immunoglobulin molecule.

221. (A) Affinity
Affinity is a measure of the strength of the non-covalent bond between a single antigen-binding site on an antibody and its corresponding epitope on the antigen. It is determined by how well the shapes and chemical properties of the two molecules complement each other. High-affinity antibodies bind more tightly and are generally more effective at neutralizing pathogens, making the selection for high-affinity responses a key goal of successful vaccination and immune development.

222. (C) Affinity is attraction; avidity is total binding strength to a multivalent antigen
While affinity measures the strength of a single interaction, avidity represents the combined strength of all the binding sites on an antibody molecule with a multivalent antigen. For example, an IgM molecule may have a low affinity at each of its ten binding sites, but its overall avidity is very high because multiple sites can bind simultaneously. This high avidity makes IgM extremely effective at clumping pathogens together for easier removal by the immune system.

223. (D) Cross-reactivity
Cross-reactivity occurs when an antibody that was produced against one specific antigen also binds to a different antigen that possesses a structurally similar epitope. This phenomenon is common in nature and can be either beneficial, providing broad protection against related pathogens, or problematic, leading to false-positive results in diagnostic tests. Understanding the extent of cross-reactivity is essential for designing accurate serological assays and for investigating the underlying causes of various autoimmune conditions in livestock.

224. (C) Cross-reactivity
In many immunodiagnostic assays, a false-positive result can occur if the antibodies used in the test cross-react with other proteins or antigens that are not the actual target. This reduces the specificity of the assay, making it difficult to accurately diagnose a specific infection. Researchers must carefully select and validate antibodies to minimize cross-reactivity, ensuring that the diagnostic test is highly specific to the pathogen of interest within the complex environment of an animal's serum or tissue.

225. (A) I, III, IV and V
Most modern diagnostic techniques, including ELISA, Western blotting, the fluorescent antibody technique, and agar gel immunodiffusion, rely on the high specificity of antigen-antibody interactions. These assays allow veterinarians to detect and quantify either the pathogen itself or the animal's immune response to it. In contrast, PCR is a molecular technique that targets and amplifies specific DNA sequences, making it a powerful tool for direct pathogen detection rather than measuring an immunological reaction.

226. (D) A secondary anti-bovine immunoglobulin antibody
In an indirect ELISA for Brucellosis, the cow's serum is added to a plate coated with Brucella antigen. Any specific antibodies present will bind to the antigen. Then, a secondary antibody, which is conjugated to an enzyme and specifically recognizes bovine immunoglobulins, is added. When a substrate is provided, the enzyme catalyzes a color change that is proportional to the amount of Brucella antibody in the original sample, allowing for a sensitive and quantitative diagnosis.

227. (A) Agar Gel Immunodiffusion (AGID)
Agar Gel Immunodiffusion is a simple but effective serological test where antigen and antibody are placed in separate wells in a semi-solid agar medium. As they diffuse toward each other, they eventually meet in an area of optimal concentration. If the antibody is specific to the antigen, they will form an insoluble immune complex that appears as a visible white line of precipitation. This technique is commonly used for diagnosing several important livestock diseases, such as equine infectious anemia.

228. (C) To separate proteins by weight, followed by identification using antibodies
Western blotting is a sophisticated technique that combines protein electrophoresis with immunological detection. First, proteins from a sample are separated by size on a gel. Then, they are transferred to a membrane and probed with specific antibodies. This allows researchers to not only detect the presence of a specific

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viral or bacterial protein but also to confirm its correct molecular weight. It is often used as a confirmatory test for many infectious diseases in domestic animals.

229. (A) It has 10 identical binding sites, granting it exceedingly high avidity
IgM is a highly effective early-stage antibody because of its multivalent pentameric structure. Even if each individual binding site has a relatively low affinity, the presence of ten sites allows the molecule to bind to multiple epitopes on a single pathogen or to cross-link multiple pathogens together. This massive increase in total binding strength, or avidity, allows IgM to efficiently clear bacteria and viruses from the bloodstream long before the higher-affinity IgG response is fully developed.

230. (D) Non-covalent forces such as hydrogen bonds and van der Waals interactions
The binding of an antigen's epitope to an antibody's paratope is mediated entirely by non-covalent interactions. These include hydrogen bonds, electrostatic forces, van der Waals interactions, and hydrophobic effects. Because these bonds are individually weak, the overall strength of the interaction depends on a very high degree of physical and chemical complementarity between the two molecules. This "lock and key" fit is the molecular basis for the extreme specificity and high affinity of the immune response.

231. (B) Clumping of particulate antigens cross-linked by specific antibody molecules
Agglutination is an immunological reaction that occurs when antibodies cross-link particulate antigens, such as whole bacteria or red blood cells, into large, visible aggregates. This process is widely used in veterinary medicine for blood typing and for the rapid diagnosis of various infectious diseases. Because each antibody molecule has at least two binding sites, it can simultaneously bind to epitopes on different particles, causing them to clump together and eventually settle out of suspension.

232. (C) Direct Immunofluorescence (Direct FAT)
Direct Immunofluorescence is an ideal technique for detecting specific antigens directly within a tissue section. It involves applying a primary antibody that is already conjugated to a fluorescent dye. If the target antigen is present in the tissue, the antibody will bind, and the resulting fluorescence can be visualized using a specialized microscope. This provides a fast and highly specific method for locating pathogens, such as the rabies virus, within the nervous tissue of an affected animal.

233. (D) It can quantify antigens in complex samples without species-specific antibodies
A major advantage of competitive ELISA is its ability to measure antigens using only a single type of specific antibody, which does not need to be species-specific. In this format, the antigen in the sample competes with a known amount of labeled antigen for a limited number of antibody binding sites. This makes it a highly versatile tool for detecting and quantifying hormones, drugs, and small molecules in various livestock species where specialized secondary antibodies may not be readily available.

234. (A) To present peptide antigens to T-cells, initiating adaptive immune responses
The Major Histocompatibility Complex is a set of cell surface proteins essential for the adaptive immune system to recognize foreign antigens. MHC molecules bind to small peptide fragments derived from pathogens and present them on the cell surface. This presentation is required for T-cells to identify and respond to the presence of an infection. Without MHC-mediated presentation, the T-cell arm of the immune system would be unable to recognize and eliminate viruses or bacteria within the animal's body.

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235. (C) IV only
MHC Class I and II molecules are the primary mediators of antigen presentation, while Class III genes encode a diverse range of other immune proteins, such as complement components and cytokines. Importantly, Class III genes do not code for T-cell receptors; T-cell receptors are encoded by an entirely separate set of genes that undergo somatic recombination. The other statements correctly describe the expression patterns and basic presentation functions of the Class I and Class II MHC molecules.

236. (B) Alpha chain non-covalently associated with smaller beta-2 microglobulin
An MHC Class I molecule consists of a large, polymorphic alpha chain that is non-covalently associated with a much smaller, non-polymorphic

protein called beta-2 microglobulin. The alpha chain contains the transmembrane domain and the peptide-binding groove where the foreign antigen is held for presentation. This structure is expressed on nearly all nucleated cells in the animal's body, allowing the immune system to constantly monitor the health and internal environment of every tissue and organ.

237. (A) The peptide-binding groove (cleft)
The MHC complex is among the most polymorphic regions in the vertebrate genome. This extreme genetic variation is concentrated almost entirely in the peptide-binding groove, which is the part of the molecule that physically interacts with the foreign antigen. Having a wide diversity of MHC alleles within a population ensures that different individuals can present different sets of pathogenic peptides, providing a broader level of protection and preventing a single pathogen from evading the entire herd's immune system.

238. (C) They encode immune proteins like complement components and various cytokines
Unlike Class I and II MHC genes, which are directly involved in antigen presentation, MHC Class III genes encode a variety of other proteins that support the immune response. These include essential components of the complement system, such as C2 and C4, and various inflammatory cytokines like tumor necrosis factor. Although these genes are physically located within the MHC region on the chromosome, they serve distinct effector and regulatory functions that coordinate the innate and adaptive immune responses.

239. (D) Erythrocytes
Professional antigen-presenting cells, such as dendritic cells, macrophages, and B-lymphocytes, are specialized to capture and process foreign antigens and express them on their surface using MHC Class II molecules. This allows them to activate helper T-cells and initiate a comprehensive adaptive immune response. In contrast, erythrocytes, or red blood cells, are not nucleated in mammals and do not express MHC molecules, as their primary function is oxygen transport rather than active participation in antigen-driven immune signaling.

240. (C) Specific MHC molecules bind and present peptides more effectively to T-cells
The link between certain MHC alleles and disease resistance exists because different MHC molecules have different shapes in their peptide-binding grooves. A specific allele may be exceptionally good at binding and presenting a critical protein from a particular virus or bacterium, leading to a faster and more effective T-cell response. Consequently, animals with these "favorable" alleles are better equipped to fight off the infection, which has profound implications for selective breeding for disease resistance in livestock.

241. (B) MHC Class I - CD8+ Cytotoxic T cells
MHC Class I molecules present endogenous peptides to CD8+ cytotoxic T lymphocytes. This interaction is essential for the immune system to detect and destroy host cells that have been compromised by viruses or intracellular bacteria. On the other hand, MHC Class II molecules interact with CD4+ helper T cells to coordinate the broader immune response. This specific "MHC restriction" ensures that the correct type of T-cell is activated to deal with the specific type of threat encountered by the animal.

242. (D) As linked haplotype blocks inherited as a single unit from each parent
The genes of the Major Histocompatibility Complex are located very close together on a single chromosome and are inherited as a linked block called a haplotype. Because recombination within the MHC is relatively rare, offspring typically inherit one complete set of MHC alleles from each parent. This means that siblings have a 25 percent chance of having identical MHC haplotypes, which is a critical consideration for tissue transplantation and for studying the transmission of disease resistance in livestock populations.

243. (A) BoLA
The Major Histocompatibility Complex in cattle is officially designated as the Bovine Leukocyte Antigen system, or BoLA. It is located on bovine chromosome twenty-three and is one of the most extensively studied genetic regions in ruminants. Researchers have identified numerous BoLA alleles and have linked many of them to important health and production traits, such as resistance to mastitis and bovine leukemia

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virus, making it a key focus for modern genomic selection in the dairy and beef industries.

244. (C) It ensures the population can present an array of pathogenic viral peptides
The high degree of polymorphism and polygeny in the MHC complex is an evolutionary strategy to maximize the population's ability to survive diverse pathogens. By having many different MHC genes and alleles, a herd can present a vast array of different peptides to the immune system. This ensures that even if a new or outdated pathogen can evade the MHC molecules of some individuals, other animals in the population will likely be able to recognize it, preventing a total population collapse.

245. (A) Both A and R are true and R is the correct explanation of A
The BoLA system is a critical area of research for improving the health of dairy cattle. Extensive studies have shown that specific alleles at the BoLA-DRB3 locus are strongly associated with the animal's ability to control infections like Bovine Leukemia Virus. By identifying these genetic markers, breeders can select for animals with superior natural resistance to these economically devastating diseases, reducing the reliance on antibiotics and improving the overall sustainability and welfare of the dairy industry.

246. (D) BoLA Class II molecules
MHC Class II molecules, known as BoLA Class II in cattle, are responsible for presenting exogenous antigens derived from extracellular pathogens like bacteria. These proteins are primarily expressed on specialized antigen-presenting cells, which ingest and break down foreign material. The resulting peptides are then loaded onto BoLA Class II molecules and presented to CD4+ helper T cells, triggering the production of antibodies and other defensive measures needed to clear the infection from the livestock animal's body.

247. (B) Water Buffalo (Bubalus bubalis)
The acronym BuLA stands for Buffalo Leukocyte Antigen, which represents the Major Histocompatibility Complex of the water buffalo. Similar to the BoLA system in cattle, the BuLA complex is highly polymorphic and plays a central role in the animal's immune response. Understanding the genetic structure and allelic diversity of the BuLA system is essential for improving disease resistance and breeding programs for this important agricultural species, which is vital for milk and draft power in many regions.

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248. (D) BoLA genes exhibit complete dominance where only one parental allele is expressed
Unlike many other Mendelian traits, the genes of the Major Histocompatibility Complex are expressed codominantly. This means that the alleles inherited from both the sire and the dam are simultaneously and fully expressed on the surface of the animal's cells. This codominant expression is an immunological advantage because it doubles the variety of MHC molecules available to present foreign peptides, significantly broadening the animal's repertoire for recognizing and responding to a wider range of potential pathogens.

249. (D) High rates of point mutations and recombination over evolutionary time
The extreme polymorphism observed at MHC loci like BoLA-DRB3 has been generated over millions of years through a combination of high point mutation rates and frequent gene conversion or recombination events. These processes constantly create new allelic variants that are then subjected to strong balancing selection. This evolutionary pressure ensures that a wide variety of alleles are maintained within the population, as individuals with more diverse MHC sets generally have a survival advantage against an ever-changing landscape of infectious diseases.

250. (A) It allows expression of two MHC sets, broadening the repertoire of antigens
Heterozygosity at the BoLA loci provides a significant immunological advantage by increasing the number of unique MHC molecules expressed on an animal's cell surfaces. Since each MHC variant has a slightly different peptide-binding specificity, a heterozygote can present a more diverse array of foreign peptides to its T-cells than a homozygote. This enhanced presentation capability makes the individual more likely to mount a successful immune response against a broader spectrum of viral and bacterial pathogens in the environment.

251. (B) Enzootic Bovine Leukosis (EBL) caused by BLV
Enzootic Bovine Leukosis, caused by the Bovine Leukemia Virus, has been a major historical driver for research into the BoLA system. This disease causes significant economic losses in dairy herds due to reduced production and culling. Studies identifying BoLA alleles that confer resistance to BLV were among the first to demonstrate the practical value of MHC research in livestock. These findings paved the way for modern genetic selection strategies aimed at improving the natural disease resistance and health of cattle.

252. (B) Xenotransplantation (transplanting pig organs into humans)
The Swine Leukocyte Antigen system is a major focus of research in xenotransplantation. Because pigs are anatomically and physiologically similar to humans, their organs are potential candidates for transplanting into human patients. However, the MHC molecules are a primary cause of transplant rejection. Scientists are working to genetically engineer "SLA-knockout" pigs or to modify the SLA genes to reduce their immunogenicity, with the ultimate goal of creating a sustainable and compatible source of organs for human medical use.

253. (A) Pathogen-associated molecular patterns highly conserved across microbes
Toll-like receptors are a key part of the innate immune system that recognize pathogen-associated molecular patterns. These PAMPs are structural components that are essential for the survival or function of whole groups of microbes and are highly conserved, meaning they do not change easily. Examples include bacterial cell wall components like lipopolysaccharide or viral nucleic acids. By targeting these universal markers, TLRs allow the immune system to immediately detect a wide range of invaders without previous exposure.

254. (C) TLRs are germline-encoded, non-clonal receptors of the innate immune system
A fundamental difference between the innate and adaptive immune systems lies in their receptors. T-cell and B-cell receptors are clonally distributed and generated through random gene rearrangement, allowing them to recognize specific antigens. In contrast, Toll-like receptors are germline-encoded and expressed uniformly on all cells of a particular type, such as macrophages. They are pre-set to recognize broad categories of pathogens, providing an immediate, non-specific first line of defense that does not require the time-consuming process of clonal selection.

255. (A) P-3, Q-4, R-1, S-2
Each Toll-like receptor is specialized to recognize a specific type of pathogen-associated molecular pattern. TLR-4 targets lipopolysaccharide from Gram-negative bacteria, while TLR-5 recognizes flagellin from motile bacteria. TLR-3 and TLR-9 are involved in detecting viral and bacterial nucleic acids, respectively. This division of labor allows the innate immune system to accurately identify the general type of invader and initiate the most appropriate signaling pathways and defense mechanisms to combat the specific infection in the animal.

256. (C) Translocation of NF-kappaB to the nucleus and production of cytokines
When a Toll-like receptor binds to its ligand, it triggers a complex internal signaling cascade. A key event in this process is the activation and translocation of the transcription factor NF-kappaB from the cytoplasm into the nucleus. Once there, NF-kappaB binds to the promoters of many genes involved in the immune response, leading to the rapid production of pro-inflammatory cytokines and other defensive proteins. This coordinated response is essential for initiating inflammation and recruiting other immune cells to the site of infection.

257. (B) They are localized in endosomes to detect nucleic acids of internal pathogens
TLRs 3, 7, 8, and 9 are located on the membranes of internal cellular compartments called endosomes. This specific localization allows them to detect the nucleic acids of viruses and bacteria that have been internalized by the cell through phagocytosis or infection. By being sequestered inside the cell, these receptors can monitor the internal environment for hidden pathogens while avoiding accidental activation by the animal's own extracellular DNA or RNA, thus maintaining a balance between defense and self-tolerance.

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258. (D) Complete failure to mount an antibody response against Gram-positive bacteria
A mutation causing TLR-4 dysfunction primarily impairs the innate immune response to Gram-negative bacteria, as these organisms are the primary source of lipopolysaccharide. While this can reduce the risk of lethal endotoxic shock, it also leaves the animal more vulnerable to these specific infections. However, such a mutation would not lead to a complete failure of the antibody response against Gram-positive bacteria, which are recognized by different receptors like TLR-2 and are primarily cleared by the adaptive immune system.

259. (A) It is a critical adaptor protein used to initiate downstream signal pathways
MyD88 is a vital adaptor protein that most Toll-like receptors use to transmit signals from the cell surface into the interior of the cell. Upon TLR activation, MyD88 recruits a series of other signaling molecules that eventually lead to the activation of transcription factors like NF-kappaB. Because it is a central hub for many different TLR pathways, mutations or deficiencies in MyD88 can cause severe immunodeficiencies, leaving the animal unable to mount an effective innate immune response to many common pathogens.

260. (C) TLR-5 - Flagellated bacteria
Each Toll-like receptor has evolved to recognize a specific molecular signature of a particular group of pathogens. TLR-5 is uniquely specialized to bind flagellin, the primary protein component of bacterial flagella. This allows the immune system to specifically detect the presence of motile bacteria in the animal's body. Similarly, other TLRs are tuned to detect various fungal, viral, and bacterial components, ensuring that the innate immune system can identify and respond to almost any type of microbial threat.

261. (A) TLR signaling induces dendritic cell maturation and upregulates MHC molecules
Toll-like receptors play a critical role in bridging the innate and adaptive immune systems. When TLRs on dendritic cells are activated, they trigger the cell to mature and migrate to the lymph nodes. During this process, the dendritic cell increases its expression of MHC and co-stimulatory molecules, which are essential for effectively activating naive T-cells. This ensures that the adaptive immune response is specifically targeted toward the type of pathogen that was originally detected by the innate receptors.

262. (D) Cytokines produced by leukocytes to regulate the growth of all immune cells
Interleukins are a large and diverse family of cytokines that act as chemical messengers between different types of white blood cells, or leukocytes. They play a fundamental role in regulating almost every aspect of the immune response, including cell growth, differentiation, and activation. By coordinating the behavior of various immune cells, interleukins ensure that the body's defense against infection is properly timed, targeted, and controlled, which is essential for both resisting disease and maintaining overall health in livestock.

263. (B) Interleukin-2 (IL-2)
Interleukin-2 is often referred to as the "T-cell growth factor" because of its central role in promoting the proliferation and survival of activated T-lymphocytes. When a T-cell is stimulated by an antigen, it secretes IL-2 and also increases the expression of IL-2 receptors on its own surface. This autocrine loop drives the rapid clonal expansion of the T-cell population, ensuring there are enough specialized cells to effectively combat the specific infection in the animal's body.

264. (C) It acts as an anti-inflammatory cytokine inhibiting macrophage functions
Interleukin-10 is a powerful anti-inflammatory cytokine that plays a crucial role in preventing excessive or chronic inflammation. It is produced by various immune cells, including regulatory T-cells and macrophages, and acts by inhibiting the production of pro-inflammatory cytokines and reducing the antigen-presenting capabilities of macrophages and dendritic cells. This helps to "cool down" the immune response once a pathogen has been cleared, protecting the animal's tissues from collateral damage caused by persistent inflammation and immune activity.

265. (A) III, II, I, IV
A standard pro-inflammatory cascade begins when Toll-like receptors recognize pathogen-associated molecular patterns. This recognition triggers macrophages to phagocytize the invader and secrete pro-inflammatory cytokines like IL-1 and TNF-alpha. These chemical signals then travel through the body, inducing the

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production of acute-phase proteins from the liver and acting on the brain to cause fever. This highly coordinated sequence of events is essential for initiating a fast and effective innate immune defense against bacterial and viral infections.

266. (A) Th2 cells
Th2 cells are a specialized subset of helper T-lymphocytes that coordinate the immune response against large extracellular parasites like helminth worms. They produce a specific set of cytokines, including IL-4 and IL-5, which stimulate B-cells to undergo class switching to IgE and promote the recruitment and activation of eosinophils and mast cells. This Th2-driven humoral and cellular response is essential for neutralizing and expelling parasites from the respiratory and gastrointestinal tracts of domestic animals.

267. (B) It activates macrophages to kill pathogens and directs a Th1-type response
Interferon-gamma is a critical cytokine for the cell-mediated immune response. It is primarily produced by Th1 cells and natural killer cells and acts as the most potent activator of macrophages, significantly enhancing their ability to kill intracellular pathogens. Additionally, IFN-gamma promotes the differentiation of more Th1 cells while inhibiting the development of the Th2 subset. this ensures that the immune system remains focused on a cell-mediated defense, which is essential for fighting many viral and bacterial infections in sheep.

268. (B) One cytokine exerts different biological effects on different target cells
Pleiotropy is a common characteristic of cytokines, where a single molecule can have many different effects depending on the target cell it binds to. For example, a cytokine might stimulate a B-cell to produce antibodies but cause a T-cell to proliferate or a macrophage to become more active. This biological versatility allows the immune system to use a small number of chemical messengers to coordinate a vast and complex array of cellular activities across many different tissues and systems.

269. (A) Endotoxic (septic) shock
A cytokine storm is a dangerous systemic inflammatory reaction caused by the massive and uncontrolled release of cytokines, particularly TNF-alpha and IL-1. In livestock, this often occurs in response to high levels of bacterial endotoxins in the blood. The overwhelming surge of cytokines causes widespread blood vessel leakage, a sudden drop in blood pressure, and organ failure, leading to a life-threatening condition known as septic or endotoxic shock that requires immediate veterinary intervention.

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270. (C) IFN-gamma - Natural Killer (NK) cells and Th1 cells
Each cytokine is produced by a specific set of immune cells. Interferon-gamma is primarily secreted by natural killer cells during the early innate response and by Th1 helper T-cells during the subsequent adaptive response. These matches are essential for understanding how the immune system is organized and how different cell types communicate. For instance, IL-2 is produced by T-cells, not B-cells, and macrophages are the main source of IL-1 and TNF-alpha, rather than erythrocytes or other non-immune cells.

271. (D) Mediating the acute phase response and stimulating liver protein production
Interleukin-6 is a key mediator of the acute phase response, which is the body's rapid systemic reaction to infection or injury. One of its primary roles is to signal the liver to increase the production of acute-phase proteins, such as C-reactive protein and fibrinogen, which help to neutralize pathogens and repair damaged tissues. Additionally, IL-6 contributes to the induction of fever and plays an important role in the transition from innate to adaptive immunity in domestic animals.

272. (C) A combination of TGF-beta and IL-6
The differentiation of naive T-cells into the Th17 subset is a complex process that requires the coordinated action of multiple cytokines. In most mammals, the combination of TGF-beta and IL-6 is essential for initiating the Th17 program. These cells then produce IL-17, which is critical for recruiting neutrophils and defending mucosal surfaces against extracellular bacteria and fungi. Understanding these cytokine requirements is vital for developing vaccines that can specifically target and enhance these important mucosal defense pathways.

273. (B) By binding to transmembrane receptors, activating internal signal pathways
Cytokines communicate by binding to specific, high-affinity receptors on the surface of target

cells. Because they are large, water-soluble proteins, they cannot cross the cell membrane. Instead, the binding to the extracellular part of the receptor triggers a conformational change that activates an internal signaling pathway, such as the JAK-STAT pathway. This signal is then transmitted to the nucleus, where it alters the expression of specific genes, leading to the observed biological response in the cell.

274. (D) Fusing a B-cell with a myeloma cell to produce monoclonal antibodies
Hybridoma technology is a revolutionary method for producing large quantities of identical, highly specific antibodies. It involves fusing a short-lived, antibody-producing B-cell from an immunized animal with a "permanent" or "immortal" cancer cell called a myeloma. The resulting hybrid cell, or hybridoma, possesses the best qualities of both parents: the ability to secrete a single type of specific antibody and the capacity to grow and divide indefinitely in a laboratory culture.

275. (B) II, I, III, IV
The production of monoclonal antibodies follows a logical sequence. First, an animal is immunized with the target antigen to stimulate the production of specific B-cells. These B-cells are then harvested from the spleen and fused with myeloma cells using a chemical agent like polyethylene glycol. The resulting mixture is grown in a selective HAT medium to isolate only the successful hybridomas. Finally, these clones are screened to identify the ones producing the desired specific antibody.

276. (C) It blocks the de novo synthesis pathway, forcing use of the salvage pathway
Aminopterin is a critical component of the selective HAT medium. It works by blocking the "de novo" pathway, which is the primary method cells use to synthesize the nucleotides needed for DNA replication. By shutting down this pathway, Aminopterin forces the cells to rely on an alternative "salvage" pathway. This selective pressure is essential because only the hybridoma cells, which inherit the necessary enzymes from the original B-cells, can use this salvage pathway to survive and grow.

277. (A) They lack the HGPRT enzyme, preventing use of the salvage pathway in the cell
Myeloma cells used in hybridoma technology are specifically chosen or engineered to be deficient in the enzyme HGPRT. This enzyme is required for the salvage pathway of nucleotide synthesis. In the presence of Aminopterin, which blocks the de novo pathway, these myeloma cells have no way to produce DNA and therefore cannot survive in the HAT medium. This ensure that any unfused myeloma cells are quickly eliminated, leaving only the successfully fused hybridoma cells to proliferate.

278. (D) They exhibit high cross-reactivity and bind to multiple diverse epitopes
A defining feature of monoclonal antibodies is their extreme specificity. Because they are produced by a single clone of identical cells, every antibody molecule in a monoclonal preparation is identical and recognizes only one specific epitope on an antigen. This is the opposite of polyclonal antibodies, which are a mixture of many different antibodies that can recognize various epitopes, often leading to higher rates of cross-reactivity. This unique specificity makes monoclonal antibodies exceptionally powerful for precision diagnostic and therapeutic applications.

279. (B) Polyethylene glycol (PEG)
Polyethylene glycol is a chemical fusogen commonly used in hybridoma technology to induce the fusion of B-cells and myeloma cells. It works by altering the cell membranes, allowing them to merge when the cells come into contact. Although the fusion process is relatively inefficient, PEG significantly increases the probability of creating a successful hybridoma. Other methods, such as electrofusion using short electrical pulses, are also used but PEG remains a standard and widely available reagent in most immunology laboratories.

280. (C) They naturally have a limited lifespan in vitro and undergo senescence
While unfused B-lymphocytes possess the necessary enzymes to survive the HAT medium's selective pressure, they are naturally programmed for a very short lifespan once removed from the animal's body. These cells do not have the capacity for indefinite division and will eventually stop growing and die in a cell culture environment. This natural senescence ensures that only the immortal hybridomas,

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which have inherited the "immortality" genes from the myeloma parent, will continue to grow and dominate the culture.

281. (D) Myeloma cell - Confers the ability to divide indefinitely in cell culture
A successful hybridoma is a functional marriage between two different cell types. The B-lymphocyte provides the genetic instructions to produce a single, specific antibody. The myeloma cell, being a type of cancer cell, provides the machinery for continuous and indefinite growth in a laboratory setting. This combination allows for the creation of a stable and permanent cell line that can produce a limitless supply of a single, highly specific monoclonal antibody for use in research, diagnostics, and medicine.

282. (A) By allowing highly specific diagnostic kits with no batch-to-batch variation
The greatest impact of monoclonal antibody technology in veterinary diagnostics has been the creation of highly standardized and reliable test kits. Because monoclonal antibodies are identical and produced by the same cell line, there is virtually no variation between different batches of the product. This consistency ensures that diagnostic tests provide accurate and reproducible results every time, which is essential for monitoring animal health, controlling disease outbreaks, and ensuring the safety and quality of food products in the livestock industry.

283. (C) It must be a mutant lacking functional genes for the HGPRT or TK enzymes
For the HAT selection system to work, the myeloma cell line must be a specific mutant that lacks the genes for either hypoxanthine-guanine phosphoribosyltransferase (HGPRT) or thymidine kinase (TK). These enzymes are essential for the salvage pathway of nucleotide synthesis. By using a deficient myeloma line, researchers can ensure that these cells will only survive if they fuse with a normal B-cell that can provide the missing enzyme, thus allowing for the selective growth of only the hybridoma cells.

284. (B) The immune system will recognize mouse antibody as foreign, causing clearance
Most monoclonal antibodies are originally produced using mouse cells. When these murine antibodies are injected into a different species, like a dog or a horse, the recipient's immune system recognizes them as foreign proteins. This can trigger an immune response that rapidly clears the antibody from the bloodstream, neutralizing its therapeutic effect and potentially causing allergic reactions. This limitation has driven the development of "animalized" antibodies that are modified to be more compatible with the target species' immune system.

285. (A) Performing limiting dilution cloning to ensure the culture is from a single cell
After the initial fusion and selection, the resulting culture often contains several different hybridoma clones. To ensure that the final product is truly a monoclonal antibody, a process called limiting dilution cloning is performed. The cells are diluted to the point where, on average, only one cell is placed in each well of a culture plate. This allows for the expansion of a population from a single original cell, guaranteeing that all the antibodies produced are identical and specific to one epitope.

286. (C) Routine artificial induction of multiple ovulation in dairy cattle
Monoclonal antibodies are widely used in animal agriculture for disease diagnosis, passive immunization, and identifying specific immune cell types through flow cytometry. However, they are not typically used for the routine induction of multiple ovulation in cattle. That process, known as superovulation, is usually achieved using hormonal treatments such as follicle-stimulating hormone. While mAbs could theoretically be used to target specific hormones, traditional endocrine-based methods remain the standard practice for embryo transfer and assisted reproduction in the livestock industry.

287. (D) Thymidine
The 'T' in HAT medium stands for thymidine. The selective medium is a mixture of hypoxanthine, aminopterin, and thymidine. While aminopterin blocks the de novo synthesis of nucleotides, hypoxanthine and thymidine are provided as essential precursors for the alternative salvage pathway. Only cells that possess the enzymes HGPRT and thymidine kinase can utilize these precursors to synthesize the DNA needed for survival and division, which is the fundamental basis for isolating successful hybridoma cells in the laboratory.

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288. (C) Hypoxanthine is a precursor converted by HGPRT into purine nucleotides
In the salvage pathway, the enzyme HGPRT uses hypoxanthine as a substrate to create purine nucleotides, which are the building blocks of DNA. This pathway provides a backup method for the cell to produce DNA when the primary de novo pathway is blocked by drugs like aminopterin. In hybridoma technology, inheriting the functional HGPRT gene from the original B-cell parent is what allows the successfully fused hybridoma to survive and grow in the selective HAT medium used during the production process.

289. (B) Its high specificity and consistent affinity for a single epitope
Monoclonal antibodies are ideal for affinity chromatography because of their absolute specificity for a single epitope. When a mAb is attached to a solid support, it will only bind to its specific target antigen as a complex mixture is passed over it. All other proteins will wash away, allowing the target to be eluted in a highly pure form. This precision is essential for purifying viral antigens for vaccines or for isolating rare proteins for detailed biochemical and structural studies in animal research.

290. (A) Both A and R are true and R is the correct explanation of A
To improve the therapeutic use of monoclonal antibodies in pets, researchers create "animalized" versions by replacing the mouse-derived constant regions with those of the target species, such as a dog or cat. This process keeps the specific antigen-binding site but makes the rest of the molecule appear "native" to the recipient's immune system. This significantly reduces the risk of the antibody being rejected or causing an allergic reaction, allowing for longer and more effective treatment of chronic conditions like allergies or cancer.

291. (A) It is required for salvage pathway synthesis of pyrimidines from thymidine
Thymidine kinase is a key enzyme in the salvage pathway that specifically converts thymidine into pyrimidine nucleotides. Just like HGPRT is needed for purines, TK is essential for the cell to produce a complete set of DNA building blocks when the de novo pathway is inhibited by aminopterin. In the HAT selection system, a deficiency in either HGPRT or TK in the myeloma parent ensures that only cells fused with a normal B-cell can survive, making these enzymes critical tools for hybridoma isolation.

292. (C) An epitope is the antigenic determinant on the antigen; the paratope is the antigen-binding site on the antibody
The interaction between an antigen and an antibody is highly specific and involves two complementary structures. The epitope is the small, specific part of the antigen that is recognized by the immune system. The paratope is the corresponding part of the antibody molecule that physically binds to the epitope. This precise structural and chemical match between the epitope and paratope is what allows monoclonal antibodies to target a single specific molecule with extraordinary accuracy in both diagnostic and therapeutic applications.

293. (A) Ascites method
The ascites method is a traditional technique for producing large quantities of monoclonal antibodies in vivo. Hybridoma cells are injected into the peritoneal cavity of a mouse, where they grow as a tumor and secrete high concentrations of the antibody into the surrounding fluid, called ascites. This fluid can then be harvested and purified. While very efficient at producing large amounts of mAb, this method has become less common due to significant animal welfare concerns and the development of high-capacity in vitro cell culture systems.

294. (D) The ascites method causes pain and distress due to tumor and fluid growth
The use of the ascites method for monoclonal antibody production is now strictly regulated or banned in many countries because it causes significant pain and distress to the laboratory animals. The growth of the hybridoma tumor and the accumulation of large volumes of fluid in the abdomen are considered major welfare issues. Consequently, modern biotechnology has shifted toward using advanced bioreactors and large-scale in vitro cell culture systems, which provide a more ethical and humane way to produce high-quality monoclonal antibodies.

295. (B) Flow Cytometry - Detects fluorescently labeled antibodies bound to single cells suspended in a fluid stream
Flow cytometry is a powerful tool for screening and characterizing hybridomas. It works by passing individual cells through a laser beam

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and measuring the resulting light scatter and fluorescence. If a hybridoma is producing an antibody that binds to a specific cell-surface marker, that binding can be detected using a fluorescent label. This allows researchers to rapidly screen thousands of cells and precisely identify the clones that are producing the desired antibody, providing a high-throughput and highly accurate method for hybridoma selection.

296. (C) By selecting rare subclones that have undergone spontaneous isotype switching
While a hybridoma typically produces a single isotype of antibody, such as IgM, rare spontaneous mutations can cause a cell to switch to a different isotype, like IgG. These rare "switch variants" can be identified and isolated using sensitive screening techniques. This allows researchers to obtain a monoclonal antibody with the same antigen specificity but different biological effector functions. This manipulation is valuable because IgG antibodies are often more stable and easier to work with in many diagnostic and therapeutic applications than the larger IgM molecules.

297. (D) An antibody of the same isotype used to measure background non-specific binding
In many immunological assays, it is critical to distinguish between specific binding to the target antigen and non-specific background binding. An isotype control is an antibody that is identical in class and structure to the experimental monoclonal antibody but does not recognize the target antigen. By using this control, researchers can measure and subtract any background signal, ensuring that the results they observe are truly due to the specific interaction between their monoclonal antibody and its intended target epitope.

298. (A) Interleukin-31 (IL-31)
Lokivetmab is a specialized "caninized" monoclonal antibody used in veterinary medicine to treat atopic dermatitis in dogs. Its specific target is interleukin-31, a cytokine that is a key mediator of the itching sensation, or pruritus. By binding to and neutralizing IL-31 in the bloodstream, Lokivetmab prevents it from activating receptors on the nerves in the skin. This provides rapid and long-lasting relief from itching without the side effects often associated with traditional steroid-based treatments, significantly improving the quality of life for affected pets.

299. (B) Memory B and Memory T lymphocytes
Memory lymphocytes are the foundation of the long-term, highly specific immunity provided by the adaptive immune system. When the body is exposed to an antigen for the second time, these memory cells recognize it immediately and mount a much faster and more powerful response than during the initial exposure. This rapid recall is why vaccines are so effective and is also the principle used to generate the high-affinity B-cells needed for successful hybridoma production, ensuring that the resulting monoclonal antibodies are of the highest possible quality.

300. (B) Strain-specific antigen subtyping (serotyping)
The extraordinary specificity of monoclonal antibodies is most fundamentally utilized in serotyping, which is the process of differentiating between closely related strains or varieties of a pathogen. Because a mAb can recognize a single unique epitope, it can distinguish between two viruses or bacteria that are identical except for one small structural difference. This precision is essential for tracking disease outbreaks, identifying the source of an infection, and ensuring that vaccines are perfectly matched to the specific strains of pathogens circulating in the livestock population.

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NODIA

CHAPTER 02
Advanced Genetics

2004

1. In the nucleosome-solenoid model of eukaryotic chromatin, how many base pairs of DNA typically wrap around the histone octamer core?
(A) 10 base pairs
(B) 146 base pairs
(C) 166 base pairs
(D) 200 base pairs

2019

2. Which of the following chromosome banding techniques relies on the differential binding of quinacrine mustard to AT-rich regions?
(A) G-banding
(B) C-banding
(C) Q-banding
(D) R-banding

2018

3. In eukaryotic gene structure, what is the primary function of the TATA box located upstream of the transcription start site?
(A) To serve as the core promoter for RNA polymerase II
(B) To provide the signal for mRNA polyadenylation
(C) To serve as the binding site for the spliceosome
(D) To signal the termination of transcription events

2009

4. Which enzyme is responsible for relieving the topological strain and supercoiling ahead of the replication fork during DNA replication?
(A) DNA helicase
(B) DNA ligase
(C) Single-stranded binding protein
(D) DNA topoisomerase

2018

5. Each of the following questions contains an Assertion (A) and a Reason (R). Choose the correct option from the following:
Assertion (A): The 5' cap added to eukaryotic pre-mRNA protects the transcript from exonuclease degradation.
Reason (R): The 5' cap involves an unusual 5'-5' triphosphate linkage to a 7-methylguanosine residue.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2024

6. According to the wobble hypothesis, which base in the anticodon of tRNA can form non-standard hydrogen bonds with multiple bases in the third position of an mRNA codon?
(A) Second base
(B) Third base (3' end)
(C) First base (5' end)
(D) Both first and second bases

2002

7. Type II restriction endonucleases are most widely used in recombinant DNA technology because they:
(A) Require ATP and S-adenosylmethionine for site cleavage
(B) Cleave DNA at random sites residing far from targets
(C) Posses methylation and cleavage activities in one chain
(D) Cleave DNA at specific palindromic recognition sites

2004

8. In blue-white screening, successful insertion of a foreign DNA fragment into the multiple cloning site of a pUC vector results in:
(A) White colonies due to lacZ' gene inactivation
(B) Blue colonies due to functional beta-galactosidase
(C) Blue colonies due to resistance to ampicillin markers
(D) White colonies due to spontaneous cellular mutations

2025

9. Which method of animal gene transfer utilizes engineered nucleases to introduce double-strand

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breaks at specific genomic loci followed by homology-directed repair?
(A) Pronuclear microinjection of linear DNA
(B) CRISPR/Cas9-mediated gene targeting
(C) Retrovirus-mediated genomic transfer
(D) Embryonic stem cell gene transfection

2013

10. In Somatic Cell Nuclear Transfer (SCNT), donor cells are typically synchronized to which phase of the cell cycle prior to nuclear transfer?
(A) S phase of the cycle
(B) G0/G1 phase of the cycle
(C) G2/M phase of the cycle
(D) Late M phase of the cycle

2019

11. In the negative regulation of the lac operon, the repressor protein binds to which specific sequence to prevent transcription?
(A) Operator
(B) Promoter
(C) CAP-binding site
(D) Leader sequence

2011

12. Which of the following transcription factor motifs typically functions by coordinating a heavy metal ion to stabilize its structure for DNA binding?
(A) Leucine zipper
(B) Helix-turn-helix
(C) Zinc finger
(D) Helix-loop-helix

2002

13. Which post-translational modification involves the covalent attachment of a small protein that generally marks the target protein for proteasomal degradation?
(A) Phosphorylation
(B) Glycosylation
(C) Acetylation
(D) Ubiquitination

2019

14. Genomic imprinting in mammals is primarily established and maintained through which epigenetic mechanism?
(A) Modification via histone acetylation
(B) Activity of chromatin remodeling
(C) DNA methylation at CpG dinucleotides
(D) Non-coding RNA degradation pathways

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2008

15. Match the following functional genomics tools (List I) with their primary application (List II):
List I: (Functional Genomics Tools)
P. ESTs
Q. SAGE
R. DNA microarrays
S. RNA-Seq
List II: (Primary Application)
1. High-throughput quantification of transcripts via next-generation sequencing
2. Short concatenated sequence tags used to quantify gene expression
3. Single-pass sequencing of cDNA for rapid gene identification
4. Hybridization-based global gene expression profiling
(A) P-III, Q-II, R-IV, S-I
(B) P-II, Q-III, R-IV, S-I
(C) P-III, Q-IV, R-II, S-I
(D) P-I, Q-II, R-III, S-IV

2015

16. In two-dimensional gel electrophoresis (2D-PAGE), proteins are separated in the first dimension based exclusively on their:
(A) Molecular weight
(B) Hydrophobicity
(C) Tertiary structure
(D) Isoelectric point

2003

17. The Sanger sequencing method relies on the incorporation of dideoxynucleotide triphosphates (ddNTPs) which cause chain termination because they lack a:
(A) 3'-OH group
(B) 2'-OH group
(C) 5'-phosphate group
(D) Nitrogenous base

2025

18. Which Next-Generation Sequencing (NGS) technology utilizes the measurement of pH changes caused by the release of hydrogen ions during nucleotide incorporation?
(A) Pyrosequencing
(B) Illumina sequencing
(C) Ion Torrent sequencing
(D) SMRT sequencing

2009

19. In Genome-Wide Association Studies (GWAS), population stratification can lead to false-positive associations. Which statistical method is commonly used to correct for this?

(A) Principal Component Analysis (PCA)
(B) Chi-square test
(C) Simple linear regression
(D) ANOVA

2021

20. The accuracy of Genomic Estimated Breeding Values (GEBVs) in livestock heavily depends on the size and structure of the:
(A) Validator subset
(B) Sibling progeny
(C) Backcross generation
(D) Reference (training) population

2010

21. Which genomic prediction model assumes that the variances of marker effects are equal across all loci?
(A) Bayes A
(B) Ridge Regression-BLUP (RR-BLUP)
(C) Bayes B
(D) Bayes Cpi

2021

22. DNA shuffling is a molecular breeding technique used primarily for:
(A) Identifying Quantitative Trait Loci (QTLs)
(B) Gene drive systems for population suppression
(C) Evolution of genes to generate chimeric proteins
(D) Targeted deletion of specific genomic introns

2023

23. Heterochromatin is generally characterized by being:
(A) Transcriptionally active and lightly stained regions
(B) Regions located exclusively at the centromeres
(C) Highly rich in actively transcribed gene sequences
(D) Transcriptionally inactive and densely packed DNA

2016

24. Which chemical is typically used in G-banding to digest chromosomal proteins prior to Giemsa staining?
(A) Trypsin
(B) Quinacrine
(C) Silver nitrate
(D) Barium hydroxide

2005

25. Consider the following statements regarding the structural organization of eukaryotic genes:
I. Exons are coding regions that are retained in mature mRNA.
II. Introns are removed by the spliceosome.
III. The 5' UTR contains the polyadenylation signal.
Which of the above statement(s) is/are INCORRECT?
(A) I and II
(B) II and III
(C) I and III
(D) I, II and III

2008

26. Which DNA polymerase is primarily responsible for the synthesis of the leading strand during eukaryotic DNA replication?
(A) DNA polymerase alpha
(B) DNA polymerase epsilon
(C) DNA polymerase delta
(D) DNA polymerase gamma

2016

27. The role of the Rho protein in prokaryotic transcription is to:
(A) Facilitate termination of transcription
(B) Initiate transcription by binding the promoter
(C) Elongate the RNA transcript
(D) Cap the 5' end of the mRNA

2015

28. The degeneracy of the genetic code refers to the fact that:
(A) Multiple amino acids can be coded by a single codon
(B) The code overlaps between adjacent codons
(C) A specific amino acid can be encoded by more than one codon
(D) The code is not conserved across species

2023

29. Alkaline phosphatase is utilized in recombinant DNA cloning to:
(A) Ligate cohesive DNA ends
(B) Add a 5' phosphate group to products
(C) Cleave specific palindromic sequences
(D) Dephosphorylate the cloning vector

2007

30. Which vector can accommodate the largest insert size for cloning large genomic fragments?
(A) Plasmid
(B) Cosmid

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(C) Yeast Artificial Chromosome (YAC)
(D) Bacterial Artificial Chromosome (BAC)

2023

31. A critical advantage of retrovirus-mediated gene transfer in animals is:
(A) Ability to transfer extremely large DNA constructs
(B) Efficient and stable integration into the genome
(C) Strictly targeted integration at homologous sites
(D) Lack of transgene silencing across generations

2007

32. In oocyte enucleation during SCNT, which cellular structure is typically visualized and removed using a micromanipulator?
(A) The nucleolus
(B) The first polar body exclusively
(C) The mitochondria
(D) The metaphase II plate (chromosomes)

2011

33. In the trp operon, the presence of high intracellular levels of tryptophan leads to:
(A) Binding of the corepressor to the repressor, blocking transcription
(B) Dissociation of the repressor from the operator
(C) Activation of RNA polymerase
(D) Increased synthesis of trp operon enzymes

2022

34. Enhancers can regulate transcription by binding specific trans-acting factors; a unique feature of enhancers is that they:
(A) Only function when located exactly at the transcription start site
(B) Must be downstream of the gene they regulate
(C) Function in either orientation over long distances
(D) Transcribe small regulatory RNA molecules

2001

35. Select the correct order of events in the secretory pathway for a newly synthesized glycoprotein:
(A) Endoplasmic reticulum → Secretory vesicles → Golgi apparatus → Plasma membrane
(B) Endoplasmic reticulum → Golgi apparatus → Secretory vesicles → Plasma membrane
(C) Golgi apparatus → Endoplasmic reticulum → Secretory vesicles → Plasma membrane
(D) Secretory vesicles → Endoplasmic reticulum → Golgi apparatus → Plasma membrane

2002

36. Which epigenetic modification is generally associated with transcriptionally active euchromatin?
(A) DNA methylation
(B) Histone deacetylation
(C) Histone H3K9 methylation
(D) Histone acetylation

2015

37. Which technique provides a global overview of all transcripts by sequencing short segments from the 3' end of mRNAs?
(A) DNA microarray
(B) SAGE (Serial Analysis of Gene Expression)
(C) Chromosome walking
(D) Western blotting

2021

38. In proteomics, Matrix-Assisted Laser Desorption/Ionization (MALDI) is primarily used to:
(A) Separate proteins based on isoelectric point
(B) Digest proteins into peptides
(C) Ionize intact peptides for mass spectrometry analysis
(D) Identify protein-protein interactions

2009

39. The Maxam-Gilbert DNA sequencing method involves:
(A) Dideoxynucleotide chain termination
(B) Real-time monitoring of polymerase activity
(C) Hybridization to oligonucleotide arrays
(D) Base-specific chemical cleavage of DNA

2011

40. Sequencing-by-synthesis in Illumina technology heavily relies on the use of:
(A) Reversible terminator nucleotides
(B) Restriction enzyme digestion
(C) Nanopore electrical current shifts
(D) Emulsion PCR

2009

41. In a Manhattan plot depicting GWAS results, the x-axis typically represents:
(A) The negative logarithm of the P-value
(B) Genomic coordinates (chromosomes)
(C) The effect size of the allele
(D) Linkage disequilibrium blocks

2013

42. Genomic selection is advantageous over traditional pedigree-based selection primarily because it:
(A) Can accurately predict breeding values for young animals before they exhibit the trait

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(B) Requires phenotypic data on every individual in the selection generation
(C) Eliminates the need for a reference population
(D) Ignores markers in linkage disequilibrium with QTLs

2012

43. The GBLUP genomic prediction model utilizes which of the following instead of a traditional pedigree relationship matrix?
(A) Genomic relationship matrix (G-matrix) derived from marker data
(B) Additive genetic variance
(C) Phenotypic variance matrix
(D) Dominance deviation matrix

2002

44. Gene drive systems, often utilizing CRISPR/Cas9, function by:
(A) Inducing random mutations throughout the genome
(B) Increasing crossing-over frequencies in meiosis
(C) Suppressing expression of homologous genes in trans
(D) Forcing inheritance rates greater than 50%

2015

45. Each of the following questions contains an Assertion (A) and a Reason (R). Choose the correct option from the following:
Assertion (A): Telomeres consist of simple tandem repetitive DNA sequences that protect the ends of eukaryotic chromosomes from degradation.
Reason (R): Telomerase acts as a reverse transcriptase to synthesize these repetitive sequences using its own RNA template.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2011

46. Ag-NOR banding is primarily utilized to specifically stain and identify which chromosomal feature?
(A) Centromeric constitutive heterochromatin
(B) AT-rich regions
(C) Nucleolar Organizer Regions
(D) Telomeres

2023

47. Which element is typically recognized by the sigma factor of the prokaryotic RNA polymerase holoenzyme to initiate transcription?
(A) TATA box
(B) -10 and -35 consensus sequences
(C) Shine-Dalgarno sequence
(D) Kozak sequence

2001

48. During DNA replication, RNA primers are removed and the resulting gaps are filled by which enzyme in Escherichia coli?
(A) DNA Polymerase II
(B) DNA Polymerase III
(C) DNA Ligase
(D) DNA Polymerase I

2008

49. The spliceosome, responsible for excising introns from pre-mRNA, is composed primarily of:
(A) Carbohydrates and lipids
(B) Small nuclear ribonucleoproteins (snRNPs)
(C) DNA and non-histone proteins
(D) Single-stranded binding proteins

2015

50. Aminoacyl-tRNA synthetases are critical for translation because they ensure:
(A) Proper folding of the ribosome complex
(B) Termination of the polypeptide chain
(C) Correct tRNA and amino acid attachment
(D) Binding of mRNA to the small subunit

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2021

51. Which class of restriction endonucleases cleaves DNA approximately 24-26 base pairs away from the recognition site and requires both ATP and S-adenosylmethionine?
(A) Type I
(B) Type III
(C) Type II
(D) Type IV

2010

52. Plasmids used as cloning vectors typically contain all of the following EXCEPT:
(A) Origin of replication
(B) Selectable marker gene
(C) Centromere sequence for segregation
(D) Multiple cloning site

2005

53. Pronuclear microinjection for generating transgenic animals involves introducing DNA directly into:
(A) The blastocyst cavity

(B) The cytoplasm of an unfertilized oocyte
(C) Cultured embryonic stem cells
(D) The male or female pronucleus of a fertilized zygote

2002

54. In animal cloning via SCNT, electrofusion is applied specifically to:
(A) Remove the nucleus from the oocyte
(B) Synchronize the cell cycle of the donor cells
(C) Fuse the donor somatic cell with the enucleated oocyte and trigger activation
(D) Prevent the extrusion of the second polar body

2004

55. Match the transcription factor motif (List I) with its defining structural characteristic (List II):
List I: (Transcription Factor Motif)
P. Zinc finger
Q. Leucine zipper
R. Helix-turn-helix
S. Helix-loop-helix
List II: (Structural Characteristic)
1. Contains two alpha-helices separated by a short amino acid sequence
2. Amphipathic alpha-helices that mediate protein dimerization
3. Two alpha-helices connected by a flexible region, common in muscle regulators
4. Coordinates a metal ion for structural stability
(A) P-IV, Q-II, R-I, S-III
(B) P-IV, Q-III, R-I, S-II
(C) P-I, Q-II, R-IV, S-III
(D) P-II, Q-IV, R-III, S-I

2010

56. The attenuation mechanism in the trp operon relies on the coupling of transcription and translation. This mechanism is possible only in:
(A) Mammalian cells
(B) Eukaryotic cells
(C) Prokaryotic cells
(D) Yeast cells

2009

57. Which molecular chaperone complex in eukaryotes assists in the folding of newly synthesized proteins in a highly ATP-dependent manner?
(A) GroEL/GroES
(B) Hsp70 and Hsp90
(C) Proteasome
(D) Ubiquitin ligase

2002

58. The process of chromatin remodeling facilitates transcription primarily by:
(A) Sliding or evicting nucleosomes to expose promoter regions
(B) Methylating cytosine residues in DNA
(C) Degrading histone proteins completely
(D) Converting euchromatin to heterochromatin

2010

59. Which bioinformatic pipeline step follows the assembly of raw NGS reads into contigs during whole-genome analysis?
(A) RNA extraction
(B) Genome annotation
(C) Chromosome banding
(D) Flow cytometry

2018

60. The Yeast Two-Hybrid system is an in vivo assay primarily designed to detect:
(A) Transcriptional abundance
(B) DNA methylation patterns
(C) Protein-protein interactions
(D) Alternative splicing events

2012

61. Single-Molecule Real-Time (SMRT) sequencing developed by PacBio is characterized by:
(A) Extremely short read lengths and high accuracy
(B) Long reads from ZMW-based polymerase monitoring
(C) Chemical degradation of DNA chains
(D) Emulsion PCR on microbeads

2014

62. In the context of GWAS, Linkage Disequilibrium (LD) is defined as:
(A) The non-random association of alleles at different loci
(B) The physical breaking of chromosomes during meiosis
(C) Random segregation of traits
(D) The equal frequency of all alleles in a population

2021

63. The accuracy of Genomic Selection relies on markers being in strong linkage disequilibrium with:
(A) Enhancers only
(B) Quantitative Trait Nucleotides (QTNs) or QTLs
(C) Intronic sequences exclusively
(D) Centromeric repeats

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2019

64. The Bayesian alphabet method "Bayes B" differs from GBLUP by assuming that:
(A) All markers have an equal variance of effect
(B) Only a few markers have effects while most are zero
(C) Polygenic effects are purely epistatic
(D) DNA methylation controls trait variation

2005

65. Consider the following statements regarding marker-assisted introgression:
I. It is used to transfer a specific desirable genomic region from a donor to a recurrent parent.
II. Foreground selection targets the specific gene of interest.
III. Background selection focuses on accelerating the recovery of the recurrent parent genome.
IV. It completely eliminates the need for backcrossing.
Which of the above statement(s) is/are CORRECT?
(A) I, II and III
(B) I, III and IV
(C) I, II and IV
(D) II, III and IV

2019

66. Scaffold proteins in the metaphase chromosome play a crucial role in:
(A) Direct transcription of rRNA
(B) Replicating telomeres
(C) Excising introns
(D) Anchoring loops to maintain higher-order structure

2002

67. C-banding techniques selectively stain which specific regions of the chromosome?
(A) Telomeric segments only
(B) Actively transcribed euchromatin
(C) Nucleolar Organizer Regions
(D) Centromeric constitutive heterochromatin

2022

68. The polyadenylation signal in eukaryotic pre-mRNA typically consists of which consensus sequence?
(A) AAUAAA
(B) TATAAA
(C) CCAAT
(D) GGGCGG

2014

69. During discontinuous replication of the lagging strand, Okazaki fragments are synthesized in which direction?
(A) 3' to 5'
(B) 5' to 5'
(C) 3' to 3'
(D) 5' to 3'

2021

70. The 3' poly(A) tail of eukaryotic mRNA serves all of the following functions EXCEPT:
(A) Enhancing the overall efficiency of translation
(B) Protecting the mRNA from exonuclease degradation
(C) Serving as a template for RNA-dependent RNA polymerase
(D) Assisting in the nuclear export of mRNA molecules

2014

71. The initiation of translation in eukaryotes typically begins when the small ribosomal subunit binds to the:
(A) Shine-Dalgarno sequence
(B) 5' cap followed by scanning for the AUG codon
(C) Polyadenylated tail
(D) TATA promoter box

NODIA

2009

72. Which modifying enzyme catalyzes the transfer of the gamma-phosphate from ATP to the 5'-hydroxyl terminus of DNA or RNA?
(A) DNA ligase
(B) Alkaline phosphatase
(C) Polynucleotide kinase
(D) Terminal deoxynucleotidyl transferase

2018

73. A cosmid vector is essentially a plasmid that incorporates:
(A) Centromeres from yeast
(B) A retroviral long terminal repeat
(C) T-DNA borders from Agrobacterium
(D) The lambda phage cos site for viral packaging

2019

74. Embryonic stem cell (ESC) transfection is a powerful method for gene transfer in mice because ESCs are:
(A) Terminally differentiated
(B) Incapable of recombination
(C) Easily derived adult tissue
(D) Pluripotent and germline-capable via blastocysts

2019

75. Arrange the following steps of Somatic Cell Nuclear Transfer (SCNT) in the correct sequence:
I. Enucleation of recipient oocyte
II. Fusion of donor cell with oocyte
III. Synchronization of donor somatic cells
IV. Activation of reconstructed embryo
V. Transfer to a surrogate mother
(A) III, I, II, IV, V
(B) I, III, II, IV, V
(C) III, II, I, V, IV
(D) I, II, III, IV, V

2005

76. The basal transcription apparatus in eukaryotes includes RNA polymerase II and general transcription factors. Which factor contains the TATA-binding protein (TBP)?
(A) TFIIA
(B) TFIIB
(C) TFIID
(D) TFIIH

2015

77. The signal peptide, generally located at the N-terminus of a newly synthesized protein, directs the ribosome to the:
(A) Nucleus
(B) Endoplasmic reticulum
(C) Lysosome
(D) Mitochondrion

2010

78. In mammalian genomes, DNA methylation almost exclusively occurs at the cytosine residue within which dinucleotide context?
(A) CpG
(B) CpA
(C) CpC
(D) CpT

2017

79. DNA microarrays evaluate differential gene expression based on the principle of:
(A) Restriction fragment length polymorphism
(B) Nucleic acid hybridization
(C) Mass spectrometry
(D) Dideoxy chain termination

2016

80. A key advantage of RNA-Seq over traditional DNA microarrays is that RNA-Seq:
(A) Lacks background noise and detects novel transcripts
(B) Requires prior sequence knowledge of the genome
(C) Can only detect highly abundant transcripts
(D) Relies solely on restriction enzyme digestion

2008

81. Nanopore sequencing distinguishes individual nucleotides passing through a protein pore by measuring characteristic changes in:
(A) Fluorescent emission
(B) Ionic current flow
(C) pH level shifts
(D) Pyrophosphate release

2009

82. Which of the following best describes "population stratification" in a GWAS?
(A) The random mating of individuals
(B) Variation caused by environment
(C) Ancestry-based allele frequency differences
(D) Linkage disequilibrium between markers

2021

83. The Reference Population in genomic selection must have both:
(A) Phenotypic records and genotypic data
(B) Genotypic data only
(C) Phenotypic records only
(D) Pedigree records only without DNA data

2005

84. Bayesian models (Bayes A, B, C) are frequently employed in genomic prediction to handle the statistical issue where:
(A) Phenotypes exceed markers
(B) Epistasis masks effects
(C) Dominance is absent
(D) Markers (p) vastly exceed individuals (n)

2016

85. Each of the following questions contains an Assertion (A) and a Reason (R). Choose the correct option from the following:
Assertion (A): Directed evolution requires the generation of a large library of mutated genes followed by stringent selection.
Reason (R): DNA shuffling is a method of directed evolution that recombines homologous genes to create chimeric variants.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

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2005

86. Centromeric DNA sequences in eukaryotes are typically composed of:
(A) Transcribed single-copy genes
(B) Alpha-satellite tandem repeats
(C) Introns and exons
(D) 5' untranslated regions

2016

87. R-banding produces a pattern opposite to G-banding by denaturing DNA at high temperatures in appropriate buffer. The darkly stained R-bands correspond to:
(A) AT-rich regions
(B) Telomeric ends only
(C) Heterochromatin strictly
(D) GC-rich euchromatic regions

2009

88. In prokaryotic genes, the untranslated regions (UTRs) are located:
(A) Flanking the coding region at both the 5' and 3' ends
(B) Only at the 3' end
(C) Only at the 5' end
(D) Within the introns

2001

89. Which property is characteristic of the eukaryotic DNA replication origin?
(A) There is only one origin per chromosome.
(B) Multiple origins fire simultaneously on each chromosome.
(C) Replication occurs strictly in a unidirectional manner.
(D) Origins are completely devoid of AT sequences.

2016

90. Pre-mRNA splicing occurs via a lariat intermediate. The branch point sequence crucial for forming this lariat typically features a conserved:
(A) Adenine nucleotide
(B) Guanine nucleotide
(C) Cytosine nucleotide
(D) Thymine nucleotide

2012

91. The termination of translation is triggered when the ribosome encounters a stop codon (UAA, UAG, or UGA) which is recognized by:
(A) Release factors
(B) A specialized terminating tRNA
(C) RNA polymerase
(D) Spliceosomes

2002

92. Type I restriction endonucleases cleave DNA:
(A) At the recognition site
(B) Ten bp from the site
(C) Randomly at large distances
(D) If the origin is unmethylated

2015

93. Antibiotic selection markers in cloning vectors ensure that:
(A) The cloned insert is properly oriented
(B) Only host cells that have successfully taken up the vector can survive
(C) The vector cannot replicate
(D) The foreign DNA is expressed immediately

2023

94. The technique of pronuclear microinjection is most commonly applied in the genetic engineering of which model organism?
(A) Caenorhabditis elegans
(B) Mus musculus (mouse)
(C) Saccharomyces cerevisiae
(D) Escherichia coli

2019

95. Match the epigenetic modification (List I) with its general effect on chromatin and transcription (List II):
List I: (Epigenetic Modification)
P. DNA methylation at promoters
Q. Histone acetylation
R. Histone deacetylation
S. Chromatin remodeling (nucleosome eviction)
List II: (Effect on Chromatin and Transcription)
1. Transcriptional repression by chromatin compaction
2. Transcriptional activation by neutralizing positive charge on histones
3. Long-term silencing associated with genomic imprinting
4. Transcriptional activation by exposing promoter DNA
(A) P-III, Q-II, R-I, S-IV
(B) P-II, Q-III, R-IV, S-I
(C) P-III, Q-I, R-II, S-IV
(D) P-I, Q-IV, R-II, S-III

NODIA

2010

96. Silencers are cis-acting regulatory elements that negatively regulate gene expression by providing binding sites for:
(A) RNA polymerase
(B) Transcriptional repressors
(C) Ribosomes
(D) Spliceosomes

2013

97. N-linked glycosylation, a major post-translational modification, involves the attachment of oligosaccharides to the amide nitrogen of which amino acid residue?
(A) Serine
(B) Threonine
(C) Asparagine
(D) Tyrosine

2016

98. Which chromatin remodeling complex heavily relies on ATP hydrolysis to slide nucleosomes along the DNA?
(A) SWI/SNF complex
(B) Histone acetyltransferase (HAT)
(C) DNA methyltransferase (DNMT)
(D) Histone deacetylase (HDAC)

2002

99. The generation of Expressed Sequence Tags (ESTs) typically involves sequencing which part of cDNA clones?
(A) The central coding sequence
(B) One or both ends (5' or 3')
(C) The promoter region
(D) The introns

2016

100. In mass spectrometry-based proteomics, what does the time-of-flight (TOF) analyzer measure?
(A) Peptide isoelectric points
(B) Protein secondary structure
(C) Nucleotide sequence data
(D) Mass-to-charge ($\frac{m}{z}$) ratio

2008

101. Pyrosequencing detects nucleotide incorporation in real-time by linking the release of pyrophosphate to a light-emitting reaction catalyzed by:
(A) Beta-galactosidase
(B) Luciferase
(C) Taq polymerase
(D) Alkaline phosphatase

2014

2010

102. In a GWAS, which threshold of significance (P-value) is conventionally used to account for multiple testing corrections globally?
(A) $P < 5 \times 10^{-8}$
(B) $P < 0.05$
(C) $P < 0.01$
(D) $P > 0.10$

2007

103. The G-matrix used in Genomic Selection represents:
(A) The physical map distance between markers
(B) Realized genomic relationships among individuals based on marker sharing
(C) The genotypic variance caused by dominance alone
(D) A correlation matrix of phenotypic traits

2013

104. Which statistical approach is most commonly used to estimate the accuracy of a genomic prediction model within the reference population?
(A) Random forest
(B) k-fold cross-validation
(C) Simple linear regression
(D) Logistic regression

2011

105. Consider the following statements regarding CRISPR/Cas9:
I. Cas9 is an endonuclease that creates double-strand breaks.
II. It requires a short guide RNA (sgRNA) for target specificity.
III. It functions independently of a Protospacer Adjacent Motif (PAM).
IV. Target cleavage can lead to non-homologous end joining (NHEJ).
V. It can be used for gene knockouts and knock-ins.
Which of the above statement(s) is/are INCORRECT?
(A) III only
(B) I and II
(C) III and V
(D) II, IV and V

2003

106. The nucleosome core particle is a highly conserved structure across eukaryotes. Which of the following histones is NOT part of the octameric core?
(A) H2A
(B) H1
(C) H2B
(D) H4

2014

107. Which banding technique is primarily diagnostic for identifying the centromeric regions of human chromosomes?
(A) G-banding
(B) C-banding
(C) R-banding

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(D) Q-banding

2014

108. Prokaryotic promoter sequences responsible for initial RNA polymerase binding typically reside at which positions relative to the transcription start site?
(A) -10 and -35
(B) +1 and +10
(C) +10 and +35
(D) -50 and -100

2014

109. Single-Stranded Binding (SSB) proteins function during replication to:
(A) Unwind the double helix
(B) Relieve supercoiling
(C) Prevent separated DNA strands from reannealing
(D) Synthesize RNA primers

2023

110. The 5' cap structure on eukaryotic mRNAs consists of:
(A) 7-methylguanosine
(B) Polyadenine tract
(C) Uridine monophosphate
(D) Dideoxycytidine

2024

111. During translation elongation, an incoming aminoacyl-tRNA first binds to which site of the ribosome?
(A) A site
(B) P site
(C) E site
(D) mRNA binding site

2004

112. Type II restriction enzymes generally leave which type of ends after cleaving double-stranded DNA?
(A) Only blunt ends
(B) Only sticky (cohesive) ends
(C) Either blunt or sticky ends depending on the specific enzyme
(D) Single-stranded RNA tails

2023

113. Yeast Artificial Chromosomes (YACs) are particularly useful for:
(A) Expressing small prokaryotic genes
(B) Blue-white screening of short PCR products
(C) Rapid sequencing of cDNA
(D) Cloning very large fragments

2013

114. In embryonic stem cell-mediated gene transfer, chimeric mice are produced by:
(A) Transfecting the surrogate mother directly
(B) Using a viral vector to infect adult skin cells
(C) Injecting genetically modified ESCs into a developing blastocyst
(D) Microinjecting sperm directly into oocytes

2015

115. Consider the following statements regarding somatic cell nuclear transfer (SCNT):
I. The recipient oocyte is typically arrested at metaphase II prior to enucleation.
II. Donor somatic cells must be highly proliferative in the S phase during transfer.
III. Electrofusion is a standard method to fuse the somatic cell with the enucleated oocyte.
Which of the above statement(s) is/are CORRECT?
(A) I and II
(B) I and III
(C) II and III
(D) I, II and III

2015

116. In the lac operon, the binding of allolactose to the repressor protein causes the repressor to:
(A) Bind firmly to the operator
(B) Undergo a conformational change and release from the operator
(C) Degrade the mRNA transcript
(D) Activate cyclic AMP production

2008

117. Which structural motif found in transcription factors functions by dimerization through hydrophobic interactions of repeated leucine residues?
(A) Leucine zipper
(B) Zinc finger
(C) Helix-turn-helix
(D) Beta-barrel

2017

118. Which term refers to the process where target proteins are covalently tagged with a small 76-amino-acid protein for proteasomal degradation?
(A) Phosphorylation
(B) Sumoylation
(C) Ubiquitination
(D) Glycosylation

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2018

119. Genomic imprinting generally involves monoallelic expression of a gene. This allele-specific expression is primarily dictated by:
(A) The random inactivation of one X chromosome
(B) The parent of origin
(C) The nutritional state of the embryo
(D) Point mutations in the promoter

2023

120. In structural genomics, the term "annotation pipeline" refers to the bioinformatic process of:
(A) Sequencing raw DNA reads
(B) Synthesizing cDNA from mRNA
(C) Staining chromosomes for karyotyping
(D) Assigning locations and functions

2012

121. MALDI-TOF mass spectrometry resolves ionized molecules based on their flight time, which is directly proportional to:
(A) The square root of their mass-to-charge ($\frac{m}{z}$) ratio
(B) Their isoelectric point
(C) Their thermal stability
(D) The number of disulfide bonds

2021

122. The chain termination method of sequencing (Sanger sequencing) fundamentally requires which mixture of nucleotides?
(A) Only ddNTPs
(B) Only dNTPs
(C) A mixture of dNTPs and a small proportion of ddNTPs
(D) Ribonucleotides exclusively

2001

123. Ion Torrent sequencing technology differs from Illumina sequencing primarily because Ion Torrent:
(A) Relies on reversible terminators and fluorescence
(B) Uses nanopores to pass DNA molecules
(C) Uses SMRT bells for continuous long reads
(D) Measures H+ ion release solely

2021

124. In Genome-Wide Association Studies, what is a Quantitative Trait Nucleotide (QTN)?
(A) An unknown environmental factor affecting the phenotype
(B) A specific single nucleotide polymorphism that causally affects a quantitative trait
(C) A random marker with no linkage to the trait
(D) A chromosomal inversion

2023

125. Each of the following questions contains an Assertion (A) and a Reason (R). Choose the correct option from the following:
Assertion (A): Genomic selection reduces the generation interval in dairy cattle breeding programs.
Reason (R): Genomic Estimated Breeding Values (GEBVs) can be accurately calculated for calves as soon as their DNA is genotyped, removing the need to wait for progeny testing.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2023

126. Which Bayesian model assumes a specific fraction (pi) of markers have zero effect on the trait, allowing for a variable proportion of informative markers?
(A) Bayes A
(B) Bayes Cpi
(C) GBLUP
(D) Ridge Regression

NODIA

2001

127. A primary objective of DNA shuffling in directed evolution is to:
(A) Recombine beneficial mutations
(B) Eliminate all genetic variation
(C) Map restriction enzyme sites
(D) Prevent crossing over in meiosis

2021

128. Euchromatin is distinguished from heterochromatin by its:
(A) High condensation during interphase
(B) Localization strictly at centromeres
(C) Decondensed structure and transcriptional activity
(D) Lack of histone proteins

2014

129. The characteristic banding pattern observed in G-banding correlates closely with:
(A) Ribosomal RNA gene clusters
(B) Telomerase activity
(C) Point mutations
(D) The distribution of GC and AT-rich isochores

2006

130. Exons in eukaryotic genes are best defined as:
(A) Sequences removed during splicing
(B) Regulatory sequences upstream of the promoter
(C) Transcribed regions that remain in the mature mRNA
(D) Sequences dictating replication origin

2024

131. During semiconservative DNA replication, which characteristic holds true?
(A) The original double helix remains completely intact.
(B) Each newly formed double helix consists of one parental strand and one newly synthesized strand.
(C) Both strands of the newly formed double helix are completely new.
(D) The DNA is cleaved into small pieces and reassembled.

2012

132. The primary role of eukaryotic RNA polymerase II is the transcription of:
(A) rRNA
(B) tRNA
(C) Pre-mRNA and some snRNAs
(D) Mitochondrial RNA

2012

133. The initiator tRNA in eukaryotic translation typically carries which amino acid?
(A) N-formylmethionine
(B) Serine
(C) Valine
(D) Unmodified methionine

2012

134. Which DNA modifying enzyme is essential for sealing the phosphodiester nicks left between Okazaki fragments?
(A) DNA Helicase
(B) DNA Topoisomerase
(C) DNA Ligase
(D) Polynucleotide kinase

2018

135. Match the vector type (List I) with its typical insert size capacity (List II):
List I: (Vector Type)
P. Plasmid
Q. Cosmid
R. BAC
S. YAC
List II: (Insert Size Capacity)
1. Up to 10 kb
2. ~35 - 45 kb
3. ~100 - 300 kb
4. Up to 1000 kb or more
(A) P-I, Q-II, R-III, S-IV
(B) P-I, Q-II, R-IV, S-III
(C) P-III, Q-I, R-II, S-IV
(D) P-II, Q-III, R-I, S-IV

2016

136. Retroviral vectors used in animal transgenesis integrate their genome via:
(A) Homologous recombination exclusively
(B) CRISPR/Cas9 nuclease activity
(C) Transient episomal maintenance
(D) Viral integrase mediating random or semi-random insertion

2002

137. Which of the following is considered a major application of Somatic Cell Nuclear Transfer (SCNT)?
(A) Sequencing whole genomes of extinct species
(B) Multiplying elite breeding livestock and preserving endangered species genetics
(C) Increasing the frequency of meiotic recombination
(D) Identifying single nucleotide polymorphisms

2014

138. In the regulation of the lac operon, catabolite repression ensures that the operon is heavily transcribed only when:
(A) Both glucose and lactose are abundant
(B) Glucose is absent and lactose is present
(C) Glucose is present and lactose is absent
(D) Both glucose and lactose are absent

2016

139. Trans-acting factors regulate eukaryotic transcription by:
(A) Being physically located on the same DNA molecule adjacent to the gene
(B) Diffusing through the nucleoplasm to bind specific cis-acting elements
(C) Replicating the DNA template
(D) Methylating the DNA

2023

140. Which of the following is a key function of molecular chaperones like Hsp70?
(A) Folding proteins correctly
(B) Adding methyl groups to DNA
(C) Cleaving signal peptides
(D) Initiating apoptosis

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2012

141. The covalent modification of histone tails by histone acetyltransferases (HATs) typically results in:
(A) Increased transcription
(B) Decreased transcription
(C) Immediate mRNA degradation
(D) Complete eviction of the histone core

2007

142. Which functional genomics tool relies on generating ~14 bp tags that are concatenated and sequenced to quantify mRNA abundance?
(A) Microarrays
(B) SAGE
(C) RNA-Seq
(D) GWAS

2009

143. In yeast two-hybrid systems, the bait protein is generally fused to:
(A) The activation domain (AD) of a transcription factor
(B) Beta-galactosidase directly
(C) Green fluorescent protein
(D) The DNA-binding domain (DBD) of a transcription factor

2023

144. Chemical degradation sequencing (Maxam-Gilbert) utilizes chemicals such as dimethyl sulfate or hydrazine to modify specific:
(A) Deoxyribose sugars
(B) Phosphate linkages
(C) Nitrogenous bases
(D) Dideoxynucleotides

2025

145. Consider the following statements regarding Next-Generation Sequencing (NGS) technologies:
I. Illumina uses bridge amplification to create clusters.
II. SMRT sequencing requires zero-mode waveguides.
III. Pyrosequencing reads fluorescent tags directly.
IV. Ion Torrent utilizes semiconductor technology.
Which of the above statement(s) is/are INCORRECT?
(A) III only
(B) I and III
(C) II and IV
(D) I, II and IV

NODIA

2015

146. Which term describes a scenario in GWAS where an apparent association is driven by subpopulation structure rather than true linkage to a QTN?
(A) Genetic drift
(B) Population stratification
(C) Genomic imprinting
(D) Epistasis

2006

147. A validation population in genomic selection is used to:
(A) Create the first generation of mutants
(B) Assess the accuracy of the prediction model built on the reference population
(C) Isolate the specific genes causing the trait
(D) Measure strictly non-heritable traits

2018

148. Which Bayesian model specifically allows each marker to have its own unique variance, differing from RR-BLUP?
(A) Bayes A
(B) GBLUP
(C) Principal Component Analysis
(D) Pedigree BLUP

2003

149. Marker-assisted introgression is a highly targeted breeding strategy aiming to:
(A) Introduce a specific allele while returning the rest of the genome to the recurrent parent type
(B) Randomly mutate the entire genome
(C) Introduce completely synthetic chromosomes
(D) Eliminate all genetic variation in the population

2024

150. Telomeric sequences in vertebrates typically consist of the tandem repeat:
(A) GATC
(B) TATAAA
(C) TTAGGG
(D) CCGG

2009

151. Which banding technique highlights the nucleolar organizer regions containing rRNA genes?
(A) Q-banding
(B) Ag-NOR banding
(C) G-banding
(D) C-banding

2001

152. Introns are correctly defined as:

(A) The coding segments of a gene
(B) Non-coding sequences that interrupt the coding region and are removed during splicing
(C) Sequences that translate into the signal peptide
(D) The core promoter elements

2001

153. Helicase separates double-stranded DNA during replication by breaking which type of bonds?
(A) Phosphodiester bonds
(B) Hydrogen bonds between base pairs
(C) Covalent bonds within the sugar-phosphate backbone
(D) Glycosidic bonds

2017

154. Spliceosome-mediated pre-mRNA splicing relies heavily on which type of RNA?
(A) rRNA
(B) tRNA
(C) snRNA
(D) snoRNA

2013

155. Arrange the following steps of translation initiation in eukaryotes in the correct order:
I. Binding of the 40S subunit to the 5' cap
II. Joining of the 60S large subunit
III. Scanning for the AUG start codon
IV. Formation of the ternary complex (eIF2-GTP-Met-tRNA)
(A) IV, I, III, II
(B) I, IV, III, II
(C) IV, III, I, II
(D) I, III, IV, II

2006

156. Restriction endonucleases evolved naturally in bacteria primarily to:
(A) Facilitate genetic recombination
(B) Defend against foreign viral (bacteriophage) DNA
(C) Replicate endogenous plasmids
(D) Assist in transcription initiation

2022

157. A major limitation of using standard plasmids for large genomic library construction is their:
(A) Requirement for eukaryotic host cells
(B) Inability to self-replicate
(C) Small insert capacity (typically $<$10 kb)
(D) High rate of mutation

2012

158. In CRISPR/Cas9 technology, the specificity of DNA cleavage is dictated directly by the:
(A) Cas9 protein structure alone
(B) Trans-activating crRNA (tracrRNA) only
(C) 20-nucleotide sequence at the 5' end of the single guide RNA (sgRNA)
(D) Homology-directed repair template

2025

159. When establishing donor cells for Somatic Cell Nuclear Transfer, serum starvation is often used to:
(A) Force cells into rapid mitosis
(B) Synchronize cells into the quiescent G0 phase
(C) Induce apoptosis
(D) Trigger DNA replication

2010

160. The regulatory gene (lacI) of the lac operon synthesizes a repressor protein that is:
(A) Expressed only in the presence of lactose
(B) Constitutively expressed at low levels
(C) Expressed only in the presence of glucose
(D) Regulated by attenuation

2004

161. Enhancers and promoters interact physically over long genomic distances through the formation of:
(A) Double-stranded RNA
(B) Chromatin loops mediated by proteins like cohesin
(C) Covalent DNA crosslinks
(D) Telomere clustering

2010

162. Phosphorylation, a critical post-translational modification for regulating protein activity, predominantly targets which amino acid residues?
(A) Glycine and Alanine
(B) Serine, Threonine, and Tyrosine
(C) Cysteine and Methionine
(D) Tryptophan and Phenylalanine

2008

163. CpG islands are often found near the promoters of mammalian genes. When these islands are heavily methylated, the associated gene is typically:
(A) Highly transcribed
(B) Alternatively spliced
(C) Transcriptionally silenced
(D) Rapidly mutated

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2001

164. The primary goal of generating Expressed Sequence Tags (ESTs) is to:
(A) Sequence the entire genome end-to-end
(B) Map repetitive non-coding elements
(C) Discover novel genes and evaluate expression profiles
(D) Quantify the number of centromeres

2011

165. Consider the following statements regarding 2D-PAGE proteomics:
I. The first dimension separates proteins by isoelectric point (pI).
II. The second dimension separates proteins by molecular weight using SDS.
III. It can resolve thousands of proteins on a single gel.
IV. It directly determines the amino acid sequence of the proteins.
V. It requires specialized ampholyte gradients.
Which of the above statement(s) is/are CORRECT?
(A) I, II, III and V
(B) I, III, IV and V
(C) II, III, IV and V
(D) I, II, IV and V

2022

166. Which sequencing technology is categorized as a "First-Generation" method?
(A) Sanger dideoxy sequencing
(B) Pyrosequencing
(C) Illumina sequencing
(D) Oxford Nanopore

2012

167. The "bridge amplification" step in Illumina sequencing is designed to:
(A) Repair double-strand breaks
(B) Generate dense clonal clusters
(C) Terminate strand elongation
(D) Convert DNA to RNA

2001

168. Statistical models in Genome-Wide Association Studies often include covariates to strictly control for:
(A) Laboratory temperature
(B) Population stratification and relatedness
(C) The size of the genome
(D) Intron length

2015

169. The estimation of Genomic Estimated Breeding Values (GEBVs) requires marker effects to be derived from a:
(A) Reference population with known phenotypes and genotypes
(B) Random sample of wild animals
(C) Population with genotypes only
(D) Single highly inbred line

2013

170. Which of the following best describes the GBLUP assumption regarding marker effects?
(A) Only a small subset of markers have an effect.
(B) All markers contribute equally to the genetic variance.
(C) Markers have an exponential distribution of effects.
(D) Marker effects are entirely dictated by epistasis.

2013

171. The CRISPR/Cas9-based "gene drive" achieves super-Mendelian inheritance by:
(A) Enhancing meiotic crossover frequencies
(B) Converting wild-type alleles to the drive allele via targeted cleavage and homology-directed repair
(C) Killing embryos that lack the drive allele
(D) Binding to the centromere and forcing biased segregation

NODIA

2016

172. The lowest level of DNA packaging, roughly 11 nm in diameter, is commonly referred to as the:
(A) Solenoid fiber
(B) Beads-on-a-string nucleosome array
(C) Radial loop scaffold
(D) Chromatid

2018

173. Q-banding requires observation under which type of microscope?
(A) Electron microscope
(B) Phase contrast microscope
(C) Fluorescence microscope
(D) Confocal microscope

2019

174. Which of the following sequences acts as a boundary element to prevent enhancers from activating adjacent non-target genes?
(A) Insulator
(B) TATA box
(C) Operator

(D) Shine-Dalgarno sequence

2009

175. Each of the following questions contains an Assertion (A) and a Reason (R). Choose the correct option from the following:
Assertion (A): Topoisomerase II is essential during the final stages of bacterial DNA replication.
Reason (R): It decatenates (unlinks) the newly replicated circular daughter chromosomes.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2021

176. Which RNA polymerase synthesizes 28S, 18S, and 5.8S ribosomal RNAs in eukaryotes?
(A) RNA Polymerase I
(B) RNA Polymerase II
(C) RNA Polymerase III
(D) Mitochondrial RNA Polymerase

2004

177. The "wobble" position allows the cell to function with fewer than 61 tRNAs. Which base is most prominent in wobble base pairing due to its ability to pair with U, C, or A?
(A) Guanine
(B) Adenine
(C) Inosine
(D) Cytosine

2025

178. Type III restriction endonucleases cleave DNA:
(A) At the exact site of recognition
(B) A specific, short distance away from their asymmetric recognition site
(C) Randomly at large distances
(D) Only single-stranded DNA

2025

179. The lacZ gene in a pUC vector encodes which enzyme used for blue-white screening?
(A) Beta-lactamase
(B) DNA ligase
(C) Alkaline phosphatase
(D) Beta-galactosidase

2021

180. A major limitation of pronuclear microinjection in animals is:
(A) Inability to transfer functional genes
(B) Random integration resulting in variable expression or insertional mutagenesis
(C) It only works in invertebrate species
(D) It requires highly synchronized somatic cells

2016

181. Oocyte enucleation during animal cloning is typically confirmed by:
(A) PCR analysis
(B) Staining with a fluorescent DNA dye such as Hoechst and exposure to UV light
(C) Measuring cell cycle phase
(D) Western blotting for histones

2017

182. In the trp operon, the regulatory attenuation mechanism relies on the translation of a short leader peptide containing two adjacent codons for:
(A) Tryptophan
(B) Methionine
(C) Proline
(D) Tyrosine

2019

183. Eukaryotic transcription factors featuring a helix-loop-helix (HLH) motif generally bind to DNA as:
(A) Monomers
(B) Tetramers
(C) Dimers (homo- or hetero-dimers)
(D) Octamers

2018

184. Signal peptides targeting proteins to the endoplasmic reticulum are rich in which type of amino acids?
(A) Acidic
(B) Basic
(C) Hydrophobic
(D) Polar uncharged

2025

185. Match the epigenetic mechanism (List I) with its specific molecular actor (List II):
List I: (Epigenetic Mechanism)
P. DNA Methylation
Q. Histone Acetylation
R. Histone Methylation
S. Chromatin Remodeling
List II: (Molecular Actor)
1. SWI/SNF Complex
2. HATs
3. DNMTs
4. HMTs
(A) P-III, Q-II, R-IV, S-I

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(B) P-III, Q-IV, R-II, S-I
(C) P-I, Q-II, R-III, S-IV
(D) P-II, Q-III, R-I, S-IV

2016

186. Which tool provides a holistic evaluation of steady-state mRNA levels utilizing highly parallel hybridization to spotted oligonucleotide probes?
(A) DNA Microarray
(B) 2D-PAGE
(C) Flow Cytometry
(D) Yeast Two-Hybrid

2009

187. In the Yeast Two-Hybrid system, a positive protein-protein interaction is identified by the:
(A) Reconstitution of a functional transcription factor leading to reporter gene expression
(B) Degradation of the target protein
(C) Emission of a fluorescent resonance energy term (FRET) signal
(D) Formation of a precipitate in the growth medium

2019

188. Maxam-Gilbert sequencing has largely been superseded by Sanger sequencing because it:
(A) Cannot read sequences longer than 10 base pairs
(B) Requires toxic reagents and radioisotope labeling
(C) Uses enzymes that are prone to high error rates
(D) Is incompatible with gel electrophoresis

2012

189. SMRT sequencing detects nucleotide incorporation using which specialized structural component?
(A) Semiconductor chip
(B) Zero-Mode Waveguide (ZMW)
(C) Nanopore protein
(D) Solid-phase emulsion droplet

2017

190. In a GWAS, high linkage disequilibrium (LD) implies that:
(A) Markers recombine freely at every generation
(B) Alleles at two closely spaced loci tend to be co-inherited
(C) The population is highly stratified
(D) The trait is purely polygenic

2006

191. Genomic Estimated Breeding Values (GEBVs) are calculated by summing:
(A) The phenotypic values of the ancestors
(B) The estimated effects of all genetic markers across the genome
(C) The error variance from the environment
(D) The recombination frequencies

2012

192. Ridge Regression-BLUP shrinks marker effects towards:
(A) Infinity
(B) Zero
(C) The population mean phenotype
(D) The largest marker effect

NODIA

2002

193. DNA shuffling creates chimeric sequences utilizing which key enzymatic process?
(A) Fragmentation and PCR reassembly without primers
(B) Restriction enzyme digestion followed by DNA ligase
(C) Reverse transcription using RNA-dependent RNA polymerase
(D) Homologous recombination in yeast cells

2017

194. Which histone variant replaces standard H3 at centromeres to serve as a foundation for kinetochore assembly?
(A) H2A.Z
(B) macroH2A
(C) CENP-A
(D) H3.3

2017

195. Consider the following statements regarding chromosome banding:
I. G-banding produces alternating light and dark bands.
II. Q-banding uses fluorescent quinacrine mustard.
III. C-banding selectively stains euchromatin.
Which of the above statement(s) is/are INCORRECT?
(A) I and II
(B) III only
(C) II and III
(D) I, II and III

2018

196. The -35 consensus sequence in a typical E. coli promoter is:
(A) TATAAT

(B) TTGACA
(C) CAAT
(D) GGGCGG

2006

197. DNA replication is termed "semidiscontinuous" because:
(A) The leading strand is synthesized continuously, while the lagging strand is synthesized in fragments
(B) It pauses frequently due to DNA damage
(C) It only occurs during half of the cell cycle
(D) RNA primers must be removed

2012

198. The 3' end of most eukaryotic mRNAs is characterized by a stretch of:
(A) 150-250 Adenine residues
(B) C-C-A sequence
(C) Uracil rich regions
(D) Alternating GC repeats

2008

199. During translation, the enzyme responsible for forming the peptide bond is a ribozyme embedded in the large ribosomal subunit called:
(A) Aminoacyl-tRNA synthetase
(B) Peptidyl transferase
(C) RNA polymerase
(D) DNA ligase

2006

200. Alkaline phosphatase treatment of a linearized cloning vector prevents:
(A) Vector self-ligation
(B) Foreign DNA insertion
(C) Antibiotic resistance expression
(D) DNA replication in the host

2008

201. Which cloning vector incorporates the F-plasmid origin of replication to maintain strict single-copy number stability for large inserts?
(A) pUC19
(B) YAC
(C) BAC
(D) Cosmid

2015

202. Retroviral integration into the host genome can sometimes cause cancer due to:
(A) Depletion of host nucleotides
(B) Insertional mutagenesis near oncogenes
(C) Destruction of the host mitochondria
(D) Excision of telomeres

NODIA

2017

203. Embryo reconstruction in SCNT requires artificially activating the embryo, a process that mimics fertilization by raising intracellular levels of:
(A) Magnesium
(B) Sodium
(C) Calcium
(D) Potassium

2014

204. In the absence of tryptophan, the repressor protein of the trp operon is:
(A) Active and bound to the operator
(B) Inactive and cannot bind the operator
(C) Degraded rapidly by proteases
(D) Bound to the promoter

2022

205. Select the correct order of events in CRISPR/Cas9-mediated gene knockout:
I. sgRNA binds to target DNA sequence adjacent to PAM
II. Cas9 introduces a double-strand break
III. Assembly of the Cas9-sgRNA ribonucleoprotein complex
IV. Non-homologous end joining (NHEJ) introduces an indel mutation
(A) III, I, II, IV
(B) I, III, II, IV
(C) III, II, I, IV
(D) I, II, III, IV

2025

206. Eukaryotic transcriptional activators typically possess at least two distinct domains: a DNA-binding domain and a(n):
(A) Spliceosome-binding domain
(B) Activation domain
(C) Helicase domain
(D) Repressor domain

2025

207. N-linked glycosylation begins in the lumen of which cellular organelle?
(A) Golgi apparatus
(B) Endoplasmic reticulum
(C) Lysosome
(D) Nucleus

2011

208. Which enzyme is primarily responsible for establishing de novo DNA methylation patterns during embryonic development?
(A) DNMT3a/3b
(B) DNMT1

(C) TET1
(D) HDAC

2001

209. The term "genome annotation pipeline" generally excludes which process?
(A) Gene prediction
(B) Functional assignment based on homology
(C) Wet-lab protein purification
(D) Identification of regulatory elements

2021

210. In mass spectrometry, the MALDI technique utilizes a matrix that functions to:
(A) Cleave proteins into peptides
(B) Absorb laser energy and facilitate desorption/ionization of analytes
(C) Separate peptides by size
(D) Measure the time of flight

2012

211. Sanger sequencing relies on standard DNA polymerase incorporating ddNTPs that lack a 3'-OH group. What direct consequence does this have?
(A) The template strand is degraded.
(B) The newly synthesized chain cannot be extended further.
(C) The DNA undergoes supercoiling.
(D) The primer dissociates immediately

2007

212. Sequencing-by-synthesis in the Illumina platform uses fluorescently labeled reversible terminators. "Reversible" implies that:
(A) The DNA sequence can be read backwards
(B) The terminator dye and block can be removed
(C) The polymerase can move 3' to 5'
(D) The template can be converted to RNA

2009

213. A typical GWAS relies heavily on tagging SNPs to represent variations across the genome, a strategy made viable by the presence of:
(A) Complete linkage equilibrium
(B) Linkage disequilibrium blocks or haplotypes
(C) Ubiquitous pleiotropy
(D) Identical repetitive sequences

2014

214. The term "GEBV" in genomic selection stands for:
(A) Genomic Estimated Breeding Value
(B) Genetically Engineered Breeding Variant
(C) Global Exact Breeding Vector
(D) Genomic Evaluated Backcross Variable

2014

215. Consider the following statements regarding Bayes A and Bayes B models:
I. Both model a t-distribution of marker effects.
II. Bayes B assumes a fraction (pi) of markers have zero effect.
III. Bayes A assumes all markers have some non-zero effect, with varying variances.
IV. Both are identical in their computational algorithms.
Which of the above statement(s) is/are CORRECT?
(A) I, II and III
(B) II, III and IV
(C) I, III and IV
(D) I, II and IV

2019

216. Marker-assisted introgression (MAI) utilizes molecular markers during backcrossing specifically to:
(A) Select against the donor genome at non-target loci (background selection)
(B) Decrease the mutation rate
(C) Map new genes without phenotypes
(D) Produce sterile offspring

2004

217. The solenoid model of chromatin structure, which achieves a 30 nm fiber, packs nucleosomes into a helix containing approximately how many nucleosomes per turn?
(A) 2
(B) 4
(C) 6
(D) 10

2019

218. In diagnostic cytogenetics, what specific property of G-banding makes it extremely valuable?
(A) It highlights only the sex chromosomes.
(B) It produces reproducible and distinct band patterns that uniquely identify each homologous chromosome pair.
(C) It causes the chromosomes to fluoresce green.
(D) It only stains actively transcribed genes.

2002

219. Within a eukaryotic gene, the 5' untranslated region (5' UTR) extends from the transcription start site to the:
(A) Initiation codon (AUG)
(B) First intron

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(C) Poly-A tail
(D) Stop codon

2004

220. Eukaryotic DNA replication requires licensing of origins. This licensing occurs strictly during which phase of the cell cycle?
(A) S phase
(B) G2 phase
(C) M phase
(D) G1 phase

2023

221. The pre-mRNA splicing process consists of two sequential transesterification reactions. The first reaction forms a:
(A) 2'-5' phosphodiester bond (lariat formation)
(B) 5'-3' phosphodiester bond
(C) Peptide bond
(D) Disulfide bond

2025

222. The term "degeneracy" in the genetic code means that:
(A) The genetic code is deteriorating over evolutionary time
(B) Some codons specify more than one amino acid
(C) Most amino acids are specified by more than one codon
(D) Stop codons also code for amino acids occasionally

2021

223. Polynucleotide kinase (PNK) is commonly used in molecular cloning to:
(A) Remove phosphate groups
(B) Cleave DNA molecules
(C) Methylate DNA molecules
(D) Phosphorylate the 5' ends of synthetic oligonucleotides or PCR products for ligation

2007

224. Which feature is unique to cosmids compared to standard plasmid vectors?
(A) Ampicillin resistance gene
(B) Origin of replication
(C) Cos sites required for lambda phage packaging
(D) Multiple cloning site

2023

225. Consider the following statements regarding retrovirus-mediated gene transfer:
I. It yields high efficiency of integration.
II. The size of the insert DNA is virtually unlimited.
III. It integrates randomly, which can cause insertional mutagenesis.
IV. It utilizes the viral integrase enzyme.
V. It always leads to stable germline transmission in one step.
Which of the above statement(s) is/are INCORRECT?
(A) II and V
(B) I and III
(C) III and IV
(D) I, II and IV

2025

226. In the context of SCNT, the term "reprogramming" refers to:
(A) Resetting the epigenetic state of the nucleus
(B) Altering the DNA sequence of the donor cell
(C) Forcing the oocyte into meiosis II
(D) Using a computer to design artificial genes

2025

227. The inducer of the lac operon, which binds the repressor protein in vivo, is:
(A) Allolactose
(B) Lactose directly
(C) cAMP
(D) Galactose

2008

228. Leucine zippers mediate transcription factor dimerization by aligning leucine residues that occur at every:
(A) Second position of an alpha helix
(B) Third position of an alpha helix
(C) Seventh position of an alpha helix
(D) Tenth position of an alpha helix

NODIA

2014

229. Molecular chaperones prevent protein aggregation primarily by binding to exposed:
(A) Hydrophilic regions
(B) N-linked glycosylations
(C) Phosphate groups
(D) Hydrophobic patches on unfolded or partially folded proteins

2002

230. Histone acetylation is catalyzed by HATs and generally occurs on the epsilon-amino group of which amino acid residues in the histone tails?
(A) Lysine
(B) Arginine
(C) Serine
(D) Threonine

2007

231. The bioinformatic step of identifying the specific physical location of a gene on a chromosome is part of:
(A) RNA splicing
(B) Protein purification
(C) Isoelectric focusing
(D) Genome annotation

2021

232. Two-dimensional gel electrophoresis (2D-PAGE) separates proteins in the second dimension based strictly on:
(A) Molecular mass
(B) Isoelectric point
(C) Hydrophobicity
(D) Affinity for zinc ions

2003

233. In the Maxam-Gilbert sequencing method, hydrazine is specifically used to modify:
(A) Purines (A and G)
(B) Guanine only
(C) Adenine only
(D) Pyrimidines (C and T)

2009

234. Nanopore sequencing technologies (e.g., MinION) have the distinct advantage over short-read sequencing of being able to:
(A) Generate ultra-long reads in a single run
(B) Sequence with absolutely zero errors natively
(C) Avoid the use of any polymerase or motor protein
(D) Rely entirely on chemical cleavage

2015

2014

235. The negative logarithm of the P-value ($-\log_{10} P$) is plotted on the y-axis of a Manhattan plot to:
(A) Visualize highly significant SNP associations
(B) Determine the physical distance between SNPs
(C) Map the exact effect size in kilograms
(D) Calculate the heritability of the trait

2005

236. A G-matrix constructed from genome-wide dense markers fundamentally replaces the traditional A-matrix (numerator relationship matrix) in BLUP because it:
(A) Measures expected relationships based on pedigree
(B) Captures Mendelian sampling and true relationships
(C) Is easier to compute by hand
(D) Completely ignores inbreeding

2015

237. The statistical assumption in GBLUP that all marker effects are drawn from the same normal distribution is best suited for traits that are:
(A) Highly polygenic with many genes of small effect
(B) Controlled by a single major gene
(C) Purely environmental
(D) Subject to genomic imprinting exclusively

2024

238. Directed evolution applies iterative rounds of mutagenesis and selection to:
(A) Optimize enzymes or proteins for specific desired traits, such as thermal stability
(B) Eradicate invasive species
(C) Select elite sires for dairy production
(D) Clone whole organisms

2019

239. Telomeric DNA is synthesized by telomerase, which is fundamentally a specialized type of:
(A) DNA-dependent DNA polymerase
(B) RNA-dependent DNA polymerase (reverse transcriptase)
(C) RNA-dependent RNA polymerase
(D) DNA-dependent RNA polymerase

2003

240. Which banding technique is most appropriate to visualize structural abnormalities in heterochromatic regions near the centromeres?
(A) C-banding
(B) G-banding
(C) R-banding
(D) Q-banding

2019

241. In eukaryotes, the "Kozak consensus sequence" surrounds the AUG start codon and is essential for:
(A) Efficient initiation of translation
(B) Transcription termination
(C) Spliceosome binding
(D) Polyadenylation

2006

242. During replication fork dynamics, the enzyme DNA gyrase in E. coli serves as a:
(A) Type I topoisomerase
(B) Type II topoisomerase
(C) Helicase
(D) Ligase

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2009

243. The addition of the 7-methylguanosine cap to the 5' end of pre-mRNA is catalyzed by three enzymes. The initial step involves the removal of the gamma phosphate from the 5' end by:
(A) Guanylyltransferase
(B) RNA triphosphatase
(C) Methyltransferase
(D) Poly-A polymerase

2022

244. The correct amino acid is covalently attached to the 3' CCA terminus of its tRNA by aminoacyl-tRNA synthetase via an intermediate that uses:
(A) GTP
(B) ATP
(C) UTP
(D) CTP

2012

245. Type IV restriction endonucleases are unique in that they specifically target and cleave:
(A) Unmethylated DNA
(B) Modified (e.g., methylated) DNA
(C) Single-stranded RNA
(D) Only palindromic sequences

2014

246. To prevent background non-recombinants in cloning, blue-white screening requires plating transformed bacteria on media containing:
(A) Ampicillin, X-gal, and IPTG
(B) Ampicillin only
(C) X-gal and Tetracycline
(D) Kanamycin and ONPG

2023

247. A primary advantage of CRISPR/Cas9 over earlier gene targeting methods (like ZFNs and TALENs) is that target specificity is dictated by:
(A) Complex protein engineering
(B) A simple, customizable RNA guide
(C) Viral integrase motifs
(D) The use of heavy metals

2024

248. In animal cloning, incomplete epigenetic reprogramming of the somatic donor nucleus frequently leads to:
(A) Increased lifespan of the clone
(B) Developmental anomalies like Large Offspring Syndrome
(C) Immediate chromosomal shattering
(D) Enhanced fertility

2003

249. The CAP-cAMP complex acts on the lac operon as a:
(A) Positive transcriptional activator
(B) Negative repressor
(C) Corepressor
(D) Riboswitch

2012

250. Zinc finger motifs coordinate a zinc ion typically using conserved residues of:
(A) Leucine and Valine
(B) Histidine and Cysteine
(C) Serine and Threonine
(D) Aspartate and Glutamate

2016

251. Which of the following best describes the function of ubiquitin ligase (E3) in the ubiquitination pathway?
(A) It activates ubiquitin using ATP.
(B) It conjugates ubiquitin to the target protein, providing specificity.
(C) It degrades the ubiquitinated protein directly.
(D) It de-ubiquitinates the protein.

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2016

252. The maintenance DNA methyltransferase responsible for copying methylation patterns to the newly synthesized daughter strand during DNA replication is:
(A) DNMT1
(B) DNMT3a
(C) DNMT3b
(D) MBD1

2023

253. RNA-Seq quantifies gene expression levels by calculating the number of:
(A) Spot fluorescence intensities
(B) Mapped sequencing reads aligned to a specific transcript (e.g., RPKM/FPKM/TPM)
(C) Protein spots on a 2D gel
(D) Restriction fragment sizes

2023

254. In the Yeast Two-Hybrid system, a false positive might occur if the "bait" protein inherently possesses:
(A) DNA-binding activity only
(B) Intrinsic transcriptional activation capability without interacting with the "prey"
(C) Ubiquitin ligase activity
(D) RNase activity

2001

255. In Sanger sequencing electropherograms, a heterozygous single nucleotide polymorphism (SNP) typically appears as:
(A) A single, perfectly sharp peak
(B) Two overlapping peaks of different colors at the same position
(C) A complete loss of signal
(D) A long stretch of a single repeating color

2013

256. The SMRT sequencing technology (PacBio) uniquely enables the direct detection of which DNA modification during the sequencing run?
(A) Histone acetylation
(B) DNA methylation via altered kinetics
(C) RNA splicing
(D) Ubiquitination

2012

257. What statistical issue arises in GWAS due to evaluating hundreds of thousands of SNPs simultaneously?
(A) Loss of degrees of freedom
(B) The multiple testing problem, leading to false positives
(C) Complete collinearity
(D) Inability to calculate a mean phenotype

2018

258. Genomic Estimated Breeding Values (GEBVs) allow dairy breeders to select superior bulls based on:
(A) Their milk production (phenotype)
(B) Their daughters' milk production exclusively
(C) Their genomic marker profile tested shortly after birth
(D) Their physical conformation only

2003

259. Bayesian alphabet models (Bayes A, B, C, L) in genomic prediction differ primarily in their prior assumptions about the:
(A) Recombination rate between chromosomes
(B) Distribution of marker variances and effects
(C) Number of chromosomes in the species
(D) Environmental variance

2003

260. Marker-assisted introgression typically requires how many generations of backcrossing with background selection to recover >99% of the recurrent parent genome?
(A) 1-2 generations
(B) 3-4 generations
(C) 10-15 generations
(D) 20+ generations

2024

261. The histone core octamer is wrapped by DNA in a left-handed superhelical turn. Approximately how many turns does the 146 bp of DNA make around the core?
(A) 1.67
(B) 1.0
(C) 2.5
(D) 3.1

2016

262. Chromosome banding requires arresting cells in which specific phase of mitosis to obtain highly condensed chromosomes?
(A) Prophase
(B) Metaphase
(C) Anaphase
(D) Telophase

2011

263. In prokaryotes, what is the sequence located roughly 8 bases upstream of the AUG start codon that binds to the 16S rRNA?
(A) Shine-Dalgarno sequence
(B) TATA box
(C) Kozak sequence
(D) Pribnow box

2025

264. DNA polymerase requires a free 3'-OH group to begin synthesis. In vivo, this group is provided by a short segment of:
(A) Single-stranded DNA
(B) RNA synthesized by primase
(C) A protein primer
(D) A methyl group

2009

265. The cleavage of a pre-mRNA at the polyadenylation site is directed by the sequence AAUAAA and a downstream sequence rich in:
(A) G/U residues
(B) A/T residues
(C) C/G residues
(D) Poly-A tracts

2024

266. During translation termination, release factors recognize the stop codon and catalyze the hydrolysis of the bond linking the:
(A) Ribosomal subunits
(B) Polypeptide chain to the tRNA in the P site
(C) mRNA to the ribosome
(D) Anticodon to the codon

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2005

267. Restriction enzyme EcoRI recognizes the palindromic sequence GAATTC and cuts between G and A. This generates fragments with:
(A) 3' overhangs
(B) 5' overhangs
(C) Blunt ends
(D) Hairpin loops

2002

268. A genomic library constructed in a Bacterial Artificial Chromosome (BAC) vector is preferred over a plasmid library for sequencing whole genomes because it:
(A) Has a smaller insert size, simplifying sequencing
(B) Requires fewer clones to cover the entire genome
(C) Replicates at a very high copy number, causing toxicity
(D) Excludes all intronic sequences

2002

269. Retrovirus-mediated gene transfer is limited to transferring transgenes into cells that are:
(A) Strictly non-dividing
(B) Actively dividing
(C) Terminally differentiated
(D) Devoid of a nucleus

2022

270. In CRISPR/Cas9, the Protospacer Adjacent Motif (PAM) sequence for the commonly used Streptococcus pyogenes Cas9 (SpCas9) is:
(A) 5'-NGG-3'
(B) 5'-TTTN-3'
(C) 5'-CCG-3'
(D) 5'-TAA-3'

2012

271. In the context of the trp operon, the leader sequence encodes a peptide rich in tryptophan. If tryptophan levels are low, the ribosome stalls, allowing the mRNA to form an antiterminator hairpin. This describes:
(A) The process of transcriptional attenuation
(B) The activity of catabolite repression
(C) Allosteric inhibition by end-products
(D) Positive control by activator proteins

2005

272. Helix-turn-helix (HTH) motifs bind to the DNA double helix primarily by inserting the "recognition helix" into the:
(A) Minor groove
(B) Major groove
(C) Sugar-phosphate backbone
(D) Centromere

2017

273. The initial attachment of the core oligosaccharide in N-linked glycosylation utilizes a lipid carrier embedded in the ER membrane called:
(A) Cholesterol
(B) Dolichol phosphate
(C) Phosphatidylcholine
(D) Sphingomyelin

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2025

274. Which of the following describes "genomic imprinting"?
(A) The random mutagenesis of the genome by radiation.
(B) An epigenetic phenomenon causing genes to be expressed in a parent-of-origin-specific manner.
(C) The process of staining chromosomes to reveal G-bands.
(D) The physical mapping of restriction sites.

2003

275. Expressed Sequence Tags (ESTs) are particularly useful for:
(A) Determining the complete sequence of introns
(B) Rapidly identifying transcripts and aiding in gene discovery
(C) Identifying the location of centromeres
(D) Mapping the mitochondrial DNA exclusively

2009

276. In mass spectrometry, proteins are commonly digested into smaller peptides prior to analysis using which highly specific protease?
(A) Pepsin
(B) Trypsin
(C) Chymotrypsin
(D) Papain

2018

277. The original Sanger sequencing method utilized radioactive isotopes for detection. Modern automated Sanger sequencing replaces radioisotopes with:
(A) Fluorescent dyes attached to the ddNTPs
(B) Chemiluminescent substrates
(C) Silver staining
(D) X-ray crystallography

2015

278. In Ion Torrent sequencing, if a homopolymer repeat (e.g., AAAA) is present in the template, the detector will register:
(A) Larger pH changes from released H+ ions
(B) A single pH change of standard amplitude
(C) No pH change
(D) A decrease in temperature

2019

279. To detect Quantitative Trait Nucleotides (QTNs) in a GWAS, the statistical power heavily depends on both the sample size and the:
(A) Length of the telomeres
(B) Minor Allele Frequency (MAF) of the markers
(C) Number of introns in the genome
(D) Size of the animal

2018

280. The traditional numerator relationship matrix (A-matrix) calculates the expected genetic covariance between full siblings as 0.5. The genomic relationship matrix (G-matrix) calculates the realized covariance between full siblings, which:
(A) Is always exactly 0.5
(B) Varies from 0.5 via Mendelian sampling
(C) Is always 1.0
(D) Is always 0.25

2014

281. The Bayes C model differs from Bayes B primarily by assuming that the variances for all markers with non-zero effects are:
(A) Infinite
(B) Equal (drawn from a common variance)
(C) Continuously variable across a t-distribution
(D) Exactly zero

2003

282. Gene drive systems designed to control insect vectors (like mosquitoes) aim to spread an allele through a wild population rapidly. This relies on biased inheritance exceeding the Mendelian rate of:
(A) 50%
(B) 25%
(C) 10%
(D) 1%

2017

283. Euchromatin is generally found concentrated in the:
(A) Inner nuclear matrix and chromosome arms
(B) Nuclear periphery and nucleolus
(C) Centromeres exclusively
(D) Telomeres exclusively

2018

284. Which chemical treatment is standardly applied in C-banding to denature DNA, prior to washing and Giemsa staining?
(A) Barium hydroxide
(B) Trypsin
(C) Quinacrine mustard
(D) Silver nitrate

2009

285. In eukaryotic gene structure, what is the role of an enhancer?
(A) It dictates the start site of transcription.
(B) It increases transcription rates via activators
(C) It provides the signal for mRNA splicing.
(D) It codes for a small regulatory peptide.

2011

286. During DNA replication, proofreading of the newly synthesized DNA is carried out by DNA polymerases using their:
(A) 3' to 5' exonuclease activity
(B) 5' to 3' exonuclease activity
(C) Endonuclease activity
(D) Ligase activity

2017

287. Which component of the spliceosome recognizes and binds to the 5' splice site of the intron?
(A) U1 snRNP
(B) U2 snRNP
(C) U4 snRNP
(D) U5 snRNP

2019

288. Aminoacyl-tRNA synthetases are highly specific enzymes. Typically, a single living cell contains:
(A) Only 4 synthetases (one for each base)
(B) 61 synthetases, one for each sense codon
(C) 1 universal synthetase for all amino acids
(D) 20 different synthetases, one for each standard amino acid

2001

289. Which enzyme is used in cDNA synthesis to generate a complementary DNA strand from an mRNA template?
(A) Reverse transcriptase
(B) DNA-dependent RNA polymerase
(C) Taq polymerase
(D) DNA ligase

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2007

290. Ti plasmid is a widely used cloning vector for plant transformation, derived from:
(A) E. coli
(B) Agrobacterium tumefaciens
(C) Saccharomyces cerevisiae
(D) Bacillus thuringiensis

2002

291. Transgenic animals produced via pronuclear microinjection are typically:
(A) Homozygous for the transgene in the first generation (F0)
(B) Hemizygous for the transgene, which integrates randomly as concatemers
(C) Free of any host DNA mutations
(D) Lacking the transgene in their germ cells

2018

292. In SCNT, the phenomenon where the clone shares the nuclear genome of the donor but the mitochondrial genome of the recipient oocyte is termed:
(A) Genetic chimerism
(B) Mitochondrial heteroplasmy or mitochondrial inheritance from the oocyte
(C) Somatic hypermutation
(D) Polyploidy

2016

293. The trp operon represents a classic example of a repressible system because its transcription is:
(A) Shut off in the presence of the end product (tryptophan)
(B) Turned on only when tryptophan is present
(C) Unaffected by tryptophan levels
(D) Controlled by glucose levels

2002

294. Zinc finger nucleases (ZFNs) represent an older gene editing technology that combined a DNA-cleaving domain (FokI) with a customizable:
(A) Zinc finger DNA-binding domain
(B) RNA guide
(C) Leucine zipper domain
(D) Helix-turn-helix motif

2024

295. Which of the following sequences typically signals the targeting of a protein to the proteasome for degradation?
(A) Poly-A tail
(B) Signal peptide
(C) Polyubiquitin chain
(D) N-acetylglucosamine chain

2017

296. Epigenetic marks are considered heritable. In mammals, most DNA methylation marks are erased and re-established during:
(A) Senescence
(B) Early embryonic development and gametogenesis
(C) Every mitotic division in somatic tissues
(D) Apoptosis

2023

297. In structural genomics, identifying Open Reading Frames (ORFs) is a critical step in genome annotation. An ORF is defined as a continuous stretch of codons that begins with a start codon and ends with a:
(A) Stop codon
(B) Promoter sequence
(C) Polyadenylation site
(D) Splice donor site

2005

298. Which of the following represents a quantitative method to detect protein-protein interactions directly from cell lysates based on antibody specificity?
(A) Co-immunoprecipitation (Co-IP)
(B) PCR
(C) Southern blotting
(D) SAGE

2025

299. The Genome-Wide Association Study (GWAS) approach differs from traditional linkage mapping primarily because GWAS:
(A) Relies on structured, multi-generation family pedigrees
(B) Exploits historical recombination events in unstructured populations at a population level
(C) Assesses only one candidate gene at a time
(D) Does not require genotyping

2003

300. In genomic selection, the phenomenon where marker estimates in the reference population perform poorly when applied to predicting GEBVs in a distantly related validation population is mainly due to the decay of:
(A) Expression of hybrid vigor or heterosis effects
(B) Total number of chromosomes in the species
(C) Linkage disequilibrium between markers and QTLs
(D) Rate of transcription across the entire genome

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ANSWERS

1. (B) 146 base pairs
The fundamental unit of eukaryotic chromatin is the nucleosome, which consists of a histone octamer wrapped by a specific length of DNA. This structural core involves approximately one hundred and forty-six base pairs of DNA coiled in nearly two left-handed superhelical turns. This compact arrangement facilitates higher-order packaging of the genome within the nucleus.

2. (C) Q-banding
Fluorescent staining techniques utilize quinacrine mustard to produce distinct bright and dark horizontal bands across chromosomes. This specific method highlights regions rich in adenine and thymine, which bind the dye more intensely. Observing these fluorescent patterns allows for the precise identification of individual chromosomes and the detection of structural abnormalities in specialized clinical diagnostic settings.

3. (A) To serve as the core promoter for RNA polymerase II
The core promoter of many eukaryotic genes contains a highly conserved DNA sequence rich in thymine and adenine. This specific element functions as the primary site for the assembly of the transcription initiation complex. By recruiting general transcription factors and RNA polymerase II, it ensures that the process begins accurately at the designated transcription start site.

4. (D) DNA topoisomerase
During the unwinding of the double helix, tension builds up in the form of positive supercoils ahead of the moving replication fork. Specialized enzymes mitigate this topological stress by creating transient breaks in the DNA backbone. By allowing the strands to rotate or pass through one another, these proteins prevent the DNA from becoming irreversibly tangled.

5. (A) Both A and R are true and R is the correct explanation of A.
Eukaryotic transcripts undergo processing where a modified guanine residue is attached to the beginning of the pre-mRNA. This structure utilizes a unique chemical bond involving three phosphate groups to link the nucleotide in a head-to-head orientation. This modification provides essential stability by preventing enzymatic breakdown and is vital for efficient translation initiation during protein synthesis.

6. (C) First base (5' end)
Flexibility in the pairing between the messenger RNA and transfer RNA allows a single tRNA to recognize multiple codons. This phenomenon occurs at the specific position where the first base of the anticodon meets the third base of the codon. Non-standard hydrogen bonding at this site enables efficient translation while reducing the total number of tRNAs required.

7. (D) Cleave DNA at specific palindromic recognition sites
Recombinant DNA technology relies heavily on enzymes that recognize specific, often palindromic, sequences within a double-stranded molecule. These catalysts function by cutting the phosphodiester backbone at precise locations within or very close to their target sites. Because they do not require complex cofactors like ATP for cleavage, they are highly reliable tools for molecular cloning.

8. (A) White colonies due to lacZ' gene inactivation
Bacterial cloning often utilizes a color-based system to identify successful transformants. When a foreign DNA fragment is inserted into the multiple cloning site of a specific vector, it disrupts the coding sequence of a marker enzyme. Consequently, the bacteria cannot process the chromogenic substrate, leading to the formation of colorless colonies instead of the typical blue ones.

9. (B) CRISPR/Cas9-mediated gene targeting
Modern genomic engineering utilizes a programmable system to introduce precise modifications at specific locations within the genome. A guide molecule directs an endonuclease to create a double-strand break, which the cell then repairs using internal mechanisms. This approach allows for efficient gene disruption or

NODIA

the insertion of new sequences through homology-directed repair in various animal models.

10. (B) G0/G1 phase of the cycle
Successful animal cloning requires the synchronization of the donor cell with the recipient oocyte to ensure proper nuclear reprogramming. Quiescent cells are typically used because their chromatin is in a state that is more receptive to the cytoplasmic factors of the oocyte. This coordination prevents premature DNA replication and chromosomal damage during the early stages of embryonic development.

11. (A) Operator
Bacterial gene regulation often involves a specific DNA sequence located between the promoter and the structural genes. A regulatory protein binds to this site to physically block the movement of RNA polymerase, thereby preventing the synthesis of messenger RNA. This negative control mechanism ensures that metabolic enzymes are only produced when the corresponding substrate is available in the environment.

12. (C) Zinc finger
Certain transcription factors employ a structural motif where a central metal ion stabilizes a small, functional loop of amino acids. This arrangement allows the protein to insert its alpha-helical component into the major groove of the DNA double helix. By recognizing specific base sequences, these motifs enable the precise regulation of gene expression across various eukaryotic organisms.

13. (D) Ubiquitination
The selective degradation of cellular proteins is often triggered by the covalent attachment of a small, highly conserved regulatory polypeptide. This modification typically occurs on lysine residues and serves as a molecular signal for recognition by the proteasome. Through this process, the cell can rapidly remove misfolded, damaged, or regulatory proteins to maintain proper physiological balance and function.

14. (C) DNA methylation at CpG dinucleotides
Epigenetic regulation in mammals involves the addition of methyl groups to specific cytosine residues located next to guanine. This modification is essential for establishing parent-of-origin specific expression patterns, where only one allele of a gene is active. These marks are faithfully maintained during cell division, ensuring that certain traits are inherited in a non-Mendelian, imprinted manner.

15. (A) P-III, Q-II, R-IV, S-I
Functional genomics utilizes diverse tools to profile gene expression and identify transcripts across different biological conditions. Sequence-based tags facilitate rapid identification, while concatenated markers allow for quantification. Modern next-generation technologies provide high-throughput transcriptomic data, and hybridization techniques enable global expression profiling. Integrating these varied approaches allows researchers to understand the complex regulatory landscape within a genome.

16. (D) Isoelectric point
High-resolution protein separation is achieved by utilizing two distinct physical properties in successive steps. In the initial phase, molecules migrate through a pH gradient until they reach a state where their net electrical charge is zero. This specific point of immobility allows for the precise isolation of proteins based on their intrinsic acidic or basic characteristics before size-based separation.

17. (A) 3'-OH group
DNA sequencing methods often utilize modified nucleotides that prevent the further extension of a growing molecular chain. These analogs lack the specific chemical group necessary for forming a phosphodiester bond with the next incoming base. When incorporated by a polymerase, they cause the synthesis to stop abruptly, generating fragments of varying lengths used to determine the genetic sequence.

18. (C) Ion Torrent sequencing
Certain next-generation sequencing platforms detect genetic information by monitoring chemical changes during DNA synthesis. As each nucleotide is added to the growing strand, a positively charged hydrogen ion is released into the surrounding solution. A hypersensitive semiconductor chip measures the resulting shift in acidity, allowing the system to identify the sequence without the need for fluorescent dyes.

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19. (A) Principal Component Analysis (PCA)
Association studies can be biased by differences in ancestral backgrounds among individuals, which may lead to incorrect conclusions regarding genetic markers. To address this, researchers use mathematical techniques to identify and adjust for internal population subgroups. By incorporating these derived components into the statistical model, the influence of population structure is minimized, thereby improving the reliability of results.

20. (D) Reference (training) population
The precision of genetic evaluations in modern livestock breeding depends heavily on the quality of the initial data set used for calibration. This group must consist of individuals who possess both detailed genetic marker information and accurate physical performance records. A larger and more representative group ensures that the mathematical models can effectively predict the genetic potential of young animals.

21. (B) Ridge Regression-BLUP (RR-BLUP)
Genomic prediction models utilize different assumptions regarding the contribution of markers to a specific trait. One common approach treats all genetic variants as having an equal influence by assigning them the same variance in the statistical analysis. This simplifies the computation and is particularly effective for complex traits that are influenced by a vast number of small genetic effects.

22. (C) Evolution of genes to generate chimeric proteins
Directed evolution techniques involve the recombination of related genetic sequences to create novel variants with improved functions. By fragmenting parental genes and allowing them to reassemble through a process of molecular crossover, researchers can produce a diverse library of chimeric molecules. Subsequent screening identifies individuals with superior properties, such as enhanced enzymatic activity or increased structural stability.

23. (D) Transcriptionally inactive and densely packed DNA
Chromatin exists in different states of compaction that reflect its functional status within the cell. Highly condensed regions are typically characterized by a lack of gene expression and stain darkly under a microscope. These areas often contain repetitive sequences and play critical roles in maintaining structural integrity and regulating the accessibility of the genome to the transcriptional machinery.

24. (A) Trypsin
Standard chromosome identification relies on creating a characteristic pattern of light and dark horizontal stripes. Prior to staining, the samples are treated with a specific protease to partially break down the associated chromosomal proteins. This enzymatic digestion makes the DNA more accessible to the dye, resulting in a highly reproducible banding pattern used for karyotyping and clinical diagnostics.

25. (C) I and III
Eukaryotic gene architecture includes sequences that are eventually translated and regions that regulate the process. While coding segments are preserved in the final transcript, the leader sequence at the beginning of the molecule does not typically contain the signal for adding the tail. Errors in understanding these components can lead to incorrect interpretations of how genes are structured and expressed.

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26. (B) DNA polymerase epsilon
Eukaryotic cells utilize specialized enzymes to replicate each strand of the double helix with high fidelity. One particular polymerase is primarily responsible for the continuous synthesis of the strand that moves in the same direction as the unwinding fork. This enzyme ensures rapid and accurate duplication of the majority of the genome during the synthesis phase of the cell.

27. (A) Facilitate termination of transcription
In many bacteria, the process of messenger RNA synthesis requires a specific protein to stop the elongation of the transcript. This factor moves along the nascent RNA molecule and, upon reaching a specific site, utilizes energy to displace the polymerase from the DNA template. This mechanism ensures that transcription ends precisely at the correct location for functional gene expression.

28. (C) A specific amino acid can be encoded by more than one codon
The genetic code is structured so that multiple three-nucleotide sequences can signal for the same building block during protein synthesis. This redundancy provides a protective mechanism

against certain mutations, as a change in a single base may not necessarily alter the resulting protein sequence. This characteristic is universal across almost all living organisms and is fundamental to molecular biology.

29. (D) Dephosphorylate the cloning vector
Molecular cloning procedures often involve an enzymatic step to remove the phosphate group from the ends of a linearized circular DNA molecule. This prevents the vector from simply closing back on itself during the ligation reaction. By ensuring the ends cannot rejoin without an insert, this treatment significantly increases the efficiency of producing recombinant molecules containing the desired foreign DNA.

30. (C) Yeast Artificial Chromosome (YAC)
Mapping complex genomes requires vectors that can carry exceptionally long segments of DNA. Certain engineered systems utilize the essential structural elements of a fungal chromosome, such as centromeres and telomeres, to maintain stability. These tools allow researchers to clone and study fragments spanning hundreds of thousands of base pairs, which is essential for constructing comprehensive physical genomic maps.

31. (B) Efficient and stable integration into the genome
Transferring genetic material into animal cells can be achieved using modified viruses that naturally insert their own sequence into the host's DNA. This method is highly valued because it ensures that the new gene becomes a permanent part of the cellular blueprint. Consequently, the transgene is faithfully passed on to all daughter cells, allowing for long-term expression and study.

32. (D) The metaphase II plate (chromosomes)
Cloning through nuclear transfer involves the delicate removal of the native genetic material from an egg cell. Because the chromosomes are not enclosed within a nucleus at this specific developmental stage, the operator must identify and extract the spindle-associated bundle. Precise removal of these structures ensures that only the donor nucleus provides the genetic blueprint for the resulting embryo.

33. (A) Binding of the corepressor to the repressor, blocking transcription
Bacterial metabolism is often regulated by the availability of specific nutrients. When a certain amino acid reaches a high concentration inside the cell, it binds to a regulatory protein, changing its shape. This activated complex then attaches to the DNA, preventing the synthesis of enzymes that would otherwise produce more of that amino acid, thereby conserving cellular resources.

34. (C) Function in either orientation over long distances
Specific DNA sequences can significantly boost the expression of genes even when located far away from the starting point. Unlike other regulatory elements, these segments are versatile and can operate regardless of their direction or whether they are upstream or downstream. They interact with the promoter through the formation of physical loops in the chromatin, bringing distant factors together.

35. (B) Endoplasmic reticulum → Golgi apparatus → Secretory vesicles → Plasma membrane
Proteins destined for export are synthesized and modified through a series of specialized cellular compartments. The process begins with initial folding and sugar attachment in one organelle before the molecules are transported to a processing center for further refinement. Finally, they are packaged into small containers that travel to the cell's outer boundary, where they are released into the surroundings.

36. (D) Histone acetylation
Gene expression is influenced by the chemical modification of the proteins around which DNA is wrapped. The addition of specific groups to these protein tails reduces their positive charge, loosening their grip on the negatively charged DNA. This creates a more open and accessible structure, which is characteristic of regions where transcription factors and enzymes can easily initiate gene activity.

37. (B) SAGE (Serial Analysis of Gene Expression)
Quantifying the abundance of various transcripts involves capturing short, representative sequences from each messenger RNA molecule. These segments are then linked together into longer chains for efficient sequencing and analysis. By counting the frequency of each unique tag,

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researchers can gain a comprehensive overview of which genes are active and their relative levels of expression in a sample.

38. (C) Ion Torrent sequencing
Proteomic analysis often utilizes a specialized ionization technique where molecules are embedded in a solid matrix and hit with a light beam. This process converts the proteins or peptides into a gaseous state without breaking them apart. Once charged, these particles can be accurately measured by their speed, allowing for the precise determination of their mass and identity in complex mixtures.

39. (D) Base-specific chemical cleavage of DNA
Early methods for determining the order of nucleotides relied on the use of specialized chemicals that break the DNA strand at specific bases. By treating a labeled sample with different reagents, a series of fragments is generated that reflects the positions of each nucleotide. These pieces are then separated by size to reconstruct the original sequence of the genetic material.

40. (A) Reversible terminator nucleotides
Modern high-throughput sequencing involves the use of special building blocks that stop the synthesis of a DNA strand after a single addition. Each block carries a unique fluorescent tag that reveals the identity of the added base. After the signal is recorded, the blockage is removed, allowing the next nucleotide to be incorporated and the sequence to be read step-by-step.

41. (B) Genomic coordinates (chromosomes)
Large-scale genetic studies often visualize results using a specific type of scatter plot. The horizontal axis represents the physical position of various markers across all the chromosomes in the genome. By plotting statistical significance on the vertical axis, researchers can easily identify specific genomic regions where the markers are strongly associated with the physical trait being studied in a population.

42. (A) Can accurately predict breeding values for young animals before they exhibit the trait
Selecting superior individuals for breeding is significantly improved by using genetic information rather than waiting for an animal to mature. By analyzing DNA markers early in life, breeders can estimate an individual's genetic potential with high accuracy. This approach drastically shortens the time required between generations, leading to faster genetic progress and more efficient improvement of desirable traits.

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43. (A) Genomic relationship matrix (G-matrix) derived from marker data
Modern genetic evaluations utilize a detailed mathematical table that describes how closely individuals are related based on their actual DNA similarities. Unlike traditional methods that rely on recorded family histories, this approach captures the real genetic sharing caused by random inheritance. This leads to more precise estimates of an individual's breeding value by accounting for the exact genes they inherited.

44. (D) Forcing inheritance rates greater than 50%
Certain genetic systems are designed to propagate specific traits through a population much faster than normal biological laws would allow. By ensuring that a particular gene is passed on to nearly all offspring, these tools can quickly alter the genetic makeup of an entire species. This technology is often explored for controlling invasive pests or reducing the spread of vector-borne diseases.

45. (A) Both A and R are true and R is the correct explanation of A.
Eukaryotic chromosomes are protected by repetitive sequences at their extremities which prevent the loss of essential genetic information during replication. A specialized enzyme maintains these structures by adding new repeats using an internal RNA guide. This process is crucial for cellular longevity and prevents the ends of the DNA from being recognized as damage by the cell's repair systems.

46. (C) Nucleolar Organizer Regions
Specific staining techniques are used to identify the chromosomal locations where ribosomal RNA genes are clustered. These areas are characterized by the presence of certain proteins that react with silver nitrate, producing dark spots under a microscope. Identifying these regions is vital for studying cellular function and identifying specific chromosomal rearrangements in both research and clinical diagnostic applications.

47. (B) -10 and -35 consensus sequences
The initiation of transcription in bacteria requires the recognition of specific DNA elements located

just before the gene. A specialized subunit of the polymerase enzyme identifies these conserved sequences to ensure the machinery binds at the correct location. These regions act as a biological signal that guides the enzyme to the start site, allowing the synthesis of RNA to begin.

48. (D) DNA Polymerase I
During the duplication of the genome, short segments of RNA are initially used to start the process. Once synthesis is underway, these temporary primers must be removed and replaced with the correct DNA nucleotides. A versatile enzyme handles this task by simultaneously chewing away the RNA and filling the resulting gap, ensuring the genetic code is continuous and accurate.

49. (B) Small nuclear ribonucleoproteins (snRNPs)
The removal of non-coding segments from pre-messenger RNA is performed by a large molecular complex found within the nucleus. This machinery is composed of specific proteins paired with small RNA molecules that recognize the boundaries of the sequences to be excised. By precisely cutting and joining the remaining parts, it ensures that the resulting molecule can be correctly translated.

50. (C) Correct tRNA and amino acid attachment
The accuracy of protein synthesis depends on the precise pairing of amino acids with their corresponding transfer molecules. Specialized enzymes catalyze this essential step by recognizing both the specific structure of the amino acid and the anticodon of the tRNA. This ensures that the genetic code is translated faithfully, as the ribosome simply follows the instructions provided by these pre-charged molecules.

51. (B) Type III
Certain bacterial enzymes recognize asymmetric DNA sequences and cut the double helix at a fixed distance from that site. These proteins operate as complex units that require energy and specific methyl donors to perform their function. Because they cleave outside of their recognition sequence, they are distinct from the more commonly used tools that cut exactly at the target site.

52. (C) Centromere sequence for segregation
Basic cloning tools are small, circular DNA molecules that can replicate independently within a bacterial host. They must contain a starting point for duplication, a way to select for their presence, and a convenient location for inserting foreign DNA. However, they do not naturally require the complex structural elements used by eukaryotic chromosomes to ensure proper distribution during cell division.

53. (D) The male or female pronucleus of a fertilized zygote
Creating genetically modified animals often involves the direct injection of DNA into a newly fertilized egg. The genetic material is introduced into one of the two distinct nuclei visible shortly after sperm entry. This early intervention increases the likelihood that the new sequence will be integrated into the genome and present in every cell of the developing organism and its offspring.

54. (C) Fuse the donor somatic cell with the enucleated oocyte and trigger activation
In animal cloning, a short pulse of electricity is used to join the donor cell with an egg that has had its own nucleus removed. This electrical treatment creates temporary pores in the cell membranes, allowing the two entities to merge into one. Additionally, the shock serves as a signal that mimics fertilization, prompting the reconstructed cell to begin embryonic development.

55. (A) P-IV, Q-II, R-I, S-III
Proteins that regulate gene expression use various structural motifs to interact with DNA or other proteins. Some utilize metal ions for stability, while others feature specialized helices that allow two protein chains to zip together. Understanding these different shapes helps scientists determine how these factors recognize their targets and how they work in pairs to control the complex machinery of transcription.

56. (C) Prokaryotic cells
Certain regulatory mechanisms rely on the fact that RNA synthesis and protein production occur in the same cellular compartment at the same time. This allows the ribosome to influence the folding of the nascent transcript as it emerges from the polymerase. Such close coordination is only possible in organisms that lack a nuclear envelope to separate these two fundamental biological processes.

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57. (B) Hsp70 and Hsp90
Maintaining the correct three-dimensional shape of proteins is vital for their function and prevents them from forming harmful clumps. Specialized molecular assistants facilitate this folding process by temporarily binding to newly made or stressed proteins. Using energy from ATP, these complexes guide the polypeptide chain into its active conformation, protecting the cell from the effects of misfolded molecules.

58. (A) Sliding or evicting nucleosomes to expose promoter regions
The way DNA is wrapped around proteins can block access to the genes, preventing them from being turned on. Specialized complexes use energy to reposition or remove these protein bundles, clearing the path for the transcriptional machinery. By making the promoter regions accessible, these machines play a fundamental role in regulating which genes are active in different cell types or conditions.

59. (B) Genome annotation
After raw genetic data is assembled into longer, continuous segments, the next crucial step is to identify the functional elements within those sequences. This process involves using computer programs to predict the locations of genes, regulatory regions, and other significant features. By adding this layer of information, researchers can begin to understand the biological meaning and function of the sequenced genome.

60. (C) Protein-protein interactions
Studying how molecules interact within a living cell is often done by using a system that links a physical contact to a measurable output. Two separate protein parts are brought together; if they stick to each other, they complete a functional unit that turns on a reporter gene. This assay is a powerful way to discover new pathways and understand cellular networks.

61. (B) Long reads from ZMW-based polymerase monitoring
Advanced sequencing technologies can observe a single enzyme as it builds a new DNA strand in real-time. By utilizing extremely small wells that restrict the path of light, the system can detect the incorporation of fluorescently labeled bases with high sensitivity. This approach allows for the generation of very long continuous sequences, which is ideal for assembling complex genomic regions.

62. (A) The non-random association of alleles at different loci
Genetic markers that are located close together on a chromosome are often inherited as a single unit because they are rarely separated by recombination. This statistical relationship means that the presence of one specific allele can reliably predict the presence of another nearby. This phenomenon is a cornerstone of genetic mapping and is essential for identifying the regions responsible for various traits.

63. (B) Quantitative Trait Nucleotides (QTNs) or QTLs
The effectiveness of genomic selection depends on the strength of the connection between observed markers and the actual DNA changes that influence a trait. When these two elements are frequently inherited together, the marker can serve as a reliable proxy for the hidden genetic effect. This allows breeders to estimate an individual's potential based solely on their DNA profile rather than phenotypes.

64. (B) Only a few markers have effects while most are zero
Advanced statistical models for genetic prediction often assume that most variations in the genome have no impact on the trait being studied. By focusing only on a small number of markers that are likely to have a real biological effect, these methods can provide more accurate results for certain characteristics. This approach contrasts with simpler models that treat every marker as equally influential.

65. (A) I, II and III
Targeted breeding strategies involve transferring a specific desirable trait from one source into a high-performing background. Molecular tools allow breeders to select for the exact gene of interest while simultaneously screening against unwanted genetic material from the donor. This dual approach ensures that the resulting offspring retain the original elite qualities of the parent while gaining the new beneficial characteristic.

66. (D) Anchoring loops to maintain higher-order structure
During the process of cell division, chromosomes must be tightly organized into a compact form

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to ensure they are moved correctly. A central framework of non-histone proteins provides a structure to which the long strands of DNA are attached in large, organized loops. This scaffold is essential for maintaining the characteristic shape and stability of the chromosomes throughout the mitotic phase.

67. (D) Centromeric constitutive heterochromatin
Specific staining methods are used to highlight the regions of chromosomes that remain highly condensed throughout the entire cell cycle. These areas are typically found near the primary constriction point and consist of repetitive, non-coding sequences. Because these regions do not participate in gene expression, they appear as dark blocks, providing a useful landmark for identifying and comparing different chromosomes.

68. (A) AAUAAA
The final processing of a eukaryotic transcript involves cutting the molecule at a specific point and adding a protective tail. This event is triggered by a highly conserved sequence of six nucleotides found near the end of the message. This signal ensures that the machinery terminates the process at the correct location, which is vital for the stability and function of the mRNA.

69. (D) 5' to 3'
DNA synthesis always proceeds by adding new building blocks to the growing end of a molecular chain. Because the two strands of the double helix run in opposite directions, one side must be made in short, discontinuous pieces. Despite this fragmented approach, each small segment is built in the same chemical direction as the continuous strand, ensuring the entire genome is duplicated correctly.

70. (C) Serving as a template for RNA-dependent RNA polymerase
The long string of adenine residues at the end of a mature message is essential for many aspects of its lifecycle. This tail protects the genetic information from being chewed away, helps the molecule leave the nucleus, and improves the efficiency of protein production. However, it does not typically function as a blueprint for the synthesis of new RNA molecules by cellular enzymes.

71. (B) 5' cap followed by scanning for the AUG codon
Starting protein synthesis in eukaryotes involves a coordinated search along the messenger RNA molecule. The machinery initially attaches to the modified structure at the very beginning of the transcript and then moves along the sequence. This scanning process continues until the specific three-base signal that marks the beginning of the protein is found, ensuring that translation starts at the correct position.

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72. (C) Polynucleotide kinase
Molecular biology techniques often require the addition of a chemical tag or a necessary functional group to the end of a nucleic acid strand. A specific enzyme catalyzes this transfer from a donor molecule to the starting point of the DNA or RNA. This process is essential for labeling molecules for detection or preparing them for join reactions in various cloning and sequencing procedures.

73. (D) The lambda phage cos site for viral packaging
Certain cloning tools combine the features of a small circular DNA molecule with the ability to be packaged into a virus. By including specific sequences that viral proteins recognize, these molecules can be efficiently moved into bacterial cells. This unique design allows for the stable storage and replication of much larger segments of genetic material than standard plasmids could typically handle.

74. (D) Pluripotent and germline-capable via blastocysts
Specialized cells derived from early embryos are invaluable for genetic engineering because they can develop into any tissue in the body. When these modified cells are introduced back into a developing host, they can contribute to the reproductive organs, ensuring the change is inherited. This capability makes them a powerful tool for creating complex animal models with specific genetic traits.

75. (A) III, I, II, IV, V
Creating a cloned organism involves a precise sequence of laboratory procedures. The donor cells are first brought into a resting state, while the recipient egg has its own genetic material removed. The two cells are then merged, and the resulting reconstruct is artificially stimulated to begin growing. Finally, the developing embryo is

placed into a surrogate mother to complete its development.

76. (C) TFIID
The assembly of the transcription machinery begins with a large protein complex that recognizes the core promoter of a gene. Within this unit is a specific protein that binds directly to the adenine-thymine rich sequence found in many genes. This binding event acts as a foundation, recruiting the other factors and the polymerase necessary to begin the synthesis of messenger RNA.

77. (B) Endoplasmic reticulum
Proteins that are destined for the cell surface or secretion are marked with a short sequence of amino acids at their starting end. This signal is recognized by the cell's transport machinery, which directs the entire ribosome complex to a specific membrane-bound organelle. Once attached, the growing protein chain is threaded into the interior for further processing and eventual transport to its destination.

78. (A) CpG
Chemical modifications to the genome often occur at specific sites where a cytosine is immediately followed by a guanine. These dinucleotide pairs are frequently clustered in regulatory regions and serve as the primary targets for enzymes that add methyl groups. This pattern is fundamental to mammalian epigenetics, as it controls gene activity and is essential for normal development and cellular differentiation.

79. (B) Nucleic acid hybridization
High-throughput analysis of gene expression often relies on the natural tendency of matching DNA or RNA strands to bind to each other. Thousands of unique sequences are fixed to a solid surface, and a labeled sample is washed over them. By measuring where the sample sticks, researchers can simultaneously determine which genes are active and their relative levels in the cell.

80. (A) Lacks background noise and detects novel transcripts
Modern transcriptomic methods provide a detailed view of gene activity by sequencing every RNA molecule in a sample. Unlike older techniques that only look for known sequences, this approach can discover previously unknown genes and alternative forms of existing ones. Additionally, it offers a wider range of detection and lower levels of interference, providing a more accurate picture of cellular function.

81. (B) Ionic current flow
Some advanced sequencing tools identify the individual components of a DNA strand by pulling the molecule through a microscopic hole. As the bases pass through the opening, they block the flow of electricity in a way that is unique to each type of nucleotide. By recording these characteristic electrical signals, the system can determine the genetic sequence quickly and efficiently.

82. (C) Ancestry-based allele frequency differences
Genetic studies can sometimes produce misleading results when the individuals being compared come from different ancestral backgrounds. These groups may naturally have different frequencies of certain markers regardless of any connection to a physical trait. If not properly accounted for, these underlying population differences can be mistaken for true associations, leading to incorrect scientific conclusions about the genetic basis of traits.

83. (A) Phenotypic records and genotypic data
To build a reliable system for predicting genetic potential, researchers must use a group of individuals that have been thoroughly analyzed. This foundational group must have both detailed genetic information and recorded measurements of the traits being studied. By linking these two types of data, mathematical models can learn how different parts of the genome influence an animal's performance.

84. (D) Markers (p) vastly exceed individuals (n)
Analyzing modern genetic data presents a challenge because the number of measured markers is much larger than the number of individuals in the study. Traditional statistical methods struggle with this imbalance, so specialized approaches are used to manage the vast amount of information. These techniques allow researchers to estimate the small contribution of each marker without overcomplicating the model.

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85. (B) Both A and R are true but R is not the correct explanation of A.
Improving proteins in the laboratory involves creating a vast collection of variants and then identifying the ones with the best performance. One powerful way to generate this diversity is by mixing segments of related genes together to create new combinations. While both these concepts are central to modern biotechnology, one describes a general strategy and the other a specific tool for implementation.

86. (B) Alpha-satellite tandem repeats
The central part of a chromosome, which is essential for proper movement during cell division, is composed of a very specific type of DNA. This region consists of long stretches of short, repetitive sequences that are repeated many thousands of times. These blocks provide a structural foundation for the assembly of the proteins that pull the chromosomes apart when a cell divides.

87. (D) GC-rich euchromatic regions
Certain staining techniques produce a pattern that is the reverse of the standard method. By using heat to treat the samples, specific regions of the chromosome are highlighted that are typically associated with high gene density and active transcription. These areas are characterized by a high proportion of guanine and cytosine, and they appear as dark bands in this specialized visual format.

88. (A) Flanking the coding region at both the 5' and 3' ends
Bacterial messenger RNA molecules contain more than just the information needed to build a protein. They also include segments at both ends that do not code for amino acids but are vital for the molecule's function. these regions help control the stability of the message and guide the ribosome to the correct starting point, ensuring the protein is made efficiently.

89. (B) Multiple origins fire simultaneously on each chromosome
Duplicating the massive genomes of eukaryotic cells requires a highly coordinated and efficient process. Rather than starting at a single point, replication begins at hundreds of different locations along each chromosome at the same time. This multi-site approach ensures that the entire genetic blueprint is copied quickly enough to allow the cell to divide within a reasonable period.

90. (A) Adenine nucleotide
The removal of non-coding sequences from a primary transcript involves a specialized chemical reaction that creates a loop-like structure. A specific, highly conserved nucleotide within the sequence acts as the focal point for this reaction. By forming a bond with the start of the intron, this base facilitates the precise cutting and joining required to produce a mature message.

91. (A) Release factors
When the machinery that builds proteins reaches a stop signal on the messenger RNA, the process must be halted and the new chain released. Specialized proteins, rather than transfer molecules, recognize these stop codons. These factors trigger a chemical reaction that cuts the link between the protein and the ribosome, allowing the completed polypeptide to be used by the cell.

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92. (C) Randomly at large distances
Some bacterial defense enzymes identify a specific sequence but perform their cutting action far away from that target. These complex molecules move along the DNA after binding and break the strand at an unpredictable location. Because of this random cleavage pattern, they are generally not used for precise DNA manipulation, though they remain important for understanding how bacteria protect themselves.

93. (B) Only host cells that have successfully taken up the vector can survive
Molecular cloning requires a way to distinguish between cells that have absorbed the new genetic material and those that have not. Vectors are designed with genes that provide protection against certain drugs. When grown in the presence of these chemicals, only the cells containing the vector will continue to grow, allowing researchers to isolate the successfully modified individuals.

94. (B) Mus musculus (mouse)
The direct injection of genetic material into a fertilized egg is a foundational technique in animal research. This method has been most extensively developed and utilized in the laboratory mouse, allowing for the creation of numerous transgenic lines. These models are essential for studying human diseases, understanding development,

and testing new medical treatments in a living, complex biological system.

95. (A) P-III, Q-II, R-I, S-IV
The activity of our genes is regulated by chemical changes to the DNA and its packaging proteins. Some modifications lead to long-term silencing, while others help turn genes on by loosening the chromatin or moving protein bundles out of the way. Understanding how these marks interact provides deep insight into how cells develop and respond to their environment without changing the genetic code.

96. (B) Transcriptional repressors
Specific DNA elements act as negative regulators of gene expression by providing a site for certain proteins to bind. When these factors attach to the DNA, they actively prevent the transcriptional machinery from functioning, effectively turning the gene off or reducing its activity. This control mechanism is vital for ensuring that proteins are only produced when and where they are needed.

97. (C) Asparagine
Many proteins are modified by the addition of complex sugar chains shortly after they are made. In one common form of this process, the carbohydrate is attached to a specific nitrogen atom within the side chain of a particular amino acid. This modification is crucial for the proper folding, stability, and cellular signaling of various proteins, especially those found on the cell surface.

98. (A) SWI/SNF complex
The organization of DNA into compact bundles can block the enzymes needed for gene expression. A specialized multi-protein machine uses energy to physically push these bundles along the DNA or remove them entirely. By creating gaps in the protective protein coating, this complex makes the underlying genetic information accessible, allowing the cell to respond to signals and turn on specific genes.

99. (B) One or both ends (5' or 3')
Researchers can rapidly identify the genes that are active in a specific tissue by sequencing short segments from the ends of complementary DNA molecules. These fragments provide a unique signature for each gene, allowing scientists to build a catalog of expressed transcripts. This approach is much faster than sequencing entire genes and is a powerful tool for discovering new genetic information.

100. (D) Mass-to-charge ($\frac{m}{z}$) ratio
Advanced analytical tools identify molecules based on how fast they travel through an electric field in a vacuum. By measuring the time it takes for a particle to reach a detector, the system can calculate a specific physical property that relates its weight to its electrical charge. This information is used to precisely identify proteins and their modifications in complex biological samples.

101. (B) Luciferase
Real-time detection of DNA synthesis can be achieved by linking the release of chemical energy to the production of light. As each nucleotide is added, a chain reaction occurs that eventually fuels a specialized enzyme to emit a flash. By recording these light signals, the system can determine the order of bases in the DNA molecule with high accuracy and speed.

102. (A) $P < 5 \times 10^{-8}$
When searching for genetic associations across millions of markers, researchers must use a very strict threshold to ensure the results are not just due to chance. This extremely low probability value is used to correct for the large number of statistical tests being performed. Only associations that meet this rigorous standard are considered truly significant and worthy of further biological investigation.

103. (B) Realized genomic relationships among individuals based on marker sharing
Modern genetic evaluation uses a detailed table that describes the actual amount of DNA shared between individuals. Unlike traditional methods that use average family expectations, this approach accounts for the random nature of inheritance, revealing who is truly most similar at the genomic level. This precise measure of relatedness significantly improves the accuracy of identifying superior individuals for breeding and selection.

104. (B) k-fold cross-validation
To ensure a genetic prediction model works reliably, it must be tested on data it hasn't seen before. A common strategy involves splitting the available data into several parts, using some to build the model and the rest to check its

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performance. By repeating this process multiple times, researchers can calculate a dependable estimate of how accurately the model will perform in practice.

105. (A) III only
Modern gene-editing tools require a specific recognition signal to be present in the target DNA for the enzyme to function. This short sequence is located immediately next to the site targeted by the guide molecule and is absolutely essential for the cutting process. Claims that the system can operate without this specific motif are incorrect and do not reflect its biological reality.

106. (B) H1
The core structure of the nucleosome is formed by a group of eight specialized proteins that come together to create a spool for DNA. While four types of histones make up this central unit, a fifth type is located outside the main bundle. This external protein helps stabilize the structure and is involved in the higher-order folding of the genetic material.

107. (B) C-banding
Certain diagnostic techniques are specifically designed to highlight the constitutive heterochromatin found at the primary constriction of chromosomes. By using specific chemical treatments that denature the rest of the DNA, these regions are made to stand out clearly when stained. This provides a reliable method for identifying individual chromosomes and studying structural variations in the regions that organize the cell's genetic material.

108. (A) -10 and -35
The starting point for gene expression in bacteria is marked by specific sequences located slightly before the actual beginning of the coding region. These two elements act as binding sites for the machinery that synthesizes RNA, ensuring it is positioned correctly. Their precise location relative to the start site is critical for the efficient and accurate initiation of the transcription process.

109. (C) Prevent separated DNA strands from reannealing
During the process of DNA duplication, the two strands of the double helix are pulled apart. To keep them from simply snapping back together, specialized proteins quickly bind to the exposed single strands. This temporary coating stabilizes the DNA, keeping it in an open and accessible form so that the enzymes responsible for synthesis can perform their work without interference.

110. (A) 7-methylguanosine
Eukaryotic messenger RNA molecules are modified at their starting end with a specific, protective structure. This addition involves a modified nucleotide that is attached in an unusual orientation shortly after transcription begins. This feature is vital for protecting the molecule from degradation and serves as an essential recognition signal for the machinery that initiates the production of proteins.

111. (A) A site
The synthesis of a protein chain involves the sequential addition of amino acids brought to the ribosome by specialized carriers. As each new building block arrives, its carrier molecule first enters a specific docking location within the ribosomal complex. This initial binding ensures that the genetic code on the messenger RNA is correctly matched before the new amino acid is joined to the chain.

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112. (C) Either blunt or sticky ends depending on the specific enzyme
Bacterial enzymes used for cutting DNA can leave different types of finishes on the resulting fragments. Some cut straight across both strands, while others create a staggered break that leaves short, single-stranded overhangs. The specific outcome depends entirely on the unique way each enzyme interacts with its target sequence, providing flexibility for different laboratory techniques in molecular biology and cloning.

113. (D) Cloning very large fragments
Studying massive segments of genetic material requires specialized vectors that can carry much more information than standard bacterial tools. By using elements derived from fungal cells, researchers can maintain stable fragments that are many hundreds of thousands of bases long. This capability is essential for building comprehensive maps of entire genomes and studying large-scale genetic structures in various complex organisms.

114. (C) Injecting genetically modified ESCs into a developing blastocyst
Creating animal models with specific genetic changes often involves using versatile cells grown in the laboratory. These modified cells are introduced into a host at a very early stage of its development. As the organism grows, the new cells mix with the host's own, resulting in an individual made of two different genetic types. This approach is fundamental for generating transgenic lines.

115. (B) I and III
Animal cloning requires precise management of the cellular environment and timing. The egg must be at a specific developmental stage when its own DNA is removed, and a specific merging technique is used to introduce the donor genetic material. When these conditions are met, the resulting cell can begin to grow into a new individual that is genetically identical to the donor.

116. (B) Undergo a conformational change and release from the operator
Bacterial systems for processing sugars are controlled by a regulatory protein that blocks gene expression when the sugar is absent. When the specific nutrient becomes available, a small molecule derived from it binds to the regulator, altering its shape. This change causes the protein to detach from the DNA, clearing the path for the machinery to begin producing the necessary enzymes.

117. (A) Leucine zipper
Certain proteins that regulate gene expression come together in pairs using a specialized structural motif. This arrangement features a series of specific amino acids that interact like a fastener, holding two protein chains together. This dimerization is essential for the proteins to bind correctly to their target DNA sequences, allowing them to effectively turn genes on or off as needed.

118. (C) Ubiquitination
The cell manages its protein levels by marking specific molecules for destruction. This involves the addition of a small, universal polypeptide tag to the target protein through a series of enzymatic steps. This molecular "label" is recognized by a large disposal complex that breaks down the marked protein into its basic components, ensuring that damaged or unnecessary proteins are removed.

119. (B) The parent of origin
Certain traits are expressed differently depending on which parent passed down the corresponding gene. This biological phenomenon is caused by chemical marks placed on the DNA during the formation of eggs or sperm. These marks dictate whether the maternal or paternal copy of a gene will be active in the offspring, which is vital for normal development and health in mammals.

120. (D) Assigning locations and functions
Once a genome has been sequenced, the next essential task is to make sense of the data. Specialized computer programs are used to find the exact positions of genes and predict what they do based on known patterns. This informative layer transforms a simple list of nucleotides into a useful biological map that researchers can use to study life and disease.

121. (A) The square root of their mass-to-charge ($\frac{m}{z}$) ratio
Identifying molecules in a complex sample can be done by measuring how long they take to cross a fixed distance when accelerated by an electric field. This speed depends on a specific physical relationship between the molecule's weight and its electrical charge. By accurately timing these movements, scientific instruments can determine the precise identity and composition of proteins and other biological compounds.

122. (C) A mixture of dNTPs and a small proportion of ddNTPs
Determining a genetic sequence often involves creating a collection of DNA fragments that end at every possible position. This is achieved by using a combination of normal building blocks and a small amount of special terminator molecules. As the DNA is built, the terminators are occasionally used by mistake, stopping the chain and revealing the identity of the base at that specific location.

123. (D) Measures H+ ion release solely
Some modern sequencing platforms operate by detecting the chemical signals released during the construction of a DNA strand. Every time a new base is added, a small electrical change occurs in the surrounding environment. By using sensitive electronics to monitor these shifts, the system

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can read the genetic code directly without the need for expensive lasers or complicated optical equipment.

124. (B) A specific single nucleotide polymorphism that causally affects a quantitative trait
Finding the exact genetic change responsible for a physical characteristic is a major goal of genomic research. In large-scale studies, researchers look for individual base differences that directly influence the variation observed in a population. Identifying these specific causal variants, rather than just nearby markers, provides the most accurate information for understanding biology and improving traits through selective breeding.

125. (A) Both A and R are true and R is the correct explanation of A.
Selecting the best animals for breeding is much faster when genetic information is used early in life. By analyzing an individual's DNA shortly after birth, breeders can estimate their future potential with high confidence. This eliminates the need to wait several years for the animal to mature and produce offspring, greatly increasing the speed at which traits can be improved.

126. (B) Bayes Cpi
Advanced mathematical models for genetic prediction allow for flexibility in how they treat different parts of the genome. One specific approach assumes that only a certain percentage of the measured markers actually influence the trait, while the rest are ignored. This strategy is particularly effective for identifying and utilizing the most informative genetic signals in complex biological data sets.

127. (A) Recombine beneficial mutations
Directed evolution techniques aim to create improved proteins by mimicking the natural process of recombination in the laboratory. By breaking related genes into pieces and allowing them to reassemble, researchers can generate new combinations of genetic changes. This process allows beneficial mutations from different sources to be brought together in a single molecule, leading to significantly enhanced functional properties.

128. (C) Decondensed structure and transcriptional activity
The parts of the genome that are currently being used by the cell are typically found in a more open and relaxed state. This loose packaging allows the machinery for reading genes to easily reach the DNA. These active regions are vital for producing the proteins the cell needs to function and are a key characteristic of the functional parts of the nucleus.

129. (D) The distribution of GC and AT-rich isochores
The characteristic horizontal stripes observed on chromosomes after staining are a reflection of the underlying chemical composition of the DNA. Different regions have varying proportions of the four chemical bases, which influences how they package and how they react with dyes. These patterns are highly consistent and serve as a reliable "barcode" for identifying and studying individual chromosomes.

130. (C) Transcribed regions that remain in the mature mRNA
Eukaryotic genes are composed of segments that carry the instructions for building proteins and other segments that are removed. The parts that are preserved and joined together to form the final message are essential for defining the protein's sequence. These regions are kept because they contain the critical information needed for the cell to carry out its biological instructions.

131. (B) Each newly formed double helix consists of one parental strand and one newly synthesized strand.
When a cell duplicates its genetic information, it uses the existing DNA as a guide. The original double helix is pulled apart, and each side serves as a template for building a new partner. This results in two new molecules, each containing one original piece and one newly made piece, ensuring the genetic code is faithfully preserved through each generation.

132. (C) Pre-mRNA and some snRNAs
Eukaryotic cells use a specialized enzyme to produce the molecules that will eventually be translated into proteins. This machinery is responsible for synthesizing the long primary transcripts that undergo processing within the nucleus. By creating these templates, the enzyme plays a central role in the flow of genetic information from the genome to the functional machinery of the cell.

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133. (D) Unmodified methionine
The production of a new protein always starts with a specific amino acid that signals the beginning of the chain. In eukaryotic organisms, this first building block is a standard form of a common amino acid. While other types of cells might use a slightly modified version, the use of this specific molecule is a universal feature of how these complex cells initiate translation.

134. (C) DNA Ligase
Completing the duplication of the genome requires an enzyme that can mend small breaks in the molecular backbone. During synthesis, especially on one of the two strands, the new DNA is made in many separate pieces. This specialized catalyst performs a vital "sealing" function by joining these fragments together into a single, continuous, and stable strand of genetic information.

135. (A) P-I, Q-II, R-III, S-IV
Genetic research utilizes various tools for storing and duplicating segments of DNA, with each type designed for a specific size range. Small circular molecules are ideal for short fragments, while more complex systems can carry moderate to very large pieces. Understanding these capacities allows scientists to choose the most appropriate tool for mapping entire genomes or studying individual genes.

136. (D) Viral integrase mediating random or semi-random insertion
Certain viruses have a natural ability to stitch their genetic material into the DNA of a host cell. In biotechnology, modified versions of these viruses are used to introduce new genes into animals. This process relies on a specialized viral protein that opens the host's genome and inserts the new sequence, ensuring it becomes a permanent part of the cell's blueprint.

137. (B) Multiplying elite breeding livestock and preserving endangered species genetics
The ability to create a genetically identical copy of an individual has profound applications in agriculture and conservation. By using the nucleus from a mature cell, scientists can reproduce high-performing animals or help save species that are on the brink of extinction. This technology allows for the preservation and expansion of valuable genetic lineages that might otherwise be lost forever.

138. (B) Glucose is absent and lactose is present
Bacteria are highly efficient and only produce certain metabolic enzymes when they are absolutely necessary. A specific set of genes is only fully turned on when their preferred energy source is missing and an alternative sugar is available. This dual sensing mechanism ensures the cell doesn't waste energy making proteins for processing sugars it doesn't need or cannot find.

139. (B) Diffusing through the nucleoplasm to bind specific cis-acting elements
Gene regulation in complex cells often involves proteins that are produced in one part of the cell and then travel to find their target DNA. These factors move through the nuclear fluid until they encounter specific sequences that they recognize. By binding to these sites, they can either help or hinder the machinery that reads the gene, providing flexible control over expression.

140. (A) Folding proteins correctly
Maintaining the proper shape of biological molecules is a critical task within every cell. Specialized molecular helpers assist newly made or damaged proteins in reaching their correct three-dimensional form. This prevents the proteins from clumping together into harmful structures and ensures they are able to perform their intended functions, thereby supporting the overall health and survival of the cell.

141. (A) Increased transcription
The way DNA is bundled can be changed by adding small chemical groups to the surrounding proteins. When certain enzymes attach these groups, they reduce the positive charge on the proteins, causing them to loosen their hold on the DNA. This creates a more open environment that makes it much easier for the gene-reading machinery to access and activate the genome.

142. (B) SAGE
Profiling the activity of thousands of genes simultaneously can be done by capturing and sequencing very short, representative markers from every messenger RNA molecule. These markers are linked together into long chains, allowing many of them to be read in a single experiment. By counting how often each marker appears, researchers can precisely determine which genes are most active in a sample.

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143. (D) The DNA-binding domain (DBD) of a transcription factor
Studying how proteins interact in a living system often involves splitting a gene-regulating molecule into two separate parts. One part is attached to a "target" protein that is fixed to the DNA. If another "tester" protein sticks to the target, the two halves of the regulator are brought back together, triggering a visible signal that confirms the two proteins are connected.

144. (C) Nitrogenous bases
Early methods for reading genetic information utilized specialized chemicals that specifically damage the core components of a DNA strand. By using reagents that target different types of bases, researchers can create a series of breaks at known positions. Analyzing the resulting fragments allows the original order of the genetic code to be reconstructed through a process of chemical degradation and separation.

145. (A) III only
Modern high-throughput sequencing technologies use diverse methods to read genetic information, such as cluster formation, electrical signals, or specialized optical wells. However, descriptions claiming that certain light-based systems directly read fluorescent tags without the help of enzymatic reactions are incorrect. Understanding the specific chemical and physical principles of each platform is essential for choosing the right tool for genomic research.

146. (B) Population stratification
Large-scale genetic studies can sometimes yield false signals when the group of individuals being studied contains hidden subgroups with different ancestral histories. These differences can cause certain markers to appear linked to a trait simply because they are more common in one group than another. Researchers must carefully account for these underlying structures to ensure their findings reflect true biological associations.

147. (B) Assess the accuracy of the prediction model built on the reference population
To ensure that a system for identifying the best breeding stock is reliable, it must be double-checked using a separate group of animals. This secondary group provides a way to verify that the mathematical patterns found in the original data set actually hold true in other individuals. This step is vital for confirming the model's practical utility before using it in real-world selection.

148. (A) Bayes A
Advanced statistical methods for analyzing genetic data allow for the fact that different parts of the genome have different levels of influence. While some models treat all markers as having the same impact, others allow each one to have its own unique contribution. This more flexible approach can be more accurate for predicting traits that are influenced by a few major genes.

149. (A) Introduce a specific allele while returning the rest of the genome to the recurrent parent type
Precision breeding aims to move a single beneficial trait from one variety into another without changing the rest of the genetic makeup. By using molecular markers, breeders can select for the desired gene while simultaneously ensuring that the offspring retain the elite characteristics of the original parent. This targeted approach significantly speeds up the process of improving crops and livestock with new traits.

150. (C) TTAGGG
The ends of vertebrate chromosomes are protected by a specific, repetitive sequence of six nucleotides that is repeated hundreds of times. This motif acts as a biological "cap" that prevents the loss of important genetic information and stops the DNA from unraveling or sticking to other molecules. Maintaining these protective ends is essential for the stability of the genome and cellular aging.

151. (B) Ag-NOR banding
Specialized staining techniques are used to identify the specific chromosomal locations where the genes for building cellular protein factories are located. These regions react with silver nitrate, producing dark spots that can be seen under a microscope. This method is valuable for researchers studying how cells manage their growth and for identifying structural differences in these important genomic areas across species.

152. (B) Non-coding sequences that interrupt the coding region and are removed during splicing
Many genes contain extra segments of DNA that do not carry the instructions for building a protein. These intervening sequences are copied when a gene is read but are then precisely cut out of the transcript before it is used. The removal of

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these non-coding parts is a fundamental step in the production of mature, functional messenger RNA in complex organisms.

153. (B) Hydrogen bonds between base pairs
Duplicating the genetic blueprint requires an enzyme that can pull the two strands of the DNA double helix apart. It achieves this by breaking the relatively weak connections that hold the matching bases together. By separating the strands, the enzyme provides access for the other proteins responsible for synthesis, allowing each side to serve as a template for a new strand.

154. (C) snRNA
The precise removal of non-coding segments from a primary transcript is carried out by a complex machine that uses small, specialized RNA molecules as guides. These molecules recognize the specific sequences at the boundaries of the parts to be removed. By coordinating the cutting and joining of the DNA message, they ensure that the final protein instructions are correct and continuous.

155. (A) IV, I, III, II
Starting the production of a new protein involves a carefully orchestrated series of events. A specialized initiator complex is formed first, which then binds to the starting end of the messenger RNA. The machinery scans along the transcript until it finds the correct "start" signal, after which the larger part of the factory joins in to begin the synthesis of the polypeptide.

156. (B) Defend against foreign viral (bacteriophage) DNA
Bacteria have developed natural biological systems to protect themselves from invading viruses. They produce specialized enzymes that act like molecular scissors, cutting the DNA of the intruder at specific sequences. By breaking the viral genome into pieces, the bacteria can prevent the infection from spreading, providing a sophisticated immune-like defense system that has been repurposed by scientists for genetic engineering.

157. (C) Small insert capacity (typically $<$10 kb)
While standard circular DNA molecules are easy to work with in the laboratory, they have a significant drawback when it comes to mapping large genomes. They can only carry relatively short segments of foreign DNA, which means thousands of individual clones are needed to cover an entire genome. This makes them less efficient for large-scale studies compared to more advanced tools designed for longer fragments.

158. (C) 20-nucleotide sequence at the 5' end of the single guide RNA (sgRNA)
Modern gene-editing technology relies on a simple and versatile system to find its target in the genome. A short sequence of genetic material is designed to match a specific location in the DNA. By changing this sequence, researchers can easily direct the cutting enzyme to almost any part of the genome, making it a highly precise and customizable tool for genetic manipulation.

159. (B) Synchronize cells into the quiescent G0 phase
Successful animal cloning requires that the donor cell be in a very specific state of rest. By temporarily depriving the cells of certain nutrients, researchers can cause them to stop dividing and enter a quiet phase. This synchronization is crucial because it ensures the genetic material is in the best possible condition for being "reset" when it is introduced into the egg cell.

160. (B) Constitutively expressed at low levels
Certain regulatory genes are always active, producing a small but steady amount of a specific protein. This constant presence ensures that the cell is always ready to respond to changes in its environment. By maintaining a baseline level of these regulators, the cell can quickly turn other metabolic pathways on or off as soon as the relevant chemical signals are detected.

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161. (B) Chromatin loops mediated by proteins like cohesin
Genomic regions that are located far apart can still interact with each other to control gene activity. The long strands of DNA are folded into large, organized structures that bring distant regulatory elements close to the genes they manage. These physical connections are stabilized by specialized proteins, allowing signals from across the genome to be integrated and influence the production of specific proteins.

162. (B) Serine, Threonine, and Tyrosine
The function of many proteins is controlled by the addition of a small phosphate group to specific amino acids within their structure. This modification can act like an "on-off" switch,

changing the protein's activity or location in the cell. This process is a fundamental way that cells respond to signals and manage complex internal processes like growth, movement, and division.

163. (C) Transcriptionally silenced
Regions of the genome that are rich in certain nucleotide pairs often serve as control centers for gene activity. When these areas are heavily modified with methyl groups, it usually signals the cell to stop reading the nearby genes. This silencing mechanism is essential for maintaining cell identity and for shutting down genes that are not needed in a particular tissue or at a specific time.

164. (C) Discover novel genes and evaluate expression profiles
Scientists can quickly learn about the active parts of a genome by sequencing short segments from all the messenger RNA molecules in a cell. This catalog of active transcripts helps identify new genes and shows which ones are most busy in different conditions. This approach is a fast and efficient way to explore the functional parts of the genome without sequencing everything.

165. (A) I, II, III and V
Separating complex mixtures of proteins can be done with high precision using two different physical properties. First, the molecules are moved through a pH gradient until they reach their neutral point. Then, they are separated by their weight using an electric field. This two-step process can resolve thousands of different proteins, providing a detailed snapshot of the cell's entire protein content.

166. (A) Sanger dideoxy sequencing
The first reliable method for reading genetic code utilized special building blocks that stop the synthesis of a DNA strand. By creating a collection of fragments that end at every possible base, researchers can reconstruct the original sequence. This foundational technique transformed biology and remains a standard for checking small segments of DNA, although it has been joined by newer, faster methods.

167. (B) Generate dense clonal clusters
Modern sequencing platforms often involve a step where individual DNA molecules are amplified to create small groups of identical copies on a surface. This process ensures that when the sequence is read, the signal is strong enough for the sensors to detect it. By creating these dense clusters, the system can read millions of different sequences simultaneously with high accuracy and speed.

168. (B) Population stratification and relatedness
Genetic association studies must account for the fact that participants may share similar backgrounds or be related to each other. These factors can create false patterns that look like genetic links to a trait but are actually just family or ancestral similarities. By using statistical adjustments, researchers can filter out these distracting signals and focus on the true genetic causes of traits.

169. (A) Reference population with known phenotypes and genotypes
To predict an animal's genetic potential accurately, researchers must first study a group where both the DNA and the physical performance are well-documented. This foundational information allows them to calculate the effect of each part of the genome on a particular trait. Once these relationships are understood, they can be used to evaluate other animals based only on their DNA profiles.

170. (B) All markers contribute equally to the genetic variance.
Certain genetic models assume that the overall variation of a trait is shared broadly across the entire genome. Rather than looking for a few "major" genes, these methods treat every measured marker as if it makes a small, equal contribution. This approach is particularly effective for complex traits like growth or health, which are influenced by many thousands of different genetic factors.

171. (B) Converting wild-type alleles to the drive allele via targeted cleavage and homology-directed repair
Specialized genetic systems can "force" themselves into every offspring by actively overwriting the other version of a gene. When the cell tries to repair a break made by the system, it uses the modified version as a template, ensuring the change is passed on. This biased inheritance allows a specific trait to spread through an entire population much faster than normal.

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172. (B) Beads-on-a-string nucleosome array
The most basic level of DNA packaging resembles a series of round objects linked by a thin thread. In this structure, the long strand of genetic material is wrapped around protein bundles to save space within the nucleus. This arrangement is the foundation for all further folding and is a key feature of how the massive genome is organized into a tiny cellular space.

173. (C) Fluorescence microscope
Certain chromosome identification methods utilize specialized dyes that glow when exposed to specific types of light. To see these patterns, researchers must use a microscope equipped with powerful lamps and filters. This setup allows the bright and dark bands on the chromosomes to be clearly visible, providing a detailed map for identifying individual chromosomes and detecting any structural changes or abnormalities.

174. (A) Insulator
Gene regulation requires precise boundaries to ensure that signals intended for one gene do not accidentally turn on another nearby. Specialized DNA elements act like biological "fences" that block the influence of distant enhancers. By preventing inappropriate interactions between different parts of the genome, these sequences ensure that each gene is expressed correctly and only when it is supposed to be.

175. (A) Both A and R are true and R is the correct explanation of A.
When circular chromosomes are duplicated in bacteria, they often end up linked together like the rings of a chain. A specialized enzyme is required to perform a delicate "unlinking" operation at the very end of the process. By breaking and then resealing the DNA strands, this protein allows the two new daughter chromosomes to separate and move into new cells.

176. (A) RNA Polymerase I
Eukaryotic cells use a dedicated enzyme to produce the major components of the machinery that builds proteins. This machinery is responsible for synthesizing the various RNA molecules that make up the structural core of the ribosome. By focusing exclusively on these essential parts, the enzyme ensures that the cell has a steady supply of factories to support its growth and maintenance.

177. (C) Inosine
Flexibility in how genetic information is read is often provided by a unique base found in transfer molecules. This special nucleotide has the unusual ability to pair with several different bases in the messenger RNA. This versatility allows the cell to function with fewer total transfer molecules, as a single one can recognize several different codons that all signal for the same amino acid.

178. (B) A specific, short distance away from their asymmetric recognition site
Some bacterial defense enzymes identify a particular sequence but perform their cutting action at a fixed distance from that location. Unlike common tools that cut directly at the target, these enzymes are more complex and require specific cofactors to work. Their unique way of interacting with DNA makes them useful for certain specialized laboratory procedures that require cutting outside of a known site.

179. (D) Beta-galactosidase
Color-based screening in microbiology utilizes a specific enzyme that can break down a colorless substrate into a bright blue product. Vectors used for cloning often contain a part of the gene for this enzyme. If a foreign DNA piece is successfully inserted, the gene is broken, the enzyme is not made, and the resulting colonies remain white, making them easy to identify.

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180. (B) Random integration resulting in variable expression or insertional mutagenesis
While direct injection of DNA into a fertilized egg is a common way to make transgenic animals, it has significant unpredictable aspects. The new genetic material can land anywhere in the host's genome, which might disrupt existing genes or lead to inconsistent levels of activity. This randomness means researchers must carefully check each individual to find ones where the new gene is working correctly.

181. (B) Staining with a fluorescent DNA dye such as Hoechst and exposure to UV light
In animal cloning, it is vital to confirm that the egg cell's own genetic material has been completely removed. Researchers use specialized dyes that bind to DNA and glow under ultraviolet light. By looking for the absence of this glow, they can be sure that the original chromosomes are gone before they introduce the new nucleus from the donor cell into the egg.

182. (A) Tryptophan
Certain bacterial genes are controlled by a mechanism that senses the availability of specific building blocks during the translation process itself. If a particular amino acid is scarce, the ribosome will stall at the corresponding codons in the leader sequence. This pause causes the mRNA to fold into a shape that allows the rest of the gene to be read, ensuring enzymes are produced.

183. (C) Dimers (homo- or hetero-dimers)
Many proteins that regulate gene activity function as pairs. This arrangement allows them to recognize longer and more specific DNA sequences than they could alone. By joining with either an identical partner or a different one, these factors can fine-tune how they respond to cellular signals, providing a highly flexible and precise way for the cell to manage its gene expression.

184. (C) Hydrophobic
Proteins that need to be sent to certain organelles or out of the cell carry a specific molecular "address" at their beginning. This sequence is characterized by a stretch of amino acids that do not like water. This physical property allows the sequence to easily insert into cellular membranes, guiding the protein into the correct transport pathway for further processing and eventual delivery.

185. (A) P-III, Q-II, R-IV, S-I
The complex landscape of the genome is managed by diverse molecular actors that add or remove chemical marks. Some proteins add methyl groups to the DNA, while others modify the proteins it is wrapped around or physically move them. Together, these actors control which parts of the genetic blueprint are accessible, allowing the cell to change its behavior without altering its underlying DNA.

186. (A) DNA Microarray
Measuring the activity of thousands of genes at once can be done by using a small chip covered with many different DNA probes. When a sample is washed over the chip, matching sequences stick to the probes, creating a measurable signal. This approach allows researchers to see a "global" picture of which genes are active in a specific cell or tissue at any given time.

187. (A) Reconstitution of a functional transcription factor leading to reporter gene expression
Finding out if two proteins interact can be achieved by using them to bring two halves of a gene-triggering molecule together. Each protein is attached to one half of the trigger; if they bind to each other, the trigger is completed and a specific "reporter" gene is turned on. This result, such as a color change or growth, confirms that the two proteins are connected.

188. (B) Requires toxic reagents and radioisotope labeling
Early methods for reading genetic information were groundbreaking but had significant practical drawbacks. They relied on hazardous chemicals and radioactive materials that required strict safety precautions and specialized disposal. Newer techniques that use safer dyes and enzymes have largely replaced these older methods, making DNA sequencing faster, cheaper, and more accessible to researchers in almost any laboratory setting.

189. (B) Zero-Mode Waveguide (ZMW)
Advanced sequencing technology uses microscopic wells that are so small they limit the way light travels through them. This allows sensors to focus on a single enzyme at the bottom of the well as it adds nucleotides to a DNA strand. By observing each addition in real-time, the system can generate very long sequences, which is particularly helpful for assembling complex genetic maps.

190. (B) Alleles at two closely spaced loci tend to be co-inherited
Genetic markers that are physically close to each other on a chromosome often stay together during reproduction. This non-random association means that knowing the state of one marker can tell you a lot about the state of another nearby. This principle is fundamental for mapping the genes responsible for various traits, as it allows researchers to use markers as signposts for the actual causal variants.

191. (B) The estimated effects of all genetic markers across the genome
Calculating an animal's overall genetic potential involves analyzing thousands of small DNA differences. By adding up the individual contributions of all these markers, researchers can produce a single score that reflects the

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animal's breeding value. This comprehensive approach is much more accurate than looking at only a few genes and allows for better selection of superior individuals early in their lives.

192. (B) Zero
Statistical models for genetic prediction often have to manage thousands of markers at once. To prevent the model from becoming too complex or inaccurate, these methods apply a mathematical technique that pulls the estimated effect of each marker slightly toward a neutral value. This ensures that only the most consistent and important genetic signals are highlighted, leading to more reliable predictions of breeding performance.

193. (A) Fragmentation and PCR reassembly without primers
Improving genes in the laboratory can be done by breaking them into small pieces and then letting them grow back together. During this reassembly, different versions of a gene can swap parts, creating many new and unique combinations. This process of molecular shuffling is a powerful way to discover improved proteins with better features, like increased strength or better activity in harsh conditions.

194. (C) CENP-A
The specific part of a chromosome where it attaches to the cellular machinery during division is marked by a unique protein. This variant replaces one of the standard proteins that DNA is wrapped around, creating a specialized structure that acts as a foundation. This molecular marker is essential for ensuring that chromosomes are pulled apart correctly and that each new cell receives the right information.

195. (B) III only
Different staining techniques reveal different aspects of chromosome structure. While some methods show overall patterns of light and dark, others are designed to highlight only specific regions that remain highly condensed. Claims that these specialized methods only stain the active, gene-rich parts of the genome are incorrect, as they are actually used to find the non-coding, structural areas that organize the genetic material.

196. (B) TTGACA
The initiation of transcription in bacteria is guided by two specific conserved sequences located upstream of the gene. One of these sequences is located approximately thirty-five bases before the starting point. This motif serves as a critical recognition site for the polymerase machinery, helping it to bind firmly and correctly to the DNA so that the process of making RNA can begin successfully.

197. (A) The leading strand is synthesized continuously, while the lagging strand is synthesized in fragments
DNA synthesis is restricted by the fact that it can only happen in one chemical direction. Because the two strands of the double helix run in opposite ways, only one side can be made smoothly as the fork opens. The other side must be built in short, backward steps, which are later joined together. This dual-speed approach ensures the entire genome is duplicated accurately.

198. (A) 150-250 Adenine residues
Most mature messenger RNA molecules in complex cells have a long string of a single type of nucleotide at their trailing end. This feature is not coded in the original DNA but is added after transcription. It serves multiple vital roles, including protecting the genetic message from destruction and helping the cell's machinery recognize and translate the information into a functional protein chain.

199. (B) Peptidyl transferase
Joining amino acids together to form a protein chain is performed by a specialized part of the ribosome. This activity is unique because it is carried out by the RNA itself rather than a protein. By catalyzing the formation of the chemical bond between each new building block, this ribozyme ensures the polypeptide grows correctly according to the instructions provided by the genetic code.

200. (A) Vector self-ligation
Molecular cloning procedures often involve a step to remove a specific chemical group from the ends of a cut DNA molecule. This prevents the circular vector from simply closing back up without incorporating the new gene. By ensuring the ends cannot rejoin on their own, researchers can greatly increase the chances that the final

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product will contain the desired foreign genetic material.

201. (C) BAC
Certain cloning tools are based on the natural systems that bacteria use to maintain their own extra genetic material. These engineered molecules are designed to stay in only one copy per cell, which makes them very stable even when carrying huge segments of foreign DNA. This stability is essential for mapping entire genomes and for studying large, complex genetic structures without fear of them changing.

202. (B) Insertional mutagenesis near oncogenes
While using viruses to deliver new genes is very effective, it can have dangerous side effects if the new material lands in the wrong spot. If a gene is inserted near a part of the host's DNA that controls cell growth, it might accidentally turn that gene on permanently. This disruption can lead to uncontrolled cell division, highlighting the need for careful screening in gene therapy.

203. (C) Calcium
In the process of cloning, an egg cell must be "fooled" into thinking it has been fertilized so that it will start to grow. This is achieved by artificially raising the level of a specific signal molecule inside the cell. This surge acts as a master switch that turns on the embryonic development program, allowing the reconstructed cell to begin dividing and forming a new individual.

204. (B) Inactive and cannot bind the operator
Bacterial systems for making building blocks are often self-regulating. When a specific amino acid is missing, the regulatory protein that would normally block the genes remains in an inactive form. This ensures that the machinery for producing the needed nutrient is turned on and can work at full speed. Only when the amino acid is abundant again will the regulator be activated to stop the process.

205. (A) III, I, II, IV
Modern gene editing involves a specific sequence of biological steps. First, the cutting enzyme and its guide are combined into a single functional unit. This complex then finds and binds to the matching target in the genome. Once attached, the enzyme makes a precise cut, and the cell's own repair machinery eventually introduces a small change that can disable the targeted gene.

206. (B) Activation domain
Proteins that turn genes on usually have two main parts that work together. One part finds and sticks to a specific DNA sequence, while the other part interacts with the machinery that reads the gene to get it started. This dual-function design allows the cell to precisely control which genes are active by using different combinations of these factors to respond to various internal signals.

207. (B) Endoplasmic reticulum
The process of attaching complex sugars to new proteins begins in a specialized organelle that looks like a network of flattened sacs. This modification is essential for the protein to fold correctly and to be recognized by other parts of the cell. Once this initial step is complete, the protein is moved to other areas for further refinement before being sent to its final destination.

208. (A) DNMT3a/3b
Establishing the initial patterns of chemical marks on the genome during early life is the job of a specific group of enzymes. These proteins add methyl groups to the DNA from scratch, helping to define how different cells will develop and function. This process is vital for normal growth and ensures that the correct genes are turned on or off in every tissue.

209. (C) Wet-lab protein purification
After a genome is sequenced, researchers use computer programs to predict where the genes are and what they might do. This process of adding information to the raw data is essential for understanding the biology of the organism. However, the physical process of cleaning and isolating proteins in a laboratory is a separate task that happens after the computer analysis is finished.

210. (B) Absorb laser energy and facilitate desorption/ionization of analytes
Analyzing large biological molecules often involves embedding them in a special material that can absorb light from a powerful beam. When hit by the laser, this material evaporates, carrying the molecules into the air and giving them an electrical charge. This allows the molecules to be measured and identified without being destroyed, providing a detailed view of the proteins present in a sample.

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211. (B) The newly synthesized chain cannot be extended further.
Certain DNA sequencing methods use modified building blocks that act like "dead ends" for synthesis. Because these molecules are missing a critical chemical group, the polymerase enzyme cannot add any more bases to the chain once one is incorporated. This creates a collection of DNA fragments of different lengths, which are then used to figure out the exact order of the genetic code.

212. (B) The terminator dye and block can be removed
Modern high-speed sequencing involves using special nucleotides that stop the construction of a DNA strand after only one addition. This stop is temporary, however, because the part that blocks further growth can be chemically removed. This allows the next base to be added and the sequence to be read one letter at a time, making it possible to read millions of sequences simultaneously.

213. (B) Linkage disequilibrium blocks or haplotypes
Large-scale genetic studies are possible because many DNA differences are inherited together in predictable groups. By measuring just a few representative markers in each group, researchers can infer the state of thousands of other nearby variants. This makes it much more efficient to scan the entire genome for links to traits without having to measure every single base in every person or animal.

214. (A) Genomic Estimated Breeding Value
Selecting the best individuals for breeding is improved by using a single number that summarizes their genetic potential based on DNA data. This score is calculated by combining the estimated effects of thousands of small genetic differences across the entire genome. This allows breeders to identify superior animals very early in life, leading to faster genetic progress and more efficient improvement of desirable traits.

215. (A) I, II and III
Advanced mathematical models for genetic prediction use different assumptions to manage the vast amount of DNA data. Some assume that most parts of the genome have little effect, while others allow for more variation in how much each marker contributes. These various approaches are all designed to improve the accuracy of predicting performance, although they use different internal logic and computational steps to achieve their results.

216. (A) Select against the donor genome at non-target loci (background selection)
Precision breeding using molecular markers allows researchers to quickly recover the original high-quality genome while keeping only one specific new trait. By screening for markers throughout the rest of the DNA, breeders can identify the individuals that have the least amount of "extra" material from the donor. This significantly reduces the time needed to create a new variety that is nearly identical to the parent.

217. (C) 6
The organization of DNA into a more compact form involves coiling a string of protein-wrapped bundles into a larger helix. This specific structure features about six of these bundles for every complete turn of the coil. This level of packaging is essential for fitting the long strands of the genome into the small nucleus of the cell while still keeping the information accessible to the machinery.

218. (B) It produces reproducible and distinct band patterns that uniquely identify each homologous chromosome pair.
Standard chromosome identification relies on creating a unique "barcode" of horizontal stripes on each chromosome. These patterns are so consistent that they can be used to tell every pair apart and to find even small structural mistakes. This reliability makes the technique a cornerstone of medical genetics, allowing doctors to diagnose conditions and researchers to study how the genome is organized in different species.

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219. (A) Initiation codon (AUG)
The beginning of a messenger RNA molecule contains a segment that does not code for any part of the protein. This leader sequence starts at the very beginning of the transcript and ends just before the specific three-base signal that marks the start of the protein's construction. This region is vital for helping the cell's machinery correctly identify and begin reading the genetic message.

220. (D) G1 phase
To ensure that the genome is copied exactly once during each cell division, the process is

controlled by a two-step "licensing" system. The preparation for this process happens during the rest phase before any new DNA is made. This timing ensures that every starting point is ready and waiting, so that once the signal to begin is given, the entire genome is duplicated in a single, coordinated event.

221. (A) 2'-5' phosphodiester bond (lariat formation)
The removal of non-coding segments from a primary transcript involves a unique two-step chemical reaction. In the first step, one end of the segment is folded back and attached to a specific site within the sequence, creating a loop-like structure. This precise folding and cutting is essential for joining the coding parts correctly to produce a message that can be used to build a protein.

222. (C) Most amino acids are specified by more than one codon
The genetic code is designed with a high level of redundancy, meaning that several different three-base combinations can all signal for the same amino acid. This feature provides a built-in safety net, as many small changes in the DNA might not actually change the resulting protein. This characteristic is universal across all life and is fundamental to how genetic information is stored and translated.

223. (D) Phosphorylate the 5' ends of synthetic oligonucleotides or PCR products for ligation
Molecular biology often requires the addition of a specific chemical group to the starting end of a DNA fragment. An enzyme is used to transfer this group from a donor molecule, providing the necessary energy for the fragment to be joined to another piece. This step is vital for preparing synthetic segments for use in cloning or for labeling them for detection in research.

224. (C) Cos sites required for lambda phage packaging
Certain cloning tools have been engineered to include specific signals that allow them to be "packed" into viruses. These sequences are not found in standard plasmids and provide a unique way to move large segments of DNA into bacterial cells very efficiently. This capability makes them ideal for building comprehensive collections of genetic information and for studying large-scale genomic structures that other tools cannot handle.

225. (A) II and V
Using modified viruses to deliver new genes into animals is a powerful but limited technique. While they are very good at inserting their payload into the host's DNA, they can only carry a relatively small amount of genetic material. Furthermore, the process does not always ensure that the new trait will be passed on to future generations in a single step, requiring careful breeding and screening.

226. (A) Resetting the epigenetic state of the nucleus
Cloning an animal requires that the DNA from a mature cell be completely "rebooted" so it can behave like the DNA of an embryo again. This process involves erasing the chemical marks that tell the cell to be skin, muscle, or blood, and replacing them with signals for early development. This resetting of the genetic instructions is what allows a specialized cell to grow into an entire new individual.

227. (A) Allolactose
Bacterial sugar processing is controlled by a small molecule that acts as a sensor for the presence of nutrients. When the relevant sugar is available, a version of it binds to a regulatory protein, causing it to fall off the DNA. This clears the way for the cell to begin making the enzymes needed to use that sugar, ensuring that resources are only spent when food is present.

228. (C) Seventh position of an alpha helix
Certain proteins that regulate gene activity come together in pairs using a structural motif characterized by a repeating pattern of a specific amino acid. These molecules feature an alpha helix where this amino acid appears at regular intervals, allowing two different protein chains to interlock like a zipper. This physical connection is essential for the proteins to bind to their target DNA and control gene expression.

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229. (D) Hydrophobic patches on unfolded or partially folded proteins
Maintaining the correct three-dimensional shape of biological molecules is vital for their function. Specialized molecular assistants prevent proteins from clumping together by temporarily covering up "sticky" regions that are usually hidden inside a well-folded protein. By protecting these exposed areas, the assistants give the protein time to reach its correct active form, supporting the overall health and survival of the cell.

230. (A) Lysine
The activity of genes is influenced by the chemical modification of the proteins around which DNA is wrapped. One common change involves adding a small acetyl group to a specific amino acid in the protein tails. This addition reduces the positive charge of the protein, causing it to loosen its grip on the DNA and making the genes more accessible to the machinery that turns them on.

231. (D) Genome annotation
Once the sequence of a genome is determined, the next vital step is to make sense of the vast amount of data. Researchers use specialized computer tools to identify the exact locations of genes and predict their biological roles. This process of labeling the genetic blueprint transforms a simple list of nucleotides into a functional map that can be used to study health, disease, and evolution.

232. (A) Molecular mass
High-resolution protein separation often involves a two-step process using an electric field. After the molecules have been sorted by their electrical properties, they are then separated based strictly on their physical size. This second step provides a detailed view of the different proteins in a sample, allowing researchers to see thousands of unique spots, each representing a single type of protein produced by the cell.

233. (D) Pyrimidines (C and T)
Early DNA reading methods utilized specific chemicals that target and break the molecular chain at known bases. One such chemical is used to specifically modify two of the four bases, leading to breaks only at those positions. By comparing the resulting fragments, researchers can reconstruct the original genetic sequence, providing a detailed look at the chemical makeup of the genome through this chemical degradation approach.

234. (A) Generate ultra-long reads in a single run
Some advanced sequencing tools can read very long continuous segments of DNA by pulling the molecule through a microscopic pore. Unlike other methods that break the DNA into tiny pieces, this approach keeps the sequence intact, making it much easier to assemble complex parts of the genome. This capability is particularly useful for studying structural variations and for building more complete and accurate genetic maps.

235. (A) Visualize highly significant SNP associations
Genetic association studies often display their results using a specific type of plot where statistical strength is converted into a more intuitive visual scale. By using a logarithmic transformation, even very small probabilities can be seen as tall peaks on a graph. This allows researchers to quickly identify the genomic regions that have the strongest links to the physical trait being studied in a population.

236. (B) Captures Mendelian sampling and true relationships
Modern genetic evaluations are improved by using DNA data to calculate exactly how much genetic material is shared between individuals. Unlike traditional methods that use average family expectations, this approach accounts for the random nature of how genes are passed from parents to offspring. This precise measure of relatedness provides more accurate estimates of an individual's true breeding value, leading to better selection decisions.

237. (A) Highly polygenic with many genes of small effect
Certain genetic models are based on the assumption that thousands of small genetic differences all across the genome contribute to a trait. Rather than looking for one or two major genes, these methods treat every part of the DNA as if it makes a tiny, similar contribution. This approach is ideal for complex characteristics like health or production, which are influenced by many biological pathways working together.

238. (A) Optimize enzymes or proteins for specific desired traits, such as thermal stability
Researchers can improve proteins in the laboratory by mimicking the natural process of evolution. This involves creating millions of variants and then carefully selecting the ones that work best under specific conditions. By repeating this cycle multiple times, scientists can develop enzymes that are much stronger or more efficient than those found in nature, providing powerful new tools for medicine, industry, and environmental protection.

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239. (B) RNA-dependent DNA polymerase (reverse transcriptase)
The protective caps at the ends of chromosomes are maintained by a unique enzyme that carries its own template. This catalyst is a specialized type of protein that builds DNA by reading an internal RNA sequence. By adding new repeats to the chromosome tips, the enzyme prevents the loss of essential genetic information and is vital for the long-term survival and division of many cell types.

240. (A) C-banding
Specific staining techniques are used to highlight the structural parts of chromosomes that do not carry genes. These regions are often found near the center and are composed of highly condensed, repetitive DNA. Visualizing these areas is essential for identifying individual chromosomes and for finding structural abnormalities in the regions that organize the genome during cell division, providing a valuable tool for genetic diagnosis and research.

241. (A) Efficient initiation of translation
In eukaryotic cells, the machinery that builds proteins must find the exact starting point on a messenger RNA molecule. A specific consensus sequence surrounding the start signal helps the machinery recognize the correct location to begin synthesis. Without this guiding sequence, the production of proteins would be much less efficient, potentially leading to errors in how the genetic instructions are followed by the cell.

242. (B) Type II topoisomerase
As the DNA double helix is unwound for replication, it can become dangerously over-twisted ahead of the machinery. A specialized enzyme acts as a biological "swivel" to relieve this pressure by cutting and then resealing both strands of the DNA. This activity prevents the molecule from tangling and is essential for the smooth and continuous duplication of the entire bacterial genome during cell division.

243. (B) RNA triphosphatase
The first step in adding a protective cap to a new messenger RNA involves removing a single phosphate group from the very beginning of the transcript. This modification prepares the molecule for the addition of the modified guanine residue that will eventually follow. This coordinated series of chemical reactions is vital for protecting the transcript from being destroyed and for ensuring it can be correctly translated later.

244. (B) ATP
Attaching the correct amino acid to its transfer molecule is a high-energy process that ensures the genetic code is translated faithfully. A specialized enzyme uses cellular fuel to activate the amino acid before bonding it to the carrier. This precision is fundamental to life, as once the amino acid is attached, the ribosome will place it in the growing protein chain based only on the carrier's signal.

245. (B) Modified (e.g., methylated) DNA
Certain bacterial defense enzymes have a very specific appetite and will only cut DNA that has been chemically modified. These proteins are designed to ignore the bacteria's own genetic material while attacking intruders that carry different patterns of methyl groups. This targeted cleavage provides a sophisticated way for cells to distinguish themselves from foreign invaders, offering a unique layer of protection against viral infections.

246. (A) Ampicillin, X-gal, and IPTG
To find the bacteria that have successfully taken up a new gene, researchers use a special mixture of chemicals in the growth medium. Some chemicals kill any cells that don't have the vector, while others participate in a color-changing reaction that identifies which vectors have the new gene inside. This simple visual test allows scientists to quickly pick out the correct colonies for further study.

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247. (B) A simple, customizable RNA guide
Modern gene editing is much more efficient than older methods because it uses a short piece of genetic material to find its target. Rather than having to build a complex new protein for every job, researchers can just design a new guide sequence. This flexibility and ease of use have transformed biotechnology, allowing for much faster and more precise modifications to the genomes of many different species.

248. (B) Developmental anomalies like Large Offspring Syndrome
Cloning often faces significant challenges because the "rebooting" of the donor DNA is not always perfect. If some of the chemical marks from the

original cell remain, the resulting embryo may not develop correctly. This can lead to various health problems and physical abnormalities in the offspring, highlighting how complex and delicate the process of resetting genetic instructions really is for creating healthy cloned animals.

249. (A) Positive transcriptional activator
Certain bacterial genes are controlled by a protein complex that acts as a sensor for the cell's energy levels. When the primary fuel source is low, this complex binds to the DNA to help recruit the machinery needed to turn on alternative pathways. This positive control mechanism ensures that the cell can efficiently switch its metabolism to use different sugars only when they are actually needed.

250. (B) Histidine and Cysteine
Many proteins that regulate gene activity use a specialized structural motif that is held together by a central metal ion. This ion is coordinated by two specific types of amino acids, which together create a stable "finger" that can reach into the DNA double helix. This motif allows the protein to recognize and bind to very specific genetic sequences, providing precise control over expression.

251. (B) It conjugates ubiquitin to the target protein, providing specificity.
The cell uses a sophisticated system to identify which proteins should be destroyed. Specialized enzymes act like molecular "matchmakers," recognizing a specific target and attaching a small destruction tag to it. This tagging process is vital for ensuring that only the correct proteins are sent to the disposal center, allowing the cell to precisely manage its internal environment and respond to various biological signals.

252. (A) DNMT1
To ensure that cell identity is maintained through division, the pattern of chemical marks on the DNA must be faithfully copied to each new strand. A specialized enzyme recognizes the marks on the original side of the molecule and quickly adds matching ones to the newly made side. This maintenance process is essential for keeping the correct genes turned on or off in every daughter cell.

253. (B) Mapped sequencing reads aligned to a specific transcript (e.g., RPKM/FPKM/TPM)
Modern gene expression analysis involves counting how many times every transcript is seen in a sample. By sequencing every RNA molecule and then matching them back to the original genome, researchers can precisely measure the activity of every gene. This digital approach provides a very accurate and detailed picture of cellular function, revealing which pathways are most active under different biological conditions or treatments.

254. (B) Intrinsic transcriptional activation capability without interacting with the "prey"
When using a system to find protein interactions, researchers must be careful about "false signals" caused by one of the proteins acting on its own. If the protein that is fixed to the DNA can turn on the reporter gene by itself, the system will show a connection even when none exists. This requires careful testing to ensure that the measured signal is truly caused by two proteins binding.

255. (B) Two overlapping peaks of different colors at the same position
When reading a genetic sequence, a single position where an individual has inherited two different versions of a gene will appear as a unique signal. Instead of one clear peak, the detector will see two different signals at the same time, usually shown as different colors on a computer screen. This visual "double peak" is a clear sign of genetic variation at that specific genomic location.

256. (B) DNA methylation via altered kinetics
Advanced sequencing technology can detect more than just the four standard bases; it can also "see" where the DNA has been chemically modified. As the enzyme builds a new strand, these modifications cause it to slow down or pause in a characteristic way. By measuring the exact timing of each addition, the system can map the epigenetic landscape of the genome directly during the sequencing run.

257. (B) The multiple testing problem, leading to false positives
Genetic association studies face a significant statistical challenge because they look at millions of different markers at the same time. With so many chances to find a pattern, some

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will inevitably appear to be linked to a trait just by coincidence. To avoid these false discoveries, researchers must use very strict rules to determine what counts as a true finding, ensuring their results reflect real biology.

258. (C) Their genomic marker profile tested shortly after birth
Breeders can identify the best sires for future generations very early in life by using DNA-based evaluations. By analyzing an individual's genetic markers shortly after it is born, they can estimate its future breeding value with high accuracy. This significantly reduces the time needed for selection, as there is no longer a need to wait for the animal's offspring to be born and measured.

259. (B) Distribution of marker variances and effects
Advanced mathematical models for predicting performance from DNA data differ in how they treat various parts of the genome. Some assume that all genetic changes have a small, similar effect, while others allow for a few markers to have much larger impacts. These different starting assumptions help researchers choose the best model for a specific trait, whether it is influenced by many genes or just a few.

260. (B) 3-4 generations
Breeders can quickly move a new trait into an elite variety by using molecular markers to guide the process. By selecting the offspring that are most similar to the original parent in every way except for the new gene, they can recover the entire high-quality genome in just a few years. This targeted approach is much faster and more efficient than traditional breeding methods that rely only on appearance.

261. (A) 1.67
The basic unit of genome organization involves a specific length of DNA coiling around a protein core. This coiling is very precise, with the strand making a little more than one and a half turns around the bundle. This arrangement is the first step in compacting the massive genome into the tiny space of the cell's nucleus, while still keeping the information accessible to the machinery.

262. (B) Metaphase
To see chromosomes clearly under a microscope, they must be caught at the moment when they are most tightly packed. This occurs during a specific phase of cell division when all the genetic material is lined up in the center of the cell. By stopping the cell at this point, researchers can obtain clear, distinct images that are essential for identifying individual chromosomes and detecting any abnormalities.

263. (A) Shine-Dalgarno sequence
Bacterial protein production is guided by a specific sequence located just before the start of the gene. This sequence acts like a docking station for the protein-building machinery, ensuring it is positioned correctly on the messenger RNA. This precise alignment is vital for the efficient and accurate translation of the genetic message into a functional protein, providing a fundamental control point in bacterial gene expression.

264. (B) RNA synthesized by primase
To begin making a new DNA strand, the synthesis machinery requires a pre-existing starting point. In the cell, this is provided by a short piece of a related molecule that is built first. This temporary primer provides the necessary chemical group for the DNA-building enzyme to attach its first block. Once the process is underway, the temporary primer is removed and replaced with the correct DNA components.

265. (A) G/U residues
The processing of a new messenger RNA molecule in complex cells involves cutting it at a specific point and adding a protective tail. This event is triggered by two signals near the end of the transcript: one is a conserved six-base sequence, and the other is a region rich in two specific types of nucleotides. Together, these signals ensure the message is finished at the correct location.

266. (B) Polypeptide chain to the tRNA in the P site
When the production of a protein is complete, the new chain must be released from the machinery. This occurs when a stop signal is reached, which triggers a chemical reaction that cuts the bond holding the protein to its last carrier. This final step allows the completed polypeptide to fold into its active shape and begin its work within the cell, completing the translation process.

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267. (B) 5' overhangs
Certain enzymes used to cut DNA do so in a staggered way, leaving short, single-stranded ends. These "overhangs" are very useful in molecular biology because they can easily pair

with other fragments that have matching ends. This makes it possible to stitch different pieces of DNA together with high precision, which is a fundamental requirement for creating recombinant molecules and for many other genetic engineering tasks.

268. (B) Requires fewer clones to cover the entire genome
Mapping massive genomes is much more efficient when researchers can work with very long segments of DNA. Specialized vectors that can carry huge pieces of genetic information are preferred because they allow the entire genome to be represented in a much smaller number of individual samples. This reduces the amount of work needed to build a complete map and helps keep large genetic structures intact for study.

269. (B) Actively dividing
Certain viruses used for delivering new genes into cells can only perform their job when the host cell is in the process of growing and splitting. They require the nuclear envelope to break down during division so they can reach the DNA and insert their own genetic material. This limitation is an important consideration when choosing the right tool for modifying different types of tissues or organisms in research.

270. (A) 5'-NGG-3'
Modern gene editing systems require a specific "landmark" sequence to be present in the DNA for the cutting enzyme to work. This landmark consists of three nucleotides: any base followed by two guanine bases. This signal is essential for the system to bind and perform its function correctly. Without this motif, the enzyme will ignore the DNA, even if the guide sequence is a perfect match.

271. (A) The process of transcriptional attenuation
Bacterial gene expression can be controlled by a mechanism that uses the ribosome as a sensor for nutrient levels. If a specific building block is in short supply, the ribosome will move differently along the messenger RNA. This change in speed causes the RNA to fold into a shape that allows the synthesis of the needed enzymes to continue, ensuring the cell can respond to scarcity.

272. (B) Major groove
Many proteins that regulate gene activity find their target by reaching into the larger of the two "valleys" in the DNA double helix. This specific entry point allows the protein to feel the chemical pattern of the bases inside, ensuring it binds to the correct sequence. This recognition is vital for the precise control of the genome, as it allows each factor to find its target.

273. (B) Dolichol phosphate
Attaching complex sugar chains to new proteins requires a specialized molecular "carrier" that is anchored in the membrane of the cell. This carrier holds the growing sugar chain in place while it is being built, before finally transferring the completed unit to the target protein. This process is essential for the proper folding and function of many proteins that work at the cell's surface or are exported.

274. (B) An epigenetic phenomenon causing genes to be expressed in a parent-of-origin-specific manner.
Certain genetic traits are unique because only one of the two inherited copies of a gene is active, and the choice depends entirely on which parent it came from. This biological "labeling" occurs through chemical modifications made during the formation of eggs and sperm. These marks ensure that some genes are always maternal and others always paternal, which is vital for the healthy development of mammals.

275. (B) Rapidly identifying transcripts and aiding in gene discovery
Scientists can quickly learn about the active genes in any tissue by sequencing short, unique segments from the ends of all the messenger RNA molecules. These segments serve as signatures that allow for the discovery of new genes and for the measurement of which ones are most active. This efficient approach avoids the need to sequence every base, providing a fast way to map functionality.

276. (B) Trypsin
Analyzing complex mixtures of proteins often starts with breaking them down into smaller, manageable pieces using a specialized enzyme. This catalyst cuts the protein chains only at very specific amino acids, creating a predictable set of fragments. These fragments can then be measured with high precision, allowing researchers to identify each protein in the original sample based on the unique pattern of its pieces.

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277. (A) Fluorescent dyes attached to the ddNTPs
Modern methods for reading the genetic code have replaced hazardous radioactive labels with bright, colored dyes. Each of the four different "terminator" building blocks is tagged with its own unique color. As the DNA is built, a laser detects these colors one by one, allowing a computer to automatically read and record the sequence. This transformation has made DNA sequencing much faster, safer, and more reliable.

278. (A) Larger pH changes from released H+ ions
Certain sequencing platforms identify bases by measuring the chemical changes that occur during DNA synthesis. If a template has several identical bases in a row, the system will incorporate them all at once, leading to a much larger signal. By recording the strength of these signals, the computer can determine not only which base was added but also how many of them were in a row.

279. (B) Minor Allele Frequency (MAF) of the markers
Finding the genetic causes of traits in a large population depends on how common each version of a gene is. If a particular genetic variant is very rare, it becomes much harder to find a strong statistical link between that marker and the trait. Researchers must use large groups of individuals and focus on common variations to ensure they have enough power to produce reliable scientific results.

280. (B) Varies from 0.5 via Mendelian sampling
While we expect full siblings to share about half of their DNA on average, the actual amount can vary due to the random way that genes are passed down. Modern genetic tools can measure this real sharing with high precision. This "realized" relatedness provides much more accurate information for breeding programs than traditional family trees, as it accounts for the specific genes each individual actually inherited.

281. (B) Equal (drawn from a common variance)
Advanced mathematical models for genetic prediction use various strategies to manage the vast amount of DNA information. One approach assumes that while most markers have no effect, all the ones that do have an effect contribute a similar amount of variation to the trait. This simplified assumption helps the model run more efficiently and can provide very accurate results for many complex biological characteristics.

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282. (A) 50%
Specialized genetic systems can spread through a wild population much faster than normal because they cheat the usual laws of inheritance. Instead of being passed to only half of the offspring, these systems can ensure they are present in nearly every individual in the next generation. This biased inheritance is being explored as a way to control pests or reduce the spread of dangerous diseases.

283. (A) Inner nuclear matrix and chromosome arms
The gene-rich and active parts of the genome are typically found in the more accessible regions of the nucleus. These areas are characterized by a loose, open structure that allows the cellular machinery to easily reach and read the DNA. This organization is vital for the cell to quickly respond to internal and external signals and to produce the proteins needed for its daily functions.

284. (A) Barium hydroxide
Certain staining techniques use a strong chemical treatment to specifically highlight the structural parts of chromosomes. By temporarily breaking down the DNA in other areas, researchers can make the highly condensed, repetitive regions near the center stand out clearly. This provides a reliable visual marker for identifying chromosomes and for finding any structural changes in these non-coding regions that are essential for cell division.

285. (B) It increases transcription rates via activators
Specific DNA elements act as volume knobs for gene expression, significantly boosting the production of certain proteins. These elements work by providing binding sites for specialized activator proteins, which then interact with the main transcription machinery. This ability to dial up the activity of a gene is essential for the cell to produce enough protein to meet its needs under different biological conditions.

286. (A) 3' to 5' exonuclease activity
To maintain a high level of accuracy when copying the genome, the building enzyme has a built-in "delete" function. If a wrong base is added by mistake, the enzyme can detect the error, move backward to remove the incorrect

piece, and then try again. This self-correcting ability is vital for preventing harmful mutations and ensuring that the genetic blueprint remains stable through every cell division.

287. (A) U1 snRNP
The removal of non-coding segments from a primary transcript starts with a specific molecular "scout" that finds the exact boundary of the sequence. This scout is a complex made of both protein and a small RNA molecule that matches the sequence at the starting edge of the segment. By marking this spot, it helps the rest of the machinery assemble and perform the precise cutting.

288. (D) 20 different synthetases, one for each standard amino acid
The accuracy of translating the genetic code depends on twenty specialized enzymes, each dedicated to a single amino acid. These proteins act like quality-control inspectors, ensuring that each carrier molecule is paired with its correct building block. This specificity is a cornerstone of molecular biology, as it ensures that the instructions in the DNA are faithfully turned into functional protein chains in every cell.

289. (A) Reverse transcriptase
Studying gene activity often involves converting messenger RNA into a more stable DNA form. This task is performed by a specialized enzyme that can read an RNA template and build a matching DNA strand. This unique capability, originally discovered in viruses, has become a foundational tool in modern molecular biology, allowing researchers to clone, sequence, and measure the expression of thousands of genes.

290. (B) Agrobacterium tumefaciens
Genetic engineering in plants often utilizes a natural system derived from a specific soil-dwelling bacterium. This organism has the unusual ability to transfer a piece of its own genetic material directly into the genome of a plant host. By repurposing this system, scientists can efficiently introduce new, beneficial traits into crops, such as resistance to pests or improved nutritional content, in a controlled way.

291. (B) Hemizygous for the transgene, which integrates randomly as concatemers
Animals created through direct DNA injection into a fertilized egg typically carry only one copy of the new gene, which can land anywhere in their genome. Often, multiple copies of the gene will stick together in a long chain at a single location. Because the placement is random, each individual must be carefully checked to see if the new gene is working as intended.

292. (B) Mitochondrial heteroplasmy or mitochondrial inheritance from the oocyte
Cloned animals are unique because their genetic material comes from two different sources. While the main instructions in the nucleus come from the donor, the energy-producing centers of the cell are provided by the egg. This means the resulting individual has a mix of genetic information, which can sometimes influence its development and health in ways that are different from a naturally born offspring.

293. (A) Shut off in the presence of the end product (tryptophan)
Certain bacterial metabolic pathways are designed to stop working as soon as they have produced enough of a specific nutrient. When the concentration of the end product gets high, it acts as a signal to turn off the genes responsible for its production. This negative feedback loop ensures the cell never wastes energy making building blocks that it already has in abundance.

294. (A) Zinc finger DNA-binding domain
Early gene editing tools combined a DNA-cutting enzyme with a customizable part that could find specific sequences. This targeting part was made of several protein "fingers" that were engineered to recognize a particular genetic code. While effective, this approach required building a brand-new protein for every target, making it more difficult and time-consuming than the newer, RNA-based methods used today in genetic research.

295. (C) Polyubiquitin chain
The cell manages the removal of damaged or unnecessary proteins by attaching a specific molecular "tag" to them. This tag consists of a long chain of a small, universal protein that acts like a disposal signal. When a protein carries this label, it is recognized and pulled into a large destruction complex that breaks it down into its basic components for recycling.

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296. (B) Early embryonic development and gametogenesis
Most chemical marks on the genome are not permanent; they are actively erased and reset during two critical periods of life. This cleaning happens during the formation of reproductive cells and shortly after fertilization. This resetting process is essential for ensuring that each new generation starts with a "blank slate" and that cells can develop into all the different tissues needed for a healthy organism.

297. (A) Stop codon
Identifying the functional parts of a genome involves looking for continuous stretches of genetic code that can be translated into a protein. These regions must start with a specific "begin" signal and continue without interruption until they reach a "finish" signal. Finding these segments is a key step in mapping the genome and in understanding the instructions for building all the cell's proteins.

298. (A) Co-immunoprecipitation (Co-IP)
To find out if two proteins physically stick to each other, researchers can use a "fishing" technique with specialized antibodies. By capturing one specific protein from a cell mixture, they can see if any other proteins are pulled along with it. This method provides direct evidence of protein connections and is essential for understanding the complex networks that control all biological processes in a cell.

299. (B) Exploits historical recombination events in unstructured populations at a population level
Large-scale genetic studies are a powerful way to find the causes of traits without needing detailed family trees. Instead, they look at thousands of unrelated individuals and search for markers that are more common in those with a particular characteristic. This approach uses the entire history of the population to find even small genetic effects that would be missed by traditional methods.

300. (C) Linkage disequilibrium between markers and QTLs
The ability to predict an animal's performance from its DNA depends on the connection between the measured markers and the actual causal genes. Over generations or between different breeds, these connections can break apart as the DNA is shuffled. This means a prediction model built for one group of animals may not work for another, requiring researchers to constantly update their data and models.

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CHAPTER 03
Overview of Breeding

2010

1. What is the recognized wild ancestor of modern domestic taurine cattle?
(A) Bos gaurus
(B) Bos primigenius
(C) Bos javanicus
(D) Bos mutus

2004

2. Identify the primary historical domestication center for Bos indicus cattle.
(A) Fertile Crescent
(B) Yellow River Valley
(C) Andean Highlands
(D) Indus Valley

2010

3. The domestic chicken is primarily descended from which wild species?
(A) Red Junglefowl
(B) Green Junglefowl
(C) Sri Lankan Junglefowl
(D) Grey Junglefowl

2024

4. Which pathway best describes the domestication of dogs and pigs?
(A) Prey pathway
(B) Directed pathway
(C) Commensal pathway
(D) Nomadic pathway

2024

5. The wild ancestor of the domestic sheep is commonly identified as the:
(A) Mouflon
(B) Bezoar
(C) Markhor
(D) Urial

2015

6. Which species was domesticated primarily through the directed pathway for transport?
(A) Pig
(B) Goat
(C) Cat
(D) Horse

2018

7. The domestication of the wild water buffalo occurred in which two distinct regions?
(A) Egypt and Mesopotamia
(B) India and China
(C) Europe and North America
(D) Africa and Australia

2008

8. Based on historical timelines, which livestock species was domesticated earliest?
(A) Horse
(B) Chicken
(C) Sheep
(D) Rabbit

2014

9. Identify the incorrect statement regarding domestication syndrome.
(A) It involves increased docility.
(B) It causes brain size reduction.
(C) It alters coat color patterns.
(D) It eliminates all natural instincts.

2025

10. In the context of livestock domestication, consider the following Assertion (A) and Reason (R):
Assertion (A): Taurine and indicine cattle represent two independent domestication events.
Reason (R): They evolved from different ancestral subspecies of the aurochs in distinct geographical regions.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2019

11. What is the primary evolutionary advantage gained by livestock during early domestication?
(A) Enhanced predator skills
(B) Guaranteed food and protection
(C) Increased territorial aggression
(D) Complete genetic isolation

NODIA

2002

12. The domestication of goats originated from the wild Bezoar in which region?
(A) Himalayas
(B) Zagros Mountains
(C) Alps
(D) Andes

2009

13. Which mathematical expression defines genotypic frequencies under Hardy-Weinberg equilibrium?
(A) $p + q = 1$
(B) $p^2 + 2pq + q^2 = 1$
(C) $p^2 + q^2 = 1$
(D) $2pq = 1$

2013

14. Identify the force that does not change allele frequencies in a large, random-mating population.
(A) Migration
(B) Mutation
(C) Random fertilization
(D) Genetic drift

2008

15. Calculate the frequency of the recessive allele if the homozygous recessive genotype frequency is 0.16.
(A) 0.04
(B) 0.16
(C) 0.40
(D) 0.80

2009

16. In small animal populations, random fluctuations in allele frequencies are defined as:
(A) Gene flow
(B) Stabilizing selection
(C) Genetic drift
(D) Directed mutation

2003

17. The impact of migration on the genetic frequency of a herd depends heavily on:
(A) Specific mutation rates found within the immigrant group
(B) Allele frequency difference between populations
(C) Exact chronological age of the migrating individuals
(D) Average physical body size of the native individuals

2003

18. Continuous selection against a recessive allele results in:
(A) Sudden and complete elimination of the allele in one generation
(B) Permanent fixation of the recessive allele within the population
(C) Sustained and immediate increase in the heterozygous frequency
(D) Asymptotic reduction of the frequency toward zero over time

2018

19. What effect does a high mutation rate (u) from a dominant to a recessive allele have over time?
(A) Increases recessive allele frequency
(B) Increases dominant allele frequency
(C) Eliminates genetic variance
(D) Causes immediate population extinction

2015

20. Match the evolutionary forces with their primary genetic impact:
List I: (Evolutionary Forces)
P. Mutation
Q. Migration
R. Genetic Drift
S. Selection
List II: (Genetic Impact)
1. Differential reproductive success
2. Random fixation or loss of alleles
3. Introduction of novel alleles from outside
4. Creation of new alleles fundamentally
(A) P-4, Q-3, R-2, S-1
(B) P-3, Q-4, R-1, S-2
(C) P-4, Q-2, R-3, S-1
(D) P-1, Q-3, R-2, S-4

2017

21. Effective population size (N_e) is typically lower than the actual census size because of:
(A) Unequal number of breeding males and females
(B) Equal sex ratios
(C) Random mating
(D) Absence of overlapping generations

2023

22. Identify the type of selection that favors intermediate phenotypes over extremes.
(A) Directional selection
(B) Disruptive selection
(C) Frequency-dependent selection
(D) Stabilizing selection

2004

23. The probability of fixation of a newly arisen neutral mutation is equal to:
(A) Zero

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(B) Its initial frequency
(C) One
(D) The mutation rate

2021

24. What is the fundamental assumption of the Hardy-Weinberg law regarding population size?
(A) Small
(B) Exactly one hundred
(C) Infinitely large
(D) Fluctuating periodically

2009

25. Phenotypic variance (V_P) is fundamentally partitioned into which primary components?
(A) V_A and V_D
(B) V_I and V_E
(C) V_G and V_I
(D) V_G and V_E

2004

26. Which component of genetic variance is directly transmitted from parents to offspring?
(A) Additive variance
(B) Dominance variance
(C) Epistatic variance
(D) Interaction variance

2007

27. Dominance variance arises due to interactions between alleles at:
(A) Different loci
(B) The same locus
(C) Mitochondrial genes
(D) Environmental interfaces

2009

28. Narrow-sense heritability (h^2) is the ratio of which variance to phenotypic variance?
(A) Total genetic variance
(B) Additive genetic variance
(C) Environmental variance
(D) Dominance variance

2017

29. Broad-sense heritability (H^2) encompasses which of the following?
(A) Total genetic variance
(B) Additive variance only
(C) Dominance variance only
(D) Environmental variance

2002

30. Consider the following statements regarding epistatic variance (V_I):
I. It involves interaction between alleles at different loci.
II. It is fully transmitted to offspring.
III. It is a component of non-additive genetic variance.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I

2009

31. Repeatability sets the upper limit for which genetic parameter?
(A) Epistatic variance
(B) Environmental variance
(C) Inbreeding coefficient
(D) Narrow-sense heritability

2004

32. Genotype-environment interaction ($V_{\{GE\}}$) indicates that:
(A) Genotypes maintain consistent performance levels across environments
(B) Environmental factors exert no significant effect on the phenotype
(C) Variable performance of genotypes across different environments
(D) Genetic variance components equal the environmental variance

NODIA

2023

33. Which trait typically exhibits the highest heritability in livestock?
(A) Fertility
(B) Carcass quality
(C) Milk yield
(D) Survival rate

2023

34. The deviation of a heterozygote's phenotype from the average of the two homozygotes is called:
(A) Breeding value
(B) Additive effect
(C) Environmental deviation
(D) Dominance deviation

2017

35. The sum of the average effects of the alleles an individual carries is known as its:
(A) Breeding value
(B) Dominance deviation
(C) Epistatic value
(D) Phenotypic value

2002

36. Which factor is considered a part of temporary environmental variance?
(A) Herd management system
(B) Genetic make-up
(C) Daily fluctuations in weather
(D) Breed origin

2015

37. Which of the following is an elite indigenous dairy cattle breed of India?
(A) Sahiwal
(B) Amritmahal
(C) Khillari
(D) Kangayam

2006

38. Identify the exotic dairy breed known for producing milk with the highest fat percentage.
(A) Holstein Friesian
(B) Brown Swiss
(C) Ayrshire
(D) Jersey

2008

39. Which Indian cattle breed is renowned strictly for its excellent draft capabilities?
(A) Red Sindhi
(B) Amritmahal
(C) Gir
(D) Tharparkar

2013

40. Consider the following statements describing dual-purpose cattle breeds in India:
I. Hariana is a prominent dual-purpose breed.
II. They are bred exclusively for beef production.
III. Ongole exhibits dual-purpose characteristics.
IV. Their cows are moderate milk yielders while bullocks are good draft animals.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) I, III and IV
(C) II, III and IV
(D) I and IV

2010

41. The Gir cattle breed is geographically native to which Indian state?
(A) Punjab
(B) Haryana
(C) Tamil Nadu
(D) Gujarat

2004

42. Which exotic dairy breed produces the highest average volume of milk per lactation?
(A) Holstein Friesian
(B) Guernsey
(C) Jersey
(D) Red Dane

2022

43. Karan Swiss is a crossbred cattle strain developed by crossing:
(A) Hariana and Holstein
(B) Sahiwal and Brown Swiss
(C) Tharparkar and Jersey
(D) Red Sindhi and Ayrshire

2016

44. What is the distinguishing phenotypic feature of the Kankrej breed?
(A) Polled head
(B) Lyre-shaped horns
(C) Pure black coat
(D) Absence of a hump

2017

45. Which of these is a widely recognized exotic beef cattle breed?
(A) Hereford
(B) Brown Swiss
(C) Sahiwal
(D) Red Sindhi

2025

46. The Tharparkar breed is predominantly adapted to which agro-climatic condition?
(A) High altitude cold deserts
(B) Humid coastal regions
(C) Arid and semi-arid deserts
(D) Heavy rainfall forest zones

2021

47. Which indigenous breed is also known by the name “Lola” due to its loose skin?
(A) Gir
(B) Hariana
(C) Ongole
(D) Sahiwal

2022

48. Identify the distinguishing characteristic of Bos indicus cattle compared to Bos taurus.
(A) Absence of a hump
(B) Smaller dewlap
(C) Prominent hump and large dewlap
(D) Thicker winter hair coat

2022

49. What is the diploid chromosome number in riverine buffaloes?
(A) 48

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(B) 50
(C) 60
(D) 38

2011

50. Consider the following statements regarding Indian buffalo breeds:
I. Murrah is the highest milk-producing breed.
II. Bhadawari milk has the highest fat percentage.
III. Surti buffaloes possess sickle-shaped horns.
IV. Jaffarabadi is one of the heaviest breeds.
V. Swamp buffaloes are primarily used for dairy in India.
Which of the above statement(s) is/are correct?
(A) I, II, III and IV
(B) II, III, IV and V
(C) I, III, IV and V
(D) I, II and IV

2015

51. The Bhadawari buffalo is famous for which specific economic trait?
(A) High milk fat content (up to 13%)
(B) Extreme body weight
(C) Longest lactation period
(D) High-speed draft work

2009

52. Which buffalo breed is characterized by "wall eyes" (white iris)?
(A) Nili-Ravi
(B) Murrah
(C) Surti
(D) Mehsana

2025

53. Jaffarabadi buffaloes originate from which region?
(A) Punjab
(B) Haryana
(C) Andhra Pradesh
(D) Saurashtra (Gujarat)

2019

54. The Mehsana buffalo is considered a natural cross between which two breeds?
(A) Murrah and Surti
(B) Murrah and Nili-Ravi
(C) Jaffarabadi and Bhadawari
(D) Toda and Surti

2017

55. What is the diploid chromosome number of swamp buffaloes?
(A) 48
(B) 50
(C) 52
(D) 54

2012

56. Which buffalo breed is reared by the pastoralist tribe in the Nilgiri hills?
(A) Chilika
(B) Banni
(C) Kalahandi
(D) Toda

2012

57. Identify the primary utility of swamp buffaloes in Southeast Asian countries.
(A) High-yield milk production
(B) Draft power in paddy fields
(C) Carpet wool production
(D) Fast-track racing

NODIA

2013

58. The Banni buffalo, known for thriving in harsh conditions, is native to:
(A) Rajasthan
(B) Gujarat (Kutch)
(C) Maharashtra
(D) Madhya Pradesh

2010

59. Which physical trait is most characteristic of the Murrah buffalo?
(A) Long, straight horns
(B) Sickle-shaped horns
(C) Drooping, heavy horns
(D) Tightly curled, short horns

2013

60. Which of the following is the correct sequence of buffalo breeds from highest to lowest average lactation milk yield?
(A) Murrah, Mehsana, Surti, Bhadawari
(B) Surti, Bhadawari, Mehsana, Murrah
(C) Mehsana, Murrah, Bhadawari, Surti
(D) Bhadawari, Surti, Murrah, Mehsana

2015

61. The Merino breed of sheep is universally renowned for producing:
(A) Fine apparel wool
(B) High-quality mutton
(C) Carpet wool
(D) Abundant milk

2025

62. Which Indian sheep breed is primarily recognized for superior mutton quality?
(A) Chokla

(B) Magra
(C) Nali
(D) Nellore

2015

63. Identify the Indian goat breed famous for its dual-purpose (milk and meat) utility and Roman nose.
(A) Jamunapari
(B) Black Bengal
(C) Barbari
(D) Chegu

2010

64. The Pashmina fiber is harvested from which goat breed?
(A) Changthangi
(B) Angora
(C) Boer
(D) Sirohi

2006

65. The Angora goat is the source of which valuable commercial fiber?
(A) Mohair
(B) Cashmere
(C) Shahtoosh
(D) Merino wool

2006

66. Which Indian goat breed is highly prolific and famous for excellent meat quality and valuable skin?
(A) Beetal
(B) Osmanabadi
(C) Malabari
(D) Black Bengal

2007

67. The Karakul sheep is specifically bred for:
(A) Fine wool
(B) Pelt (lamb skin)
(C) Mutton
(D) Milk

2024

68. Which of the following sheep breeds is native to the cold arid region of Rajasthan and produces good carpet wool?
(A) Chokla
(B) Gaddi
(C) Deccani
(D) Hassan

2002

69. Identify the highly prolific Indian sheep breed known for carrying the FecB (Booroola) gene.
(A) Malpura
(B) Marwari
(C) Patanwadi
(D) Garole

2008

70. Regarding the genetics of sheep prolificacy, consider the following Assertion (A) and Reason (R):
Assertion (A): The Garole sheep exhibits exceptional litter size compared to other Indian sheep.
Reason (R): It possesses a natural mutation in the BMPR1B (FecB) gene which increases ovulation rate.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2022

71. Which exotic goat breed is widely known as the "Queen of Goats" for its high milk production?
(A) Toggenburg
(B) Saanen
(C) Alpine
(D) Anglo-Nubian

2003

72. The Boer goat is an exotic breed primarily utilized for:
(A) Meat
(B) Milk
(C) Fiber
(D) Pelt

2003

73. Which exotic poultry breed is the primary genetic base for modern commercial white egg layers?
(A) White Leghorn
(B) Rhode Island Red
(C) White Plymouth Rock
(D) Sussex

2015

74. Modern commercial broilers are predominantly developed using crosses that include which breed?
(A) White Leghorn
(B) Minorca
(C) Ancona
(D) White Cornish

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2019

75. Identify the renowned dual-purpose poultry breed that lays brown eggs.
(A) Rhode Island Red
(B) White Leghorn
(C) Cornish
(D) Silkie

2016

76. Which indigenous Indian poultry breed is famous for its fighting prowess and stamina?
(A) Kadaknath
(B) Chittagong
(C) Busra
(D) Aseel

2006

77. The Kadaknath breed of poultry is unique because it exhibits:
(A) Fibromelanosis (black meat and organs)
(B) Complete absence of feathers
(C) Production of green-shelled eggs
(D) A massive body weight exceeding 5 kg

2014

78. In poultry breeding, strains utilized for commercial broiler production must excel in:
(A) Maximization of total lifetime egg production cycles
(B) Increased density and quality of the external plumage
(C) Extended biological lifespan and overall bird longevity
(D) Rapid growth rates and efficient feed conversion ratios

2010

79. The Naked Neck gene (Na) in poultry is economically advantageous in which environment?
(A) Sub-zero cold climates
(B) Hot and humid tropical climates
(C) High altitude mountains
(D) Environments with heavy predators

2009

80. Match the poultry breeds to their utility class:
List I: (Poultry Breeds)
P. White Leghorn
Q. Cornish
R. Rhode Island Red
S. Aseel
List II: (Utility Class)
1. Dual-purpose
2. Indigenous game bird
3. Meat type
4. Egg type
(A) P-4, Q-3, R-1, S-2
(B) P-3, Q-4, R-2, S-1
(C) P-4, Q-1, R-3, S-2
(D) P-2, Q-3, R-1, S-4

2024

81. Which breed belongs to the Mediterranean class of poultry?
(A) Plymouth Rock
(B) Minorca
(C) Brahma
(D) Sussex

2018

82. The Plymouth Rock is categorized under which class of poultry?
(A) American
(B) Asiatic
(C) English
(D) Mediterranean

2019

83. The characteristic feather pattern of the Barred Plymouth Rock is an example of:
(A) Sex-influenced trait
(B) Sex-linked trait
(C) Holandric trait
(D) Mitochondrial inheritance

2006

84. Brahma and Langshan breeds belong to which poultry class?
(A) English
(B) American
(C) Mediterranean
(D) Asiatic

2017

85. The National Bureau of Animal Genetic Resources (NBAGR) is headquartered in:
(A) Karnal
(B) New Delhi
(C) Hyderabad
(D) Izatnagar

NODIA

2016

86. Which conservation strategy involves preserving live populations of native breeds in their natural habitat?
(A) Ex situ in vitro
(B) Cryopreservation
(C) Genomic banking
(D) In situ

2005

87. Cryopreservation of semen and embryos is an example of:
(A) In vivo conservation
(B) Ex situ conservation
(C) In situ conservation
(D) Phenotypic characterization

2025

88. The primary mandate of NBAGR does not include:
(A) Registration of new animal breeds
(B) Characterization of animal genetic resources
(C) Commercial sale of dairy products
(D) Conservation of threatened breeds

2013

89. Upon successful registration of a newly identified breed, NBAGR issues a unique:
(A) Barcode index
(B) Patent certificate
(C) Trademark license
(D) Accession number

2021

90. Identify the correct sequence for the following standard steps of breed registration by NBAGR:
I. Evaluation by the Breed Registration Committee
II. Submission of application with breed descriptors
III. Issue of Accession Number
IV. Phenotypic and genetic characterization
(A) IV, II, I, III
(B) II, IV, I, III
(C) IV, I, II, III
(D) II, I, IV, III

2013

91. The categorization of a breed as "Endangered" by FAO is primarily based on:
(A) Standard dairy performance and milk yield parameters
(B) Population size and number of active breeding females
(C) Specific geographical location and regional distribution
(D) Observed frequencies of distinct coat color variations

2008

92. Phenotypic characterization of livestock genetic resources primarily requires data on:
(A) Whole genome sequences
(B) Morphological traits and biometry
(C) Transcriptome profiles
(D) Mitochondrial haplogroups

NODIA

2017

93. Molecular characterization of livestock breeds is most commonly performed using:
(A) Phenotypic descriptors
(B) Microsatellite markers and SNPs
(C) Blood glucose levels
(D) Rumen microbial counts

2025

94. The preservation of somatic cells for future cloning purposes falls under:
(A) In situ conservation
(B) Ex situ in vivo conservation
(C) Ex situ in vitro conservation
(D) Population expansion

2005

95. The concept of a "Core Breeding Tract" refers to:
(A) Native geographic area of breed origin and maintenance
(B) Authorized laboratory facilities where semen is stored
(C) Large-scale commercial feedlots for intensive production
(D) International quarantine centers for disease monitoring

2015

96. Which entity evaluates and approves the registration of new livestock breeds in India?
(A) ICAR headquarters directly
(B) State Animal Husbandry Departments
(C) Breed Registration Committee (BRC) under ICAR
(D) Food and Agriculture Organization (FAO)

2018

97. In domestic mammals, the heterogametic sex is:
(A) Male (XY)
(B) Female (XX)
(C) Female (ZW)
(D) Male (ZZ)

2024

98. In poultry, the sex chromosomes are denoted as Z and W. Which sex is heterogametic?
(A) Male (ZZ)
(B) Male (ZW)
(C) Female (ZZ)
(D) Female (ZW)

2009

99. The critical gene responsible for initiating male sex determination in mammals is located on the Y chromosome and is called:
(A) SRY
(B) SOX9
(C) DMRT1
(D) DAX1

2018

100. Consider the following statements regarding sex chromosome aneuploidy in mammals:
I. XXY causes Klinefelter's syndrome equivalent.
II. XO causes Turner's syndrome equivalent.
III. XXX causes fertile male syndrome.
Which of the above statement(s) is/are incorrect?
(A) I
(B) II, III
(C) III
(D) I, II

2004

101. Triploidy ($3n$) in poultry usually results in:
(A) Exceptional egg production
(B) Early embryonic death or intersex individuals
(C) Perfect male fertility
(D) Increased lifespan

2025

102. An individual exhibiting both male and female phenotypic characteristics in different parts of its body is called a:
(A) Freemartin
(B) Gynandromorph
(C) Hermaphrodite
(D) Pseudohermaphrodite

2017

103. Freemartinism in cattle predominantly occurs due to:
(A) Ingestion of harmful fungal toxins in the maternal diet
(B) Specific single gene mutation located on the X chromosome
(C) Placental vascular anastomosis in heterosexual twin pairs
(D) Occurrence of polyspermy during the fertilization process

2023

104. A freemartin calf is genetically:
(A) A normal male
(B) A fertile female
(C) A triploid individual
(D) A sterile female chimera

2003

105. Which gene is considered the master sex-determining switch in birds, located on the Z chromosome?
(A) DMRT1
(B) SRY
(C) FOXL2
(D) AMH

2017

106. In poultry, sex-linked traits like feather sexing rely on genes located on which chromosome?
(A) Autosome 1
(B) W chromosome
(C) Mitochondrial DNA
(D) Z chromosome

2013

107. The presence of horns in certain sheep breeds behaves as dominant in males and recessive in females. This is an example of:
(A) Sex-influenced inheritance
(B) Sex-linked inheritance
(C) Sex-limited inheritance
(D) Y-linked inheritance

2002

108. Which ploidy level is standard for somatic cells of normal domestic livestock?
(A) Haploid (n)
(B) Triploid ($3n$)
(C) Diploid ($2n$)
(D) Tetraploid ($4n$)

2025

109. Pre-zygotic isolating mechanisms function to:
(A) Prevent the survival of hybrid embryos
(B) Reduce the fitness of F2 hybrids
(C) Induce sterility in hybrid offspring
(D) Prevent mating or fertilization between species

2014

110. Consider the following statements regarding post-zygotic isolation mechanisms:
I. Hybrid inviability
II. Hybrid sterility
III. Temporal isolation
IV. Hybrid breakdown
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) II, III and IV
(C) I, III and IV
(D) I, II and III

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2004

111. Which mechanism prevents mating due to species breeding at different times of the year?
(A) Spatial isolation
(B) Temporal isolation
(C) Behavioral isolation
(D) Mechanical isolation

2019

112. The inability of sperm from one species to fertilize the egg of another species is termed:
(A) Mechanical isolation
(B) Gametic isolation
(C) Hybrid inviability
(D) Hybrid breakdown

2024

113. Speciation that occurs due to geographic separation of populations is known as:
(A) Sympatric speciation
(B) Parapatric speciation
(C) Artificial speciation
(D) Allopatric speciation

2016

114. The classic example of hybrid sterility in equine species, resulting from a male donkey and a female horse, is the:
(A) Hinny
(B) Mule
(C) Zorse
(D) Zeedonk

2021

115. Haldane's rule states that in species hybrids, if one sex is absent, rare, or sterile, it is usually the:
(A) Heterogametic sex
(B) Homogametic sex
(C) Female sex exclusively
(D) Larger sex

2004

116. According to Haldane's rule, a sterile avian hybrid is most likely to be:
(A) Male (ZZ)
(B) Intersex (ZO)
(C) Supermale (ZZZ)
(D) Female (ZW)

2013

117. Differences in courtship rituals preventing mating between species represents:
(A) Behavioral isolation
(B) Ecological isolation
(C) Gametic isolation
(D) Mechanical isolation

2019

118. When two related species occupy the same geographic region but utilize entirely different habitats, it is called:
(A) Temporal isolation
(B) Sympatric breakdown
(C) Mechanical isolation
(D) Ecological (habitat) isolation

2022

119. Hybrid breakdown occurs when:
(A) Fertile F1 generation but weak or sterile F2 offspring
(B) Mortality of the F1 hybrid before the stage of birth
(C) Complete sterility observed in the first hybrid generation
(D) Failure of the male and female gametes to undergo fusion

2015

120. Consider the following statements regarding pre-zygotic isolating mechanisms:
I. Mechanical isolation
II. Gametic isolation
III. Behavioral isolation
IV. Ecological isolation
V. Hybrid sterility
Which of the above statement(s) is/are correct?
(A) I, II, III and IV
(B) II, III, IV and V
(C) I, III, IV and V
(D) I, II, IV and V

NODIA

2017

121. Bos indicus cattle exhibit superior heat tolerance primarily due to:
(A) High density of sweat glands and vascularized skin
(B) Presence of thick subcutaneous fat layers in body
(C) Genetic absence of a functioning thyroid gland tissue
(D) Maintenance of much lower resting respiratory rates

2001

122. Which adaptation helps native desert sheep breeds minimize water loss?
(A) Constant panting
(B) Excretion of highly concentrated urine and dry feces
(C) Sweating profusely
(D) High basal metabolic rate

2009

123. Hypoxia tolerance in high-altitude animals like the Yak is genetically linked to adaptations in:
(A) Bone density
(B) Rumen microbial flora
(C) Hemoglobin oxygen affinity and heart size
(D) Hoof structure

2025

124. The expression of Heat Shock Proteins (HSPs) during thermal stress functions to:
(A) Increase body temperature further
(B) Stop all metabolic processes
(C) Prevent protein denaturation and assist in cellular repair
(D) Trigger immediate apoptosis in healthy cells

2006

125. Trypanotolerance in the N'Dama cattle breed is a classic example of:
(A) Genetic disease resistance
(B) Nutritional adaptation
(C) Thermal adaptation
(D) Behavioral adaptation

2001

126. Which morphological feature provides insulation against cold stress in sheep?
(A) Large dewlap
(B) Elongated ears
(C) Bare belly
(D) Dense fleece cover

2005

127. Evaporative cooling in poultry is primarily achieved through:
(A) Sweating from the skin
(B) Panting (respiratory evaporation)
(C) Urination
(D) Flapping wings

2016

128. Light-colored hair coats in tropical cattle breeds assist in:
(A) Absorbing solar radiation
(B) Reflecting solar radiation
(C) Camouflage from predators
(D) Attracting insects

2023

129. Photoperiodism regulates which vital physiological process in temperate sheep breeds?
(A) Digestion
(B) Hoof growth
(C) Tooth eruption
(D) Seasonal reproduction and estrus cycling

2023

130. Regarding the physiological adaptations of cattle, consider the following Assertion (A) and Reason (R):
Assertion (A): Bos indicus cattle possess large dewlaps and pendulous sheaths.
Reason (R): These structures increase the surface area to volume ratio, facilitating heat dissipation.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2024

131. Bos indicus cattle show greater resistance to which external parasite compared to Bos taurus?
(A) Ticks
(B) Leeches
(C) Tapeworms
(D) Roundworms

2011

132. The ability of the camel to withstand severe dehydration is facilitated by:
(A) Internal storage of pure water in the fatty hump
(B) Oval-shaped red blood cells resistant to osmotic lysis
(C) Total physiological absence of functional kidneys
(D) Mechanism of continuous and profuse dermal sweating

2017

133. Positive assortative mating is defined as the mating of individuals that are:
(A) Less related than average
(B) Phenotypically more similar than expected by chance
(C) Phenotypically dissimilar
(D) Genetically identical only

2017

134. What is the primary genetic consequence of positive assortative mating?
(A) Increases heterozygosity for the traits involved
(B) Maintains Hardy-Weinberg equilibrium
(C) Increases homozygosity for the traits involved
(D) Induces random genetic drift

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2014

135. Negative assortative mating (disassortative mating) involves pairing individuals that are:
(A) Highly inbred
(B) Genotypically identical
(C) From the same geographical origin
(D) Phenotypically opposite or dissimilar

2018

136. The phenotypic consequence of negative assortative mating is typically:
(A) Increased phenotypic variation in the next generation
(B) Fixation of extreme phenotypes
(C) Formation of two distinct subpopulations
(D) Increased uniformity (reduction in phenotypic variance)

2004

137. Which mating strategy is best suited to correct a specific conformational defect in a herd?
(A) Random mating
(B) Positive assortative mating
(C) Negative assortative mating (Corrective mating)
(D) Intense inbreeding

2019

138. Positive assortative mating affects genetic variance by:
(A) Decreasing additive genetic variance
(B) Eliminating dominance variance completely
(C) Having no effect on variance
(D) Increasing additive genetic variance

2016

139. Mating the best performing males to the best performing females is an example of:
(A) Positive assortative mating
(B) Disassortative mating
(C) Negative assortative mating
(D) Crossbreeding

2016

140. Match the mating systems with their genetic outcomes:
List I: (Mating Systems)
P. Positive assortative mating
Q. Negative assortative mating
R. Inbreeding
S. Outcrossing
List II: (Genetic Outcomes)
1. Increases heterozygosity across the genome
2. Increases homozygosity for specific selected traits
3. Increases homozygosity across the entire genome
4. Increases intermediate phenotypes for specific traits
(A) P-2, Q-4, R-3, S-1
(B) P-3, Q-1, R-2, S-4
(C) P-4, Q-2, R-1, S-3
(D) P-1, Q-3, R-4, S-2

NODIA

2007

141. Unlike inbreeding, positive assortative mating increases homozygosity:
(A) Only at loci affecting the specific trait selected
(B) Across the entire genome simultaneously and equally
(C) Exclusively for lethal and deleterious recessive alleles
(D) Specifically within the male members of the population

2007

142. A breeder consistently mates tall bulls with short cows. This is:
(A) Positive assortative mating
(B) Linebreeding
(C) Random mating
(D) Negative assortative mating

2004

143. Which mating system is theoretically expected to yield a bimodal distribution of phenotypes over many generations?
(A) Negative assortative mating
(B) Random mating
(C) Positive assortative mating
(D) Crossbreeding

2019

144. The limits of positive assortative mating are primarily dictated by:
(A) Drastic increase of population-wide heterozygosity
(B) Massive levels of extreme outbreeding depression
(C) Local mutation rates eventually becoming zero
(D) Exhaustion of additive genetic variance for the trait

2015

145. Inbreeding is defined as the mating of individuals that are:
(A) More closely related than the average relationship in the population
(B) From completely different breeds
(C) Less closely related than the average

III. It produces purebred offspring.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I

2022

171. A major advantage of rotational crossbreeding systems is that they:
(A) Require purchasing all replacement females from outside
(B) Retain high levels of heterosis while generating their own replacement females
(C) Eliminate heterosis completely
(D) Produce offspring identical to a single pure breed

2002

172. In a continuous two-breed rotational cross (criss-crossing) at equilibrium, what percentage of maximum F1 heterosis is retained?
(A) 50%
(B) 66.7%
(C) 85.7%
(D) 100%

2005

173. In a continuous three-breed rotational cross at equilibrium, the retained heterosis is approximately:
(A) 50%
(B) 66.7%
(C) 85.7%
(D) 93.7%

2023

174. A terminal crossing system is specifically designed so that:
(A) All offspring (both male and female) are marketed/slaughtered.
(B) All crossbred females are retained as replacements.
(C) The herd gradually reverts to purebred status.
(D) Only males are sold, and females are inter se mated.

2023

175. Which crossing strategy best exploits breed complementarity?
(A) Breeding a dairy sire to a dairy dam of the same breed
(B) Mating a terminal meat-type sire to a highly prolific maternal crossbred dam
(C) Repeated backcrossing to a single breed
(D) Intense inbreeding

2021

176. What is the fundamental disadvantage of rotational crossing?
(A) It requires constant purchase of F1 females
(B) It results in zero heterosis
(C) It eliminates additive genetic variance
(D) It leads to wide fluctuations in breed composition between generations

2009

177. A two-tier breeding system in poultry or swine usually involves:
(A) Nucleus multiplier flocks and commercial flocks
(B) Three independent rotational breeds
(C) Grading up of non-descript animals
(D) Interspecific hybridization

2018

178. What happens to recombination loss in the F1 generation of a cross?
(A) It is at its absolute maximum
(B) It is zero because all F1 individuals inherit intact gametes from purebred parents
(C) It causes immediate sterility
(D) It acts identically to inbreeding depression

2012

179. Retained heterosis is formally calculated using:
(A) Path coefficients
(B) Wright's formula based on the breed fractions
(C) Standard deviation
(D) The heritability estimate

2009

180. Consider the following statements regarding crossbreeding:
I. It increases heterozygosity.
II. It is primarily used to fix recessive alleles.
III. It typically improves traits with low heritability like fertility.
IV. It utilizes both additive and non-additive gene effects.
Which of the above statement(s) is/are incorrect?
(A) I and III
(B) II and IV
(C) II
(D) IV

2011

181. Grading up involves the continuous mating of non-descript or native females with:
(A) Sires of different breeds in each generation
(B) Purebred sires of a single highly productive

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different breeds
(B) Maintain high relationship to a superior ancestor with low F
(C) Maximize levels of inbreeding depression very rapidly
(D) Completely eliminate all additive genetic variance

2001

159. Linebreeding is most successfully applied in:
(A) Elite herds containing an exceptionally superior sire
(B) Small flocks with average merit
(C) Commercial crossbred broiler operations
(D) Non-descript indigenous populations

2019

160. Compared to close inbreeding (like full-sib mating), linebreeding aims to:
(A) Increase the rate of inbreeding accumulation
(B) Have the exact same rate of inbreeding
(C) Produce sterile hybrids
(D) Slow down the rate of inbreeding accumulation

2006

161. An arrow diagram used in pedigree analysis visually traces:
(A) Environmental effects
(B) Pathways of genetic transmission from ancestors to descendants
(C) Mendelian segregation of independent traits
(D) The mutation pathways of alleles

2001

162. A major risk of prolonged linebreeding without intense selection is:
(A) Spontaneous mutation to entirely different species
(B) Extreme outbreeding depression
(C) Immediate increase in heterozygosity
(D) Eventual accumulation of inbreeding depression

2001

163. Coefficient of relationship ($R_{\{XY\}}$) measures:
(A) The probable proportion of identical genes shared by two individuals due to common ancestry
(B) The probability of identity by descent at a single locus
(C) The degree of phenotypic variance
(D) The environmental correlation

2005

164. What happens to the relationship between a descendant and a revered ancestor if no linebreeding is practiced over many generations?
(A) It halves with each successive generation
(B) It remains constant
(C) It doubles with each generation
(D) It immediately drops to zero

2018

165. When is linebreeding strictly not recommended?
(A) When an outstanding sire is identified
(B) When the herd is genetically superior
(C) When the herd is of average or poor genetic merit
(D) When pedigree records are meticulously kept

2016

166. In linebreeding, if an individual is mated to its own grandparent, what is the resulting inbreeding coefficient of the offspring (assuming no other common ancestors)?
(A) 0.0625
(B) 0.125
(C) 0.25
(D) 0.50

2005

167. Linebreeding requires:
(A) No pedigree records
(B) Accurate and deep pedigree records
(C) Only phenotypic records
(D) Constant introduction of outside breeds

2003

168. To successfully mitigate the adverse effects of linebreeding, a breeder must apply:
(A) Random selection
(B) Strict and intense culling of inferior animals
(C) Zero culling to preserve population size
(D) Artificial mutagenesis

2017

169. The mating of animals from two distinct breeds is termed:
(A) Crossbreeding
(B) Linebreeding
(C) Outcrossing
(D) Grading up

2003

170. Consider the following statements regarding a three-way cross:
I. It involves mating an F1 crossbred female to a purebred male of a third breed.
II. It takes advantage of maternal heterosis.

NODIA

2019

217. The standard formula to calculate percent heterosis is:

(A) $\left[\frac{F_1 - \text{Parent Average}}{\text{Parent Average}}\right] \times 100$

(B) $\left[\frac{F_1 - \text{Best Parent}}{\text{Best Parent}}\right] \times 100$

(C) $\left[\frac{\text{Parent Average} - F_1}{F_1}\right] \times 100$

(D) $\left[\frac{F_1 + \text{Parent Average}}{2}\right] \times 100$

2005

218. Individual heterosis refers to the advantage of the crossbred individual in its own performance for traits like:

(A) Conception rate of its mother
(B) Growth rate and survival
(C) Maternal milk yield
(D) Paternal libido

2008

219. Maternal heterosis is best observed in traits such as:

(A) Wool staple length of the offspring
(B) Carcass lean percentage of the offspring
(C) Milk production and weaning weight of the offspring reared by a crossbred dam
(D) Semen volume of the crossbred sire

2017

220. Consider the following steps involved in developing a synthetic breed:

I. Selection of divergent foundation breeds.
II. Crossing to create the desired foundation mix.
III. Strict inter se mating of the crossbreds.
IV. Rigorous selection for desired traits in subsequent generations.
V. Immediate backcrossing to the exotic purebred forever.

Which of the above statement(s) is/are correct?

(A) I, II, III and V
(B) I, II, III and IV
(C) II, III, IV and V
(D) I, III, IV and V

2024

221. Paternal heterosis provides advantages primarily in:

(A) Dam milk yield
(B) Offspring growth rate
(C) Sire fertility and mating capacity
(D) Egg shell thickness

2006

222. A synthetic breed is defined as:

(A) Artificial animal created solely by genetic engineering
(B) Stabilized composite population formed by crossbreeding
(C) Purebred population that has undergone severe inbreeding
(D) Sterile first-generation hybrid with no fertile progeny

2008

223. What proportion of maximum F1 heterosis is theoretically retained in a synthetic breed formed from four equally represented pure breeds?

(A) 50%
(B) 62.5%
(C) 75%
(D) 100%

2003

224. Which Indian cattle breed is a well-known synthetic breed developed in Kerala?

(A) Sunandini
(B) Sahiwal
(C) Gir
(D) Hariana

2001

225. Frieswal cattle strain was developed by combining:

(A) Holstein Friesian and Sahiwal
(B) Brown Swiss and Sahiwal
(C) Jersey and Red Sindhi
(D) Holstein Friesian and Hariana

2008

226. Avikalin and Avivastra are examples of synthetic breeds of which livestock species in India?

(A) Goat
(B) Buffalo
(C) Pig
(D) Sheep

2017

227. Retained heterosis in a synthetic breed is inversely proportional to:

(A) The number of foundation breeds
(B) The degree of inbreeding in the foundation breeds
(C) The sum of the squares of the breed fractions $(\sum p_i^2)$
(D) The environmental variance

2019

228. Inter se mating essentially means:

(A) Mating crossbred animals among themselves

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exotic or improved breed
(C) Crossbred sires
(D) Sires from their own non-descript population

2002

182. In grading up, what is the exotic genetic inheritance proportion in the first generation (F1)?
(A) 25%
(B) 50%
(C) 75%
(D) 100%

2011

183. Following two generations of backcrossing to the purebred sire in a grading up program (where F1 is the first generation), the offspring's exotic inheritance is:
(A) 50%
(B) 75%
(C) 87.5%
(D) 93.75%

2004

184. To reach roughly 96.8% purity, how many continuous generations of grading up are required?
(A) 2
(B) 3
(C) 5
(D) 8

2024

185. Theoretically, an animal is practically considered a purebred after how many generations of grading up?
(A) 1-2
(B) 3-4
(C) 5-6
(D) >10

2016

186. A significant practical limitation of grading up indigenous cattle with exotic dairy breeds in tropical climates is:
(A) Decrease in milk yield
(B) Loss of adaptability, heat tolerance, and disease resistance at higher exotic blood levels
(C) Uncontrollable increase in hybrid vigor
(D) Immediate sterility in the first generation

2007

187. The formula predicting the proportion of native germplasm remaining after n generations of grading up is:
(A) $\left(\frac{1}{2}\right)^n$
(B) $1-\left(\frac{1}{2}\right)^n$
(C) $\left(\frac{n}{2}\right)$
(D) $\frac{1}{n}$

2010

188. Grading up is most economical when applied to populations that are:
(A) Already highly selected purebreds
(B) Genetically elite nucleus herds
(C) Low-producing, non-descript animals
(D) Synthetic breeds

2004

189. To prevent inbreeding in a continuous grading up program, the breeder must strictly:
(A) Use the exact same sire for all generations
(B) Change the purebred sire in every generation
(C) Switch to a different breed every generation
(D) Mate brothers and sisters

2006

190. In the context of livestock biodiversity, consider the following Assertion (A) and Reason (R):
Assertion (A): Widespread and indiscriminate grading up poses a threat to indigenous livestock biodiversity.
Reason (R): It progressively replaces the native genome with the exotic genome, potentially leading to the extinction of native purebreds.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2018

191. In India, crossbreeding policies generally recommend restricting exotic inheritance in cattle to what level to maintain adaptability?
(A) 12.5% to 25%
(B) 50% to 62.5%
(C) 87.5% to 93%
(D) 100%

2014

192. Once the desired optimal level of exotic inheritance is reached in a crossbred population, the standard breeding strategy is:
(A) Continue grading up to 100%
(B) Backcross to the indigenous breed

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(C) Inter se mating among the crossbreds
(D) Terminal crossing with a meat breed

2009

193. A mule is the hybrid offspring of:
(A) A stallion and a jennet (female donkey)
(B) A jack (male donkey) and a mare (female horse)
(C) A zebra and a horse
(D) A zebra and a donkey

2005

194. A hinny is the hybrid offspring of:
(A) A stallion and a jennet
(B) A jack and a mare
(C) A male horse and a female zebra
(D) A camel and a llama

2006

195. What is the diploid chromosome number of a mule?
(A) 64
(B) 62
(C) 63
(D) 60

2003

196. The hybrid sterility in mules is primarily caused by:
(A) Incompatibility of mitochondrial DNA
(B) Failure of homologous chromosomes to pair correctly during meiosis
(C) Lethal recessive mutations
(D) Viral infections during gestation

2022

197. Which of the following is an example of a fully fertile interspecific hybrid?
(A) Mule
(B) Bos taurus x Bos indicus
(C) Liger
(D) Zeedonk

2013

198. The 'Beefalo' is a fertile cross between:
(A) Domestic cattle and American Bison
(B) Domestic cattle and Water Buffalo
(C) Domestic cattle and Yak
(D) Sheep and Goat

2019

199. A hybrid between a domestic cow and a male Yak is called a:
(A) Dzo
(B) Cama
(C) Zobo
(D) Cattalo

2009

200. Match the hybrid with its parent species:
List I: (Hybrids)
P. Mule
Q. Hinny
R. Liger
S. Cama
List II: (Parent Species)
1. Male Lion x Female Tiger
2. Camel x Llama
3. Jack x Mare
4. Stallion x Jennet
(A) P-3, Q-4, R-1, S-2
(B) P-4, Q-3, R-1, S-2
(C) P-3, Q-1, R-4, S-2
(D) P-1, Q-4, R-3, S-2

2024

201. According to Haldane's Rule regarding the Dzo (Cattle x Yak hybrid):
(A) Both males and females are sterile
(B) Males are sterile, females are fertile
(C) Females are sterile, males are fertile
(D) Both males and females are fully fertile

2009

202. The successful hybridization between cattle and bison implies that:
(A) They have identical chromosome numbers and highly homologous chromosomes
(B) They belong to the exact same species
(C) They exhibit complete gametic isolation
(D) Bison are essentially domestic animals

2019

203. The evolutionary significance of distant species hybridization in nature is usually limited due to:
(A) Extreme heterosis
(B) Severe inbreeding depression
(C) Pre-zygotic and post-zygotic reproductive barriers
(D) High mutation rates in hybrids

2025

204. Can a sheep and a goat successfully produce a fertile hybrid naturally?
(A) Yes, easily
(B) No, they generally face hybrid inviability or early embryonic death
(C) Yes, but only if the goat is the sire
(D) Yes, but it results in a triploid animal

2006

205. Heterosis (hybrid vigor) is formally defined as:
(A) The inferiority of crossbreds compared to purebreds

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(B) The superiority of the crossbred offspring over the average of its purebred parents
(C) The exact average of the parents' phenotypes
(D) The increase in homozygosity

2015

206. Which hypothesis of heterosis suggests that hybrid vigor is due to the masking of deleterious recessive alleles by favorable dominant alleles?
(A) Overdominance hypothesis
(B) Epistasis hypothesis
(C) Dominance hypothesis
(D) Linkage hypothesis

2017

207. The Overdominance hypothesis (East and Shull) proposes that:
(A) Homozygotes are always superior
(B) The heterozygous genotype (Aa) is fundamentally superior to both homozygous genotypes ($\forall$ and aa)
(C) Epistatic interactions alone cause heterosis
(D) Environmental variance is zero

2017

208. The Epistasis hypothesis attributes heterosis to:
(A) Favorable interactions between alleles at different loci
(B) Complete dominance at a single locus
(C) Increased homozygosity
(D) Elimination of mutations

2015

209. If the Dominance hypothesis is the sole cause of heterosis, it should theoretically be possible to:
(A) Never achieve purebred lines that match hybrid merit
(B) Isolate purebred lines performing equal to F1 hybrids
(C) Completely eliminate all the existing dominance variance
(D) Prove that heterozygotes are physiologically more robust

2023

210. Under the Overdominance hypothesis, is it possible to fix heterosis in a purebred line?
(A) Yes, by intense inbreeding
(B) Yes, by grading up
(C) No, because purebreeding increases homozygosity, losing the superior heterozygote advantage
(D) No, because dominance completely disappears

2009

211. Which traits generally exhibit the highest degree of heterosis?
(A) Highly heritable traits (e.g., carcass traits)
(B) Moderately heritable traits (e.g., growth rate)
(C) Lowly heritable traits (e.g., fertility and survival)
(D) Traits with purely additive gene action

2023

212. Negative heterosis implies that:
(A) The hybrid performs better than both parents
(B) The hybrid performs worse than the average of the parents
(C) Heterosis is only seen in the F2 generation
(D) The hybrid has negative additive variance

2021

213. Heterosis and inbreeding depression are essentially:
(A) Unrelated phenomena
(B) Identical genetic processes
(C) Two sides of the same genetic coin (opposite effects on heterozygosity)
(D) Both caused by increased homozygosity

2014

214. The reduction in performance of the F2 generation compared to the F1 generation is primarily attributed to:
(A) Increased heterosis
(B) Recombination loss (breakup of favorable epistatic gene combinations)
(C) Increased maternal heterosis
(D) Environmental degradation

2001

215. The degree of heterosis achieved in a cross is generally proportional to:
(A) The genetic similarity of the parent breeds
(B) The genetic divergence (distance) between the parent breeds
(C) The level of inbreeding of the crossbreds
(D) The size of the parent populations

2015

216. Which of the following does not significantly contribute to the physiological expression of heterosis?
(A) Increased metabolic efficiency
(B) Greater resistance to environmental stress
(C) Accelerated mutation rate
(D) Improved partitioning of nutrients

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population
(D) Sharing the same phenotype only

2024

146. The most prominent phenotypic result of inbreeding is:
(A) Heterosis
(B) Hybrid vigor
(C) Increased additive variance
(D) Inbreeding depression

2022

147. Traits most susceptible to inbreeding depression are those associated with:
(A) Carcass quality
(B) Fitness, reproduction, and survival
(C) Structural conformation
(D) Coat color

2023

148. Wright's coefficient of inbreeding (F) measures the probability that two alleles at a locus in an individual are:
(A) Identical by descent (IBD)
(B) Alike in state only
(C) Completely different
(D) Mutated

2019

149. Calculate the inbreeding coefficient (F) of the offspring resulting from a half-sib mating (assuming no previous inbreeding).
(A) 0.0625 (6.25%)
(B) 0.125 (12.5%)
(C) 0.25 (25%)
(D) 0.50 (50%)

2013

150. Calculate the inbreeding coefficient (F) of the offspring resulting from a full-sib mating (assuming no previous inbreeding).
(A) 0.125 (12.5%)
(B) 0.25 (25%)
(C) 0.50 (50%)
(D) 0.75 (75%)

2008

151. The phenomenon where a highly inbred sire consistently stamps his characteristics on his offspring is called:
(A) Hybrid vigor
(B) Genetic prepotency
(C) Overdominance
(D) Epistasis

2011

152. Inbreeding exposes hidden recessive alleles because it increases:
(A) Heterozygosity
(B) Mutation rate
(C) Homozygosity
(D) Genetic drift

2025

153. The process of eliminating deleterious recessive alleles from a population through intense inbreeding and strict selection is known as:
(A) Grading up
(B) Purging the genetic load
(C) Rotational crossing
(D) Outcrossing

2007

154. Which method constructs a numerator relationship matrix to easily calculate inbreeding coefficients in large pedigrees?
(A) Path coefficient method
(B) Tabular method
(C) Diallel method
(D) Hardy-Weinberg method

2016

2001

155. What is the value of the inbreeding coefficient (F) for individuals in the base population?
(A) 1.0
(B) 0.5
(C) 0.0
(D) -1.0

2016

156. In Wright's path coefficient formula, what does the factor $(1 + F_A)$ represent?
(A) The correction for the inbreeding of the common ancestor A
(B) The dominance effect
(C) The number of generations
(D) The environmental variance

2018

157. Linebreeding is fundamentally a specialized form of:
(A) Outcrossing
(B) Inbreeding
(C) Crossbreeding
(D) Species hybridization

2018

158. The primary objective of a linebreeding program is to:
(A) Introduce novel genes from completely

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(B) Mating back to the parent breeds
(C) Mating only brothers and sisters
(D) Mating to a completely different species

2013

229. A diallel cross involves:
(A) Mating a single sire to multiple dams
(B) Mating a single dam to multiple sires
(C) All possible crosses among a set of parental lines
(D) Repeated backcrossing to a single parental line

2005

230. Which of the following represents the correct selection of Griffing's Method I diallel design?
(A) Parents, F1s, and reciprocal F1s are all included
(B) Only Parents and F1s are included
(C) Only F1s and reciprocal F1s are included
(D) Only F1s are included

2025

231. Griffing's Method 2 diallel design includes:
(A) Parents + F1s + reciprocals
(B) Parents + F1s (no reciprocals)
(C) F1s + reciprocals (no parents)
(D) F1s only

2008

232. Griffing's Method 4 diallel design includes:
(A) Parents + F1s
(B) F1s + reciprocals
(C) Only F1s (no parents, no reciprocals)
(D) Parents + reciprocals

2009

233. In diallel analysis, differences between reciprocal crosses ($A \times B$ vs $B \times A$) primarily indicate the presence of:
(A) Additive gene action
(B) Maternal effects and/or sex-linked genes
(C) Epistatic interactions
(D) Environmental bias

2005

234. In Griffing's analysis, if the parental lines are specifically chosen by the breeder and not random, which statistical model is appropriate?
(A) Model I (Fixed effects)
(B) Model II (Random effects)
(C) Model III (Mixed effects)
(D) Threshold model

2019

235. To estimate population genetic variances directly from a diallel, the parents must be a random sample. This requires:
(A) Model I
(B) Model II
(C) Fixed effects modeling
(D) Elimination of reciprocals

2001

236. The General Combining Ability (GCA) variance component in a diallel corresponds fundamentally to:
(A) Additive genetic variance
(B) Dominance variance
(C) Epistatic variance
(D) Maternal variance

2007

237. The Specific Combining Ability (SCA) variance component corresponds fundamentally to:
(A) Additive genetic variance
(B) Non-additive genetic variance (Dominance and Epistasis)
(C) Environmental variance
(D) Cytoplasmic inheritance

2018

238. Diallel crosses are highly resource-intensive because:
(A) The number of required crosses increases linearly with the number of parents
(B) The number of required crosses increases quadratically with the number of parents
(C) They require cloning technology
(D) They only work with inbred lines

2010

239. For n parental lines, the total number of cross combinations in a full diallel (Method I) is:
(A) $\frac{n(n-1)}{2}$
(B) n
(C) n^2
(D) $2n$

2019

240. Identify the correct sequence for the following standard steps of Griffing's diallel analysis:
I. Estimate GCA and SCA variance components
II. Perform the crossing design and collect phenotypic data
III. Estimate specific genetic effects for each parent and cross

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IV. Perform ANOVA for general block and treatment effects

(A) II, IV, I, III
(B) II, I, IV, III
(C) IV, II, I, III
(D) I, II, III, IV

2003

241. A partial diallel cross is employed primarily to:
(A) Eliminate the additive variance from population
(B) Increase the degree of inbreeding in the lines
(C) Reduce crosses while estimating combining ability
(D) Maximize maternal effects within the population

2001

242. In a partial diallel, a specific line is crossed with:
(A) All other lines
(B) Only a structured subset (s) of the other lines
(C) Itself only
(D) Completely unrelated species

2008

243. A triallel cross involves mating an F1 hybrid to:
(A) One of its own parents
(B) A third unrelated inbred line or breed
(C) Another identical F1 hybrid
(D) A completely different species

2017

244. A quadriallel (double cross) involves mating:
(A) Two different F1 hybrids $(A \times B) \times (C \times D)$
(B) One F1 hybrid and two pure lines
(C) Four purebreds sequentially to one dam
(D) Four sires to one dam

2014

245. Triallel and quadriallel crosses are particularly useful for estimating which type of genetic variance?
(A) Additive only
(B) Epistatic interactions
(C) Mutational variance
(D) Cytoplasmic variance

2004

246. Kempthorne's design is heavily utilized for the statistical analysis of:
(A) Simple outcrosses
(B) Assortative mating
(C) Partial, triallel, and quadriallel crosses
(D) Mass selection

2018

247. The primary disadvantage of triallel and quadriallel crosses in large livestock is:
(A) Lack of statistical models
(B) Extreme time requirement (generation interval) and cost
(C) They cause immediate sterility
(D) They prevent heterosis

2002

248. In estimating epistasis, a double cross allows partitioning of interactions into:
(A) AxA, AxD, and DxD interactions
(B) Additive by environmental effect
(C) Dominance by environmental effect
(D) No partition is actually possible

2019

249. Circulant partial diallel designs ensure that:
(A) Every parent is involved in exactly the same number of crosses (s)
(B) No parent is crossed with another
(C) Only males are evaluated
(D) Only random mating occurs

2013

250. In the evaluation of inbred lines, consider the following Assertion (A) and Reason (R):
Assertion (A): Partial diallels are often preferred over full diallels when evaluating a very large number of inbred lines.
Reason (R): A full diallel becomes physically and financially impossible due to the exponential increase in required cross combinations.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2023

251. The statistical efficiency of a partial diallel heavily depends on:
(A) The number of lines sampled
(B) The number of crosses per line (s)
(C) Both A and B
(D) The color of the animals

2024

252. Which mating design is the most complex but provides the most detailed partitioning of epistatic variance?
(A) Single pair mating
(B) Diallel cross
(C) Quadriallel cross

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(D) Topcross

2018

253. General Combining Ability (GCA) is defined as the:
(A) Average performance of a line in hybrid combinations
(B) Performance of a specific cross minus the parent average
(C) Performance of the worst progeny
(D) Superiority of a heterozygote

2013

254. GCA is mathematically expressed as a deviation from the:
(A) Best performing line
(B) Overall population mean of the crosses
(C) Environmental mean
(D) Inbreeding coefficient

2010

255. Specific Combining Ability (SCA) evaluates:
(A) The overall additive genetic value of the sire
(B) Cross performance deviating from parent GCA sums
(C) Degree of phenotypic uniformity in purebreds
(D) Exact mutational rate within a specific cross

2025

256. If a trait is governed entirely by additive gene action, the SCA variance will be:
(A) Equal to GCA variance
(B) Exceptionally large
(C) Theoretically zero
(D) Negative

2024

257. GCA is traditionally estimated by evaluating the performance of:
(A) Full-sib families
(B) Half-sib families
(C) Clones
(D) Unrelated individuals

2014

258. SCA is estimated by evaluating the variance between:
(A) Half-sib families
(B) Full-sib families (specific crosses)
(C) Sire groups
(D) Dam groups only

2009

259. A high ratio of GCA variance to SCA variance indicates that the trait should be improved primarily through:
(A) Crossbreeding
(B) Selection (purebreeding)
(C) Random mating
(D) Cloning

2012

260. Match the combining abilities with their optimal breeding strategies:
List I: (Combining Abilities)
P. High GCA variance
Q. High SCA variance
R. Low heritability
S. High heritability
List II: (Breeding Strategies)
1. Pure line selection
2. Crossbreeding to exploit heterosis
3. Inter-family selection
4. Mass selection
(A) P-1, Q-2, R-3, S-4
(B) P-2, Q-1, R-4, S-3
(C) P-4, Q-3, R-1, S-2
(D) P-1, Q-4, R-2, S-3

2018

261. In poultry breeding, standard purebred selection plateaus when additive variance is exhausted. Further improvement relies on:
(A) Inbreeding solely
(B) Exploiting SCA through systematic crossbreeding
(C) Negative assortative mating
(D) Mass culling

2008

262. The variance of GCA (σ^2_{GCA}) in terms of additive genetic variance (σ^2_A) is:
(A) $\sigma^2_{GCA} = \sigma^2_A$
(B) $\sigma^2_{GCA} = \frac{1}{2}\sigma^2_A$
(C) $\sigma^2_{GCA} = \frac{1}{4}\sigma^2_A$
(D) $\sigma^2_{GCA} = 2\sigma^2_A$

2007

263. The variance of SCA (σ^2_{SCA}) fundamentally includes what proportion of dominance variance (σ^2_D)?
(A) $\frac{1}{4}\sigma^2_D$
(B) $\frac{1}{2}\sigma^2_D$
(C) σ^2_D
(D) $2\sigma^2_D$

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10. (A) Both A and R are true and R is the correct explanation of A.
Taurine cattle and indicine cattle are the results of two independent domestication events involving different subspecies of the aurochs. Bos taurus originated in the Near East from Bos primigenius primigenius, while Bos indicus descended from Bos primigenius namadicus in South Asia. This geographic and genetic separation explains the distinct physiological differences observed between these two major cattle lineages.

11. (B) Guaranteed food and protection
During the early stages of domestication, livestock gained a significant evolutionary advantage through the provision of guaranteed food sources and protection from natural predators. This human-mediated environment reduced the selective pressures found in the wild, allowing for higher survival rates of offspring. In exchange for these benefits, humans obtained a reliable supply of animal products and labor for various tasks.

12. (B) Zagros Mountains
The domestication of goats is traced back to the wild Bezoar ibex, Capra aegagrus, in the Zagros Mountains of modern-day Iran and Iraq. Around ten thousand years ago, early farmers began managing these animals for their meat, milk, and skins. This region served as a primary domestication center from which domesticated goats eventually spread throughout the Mediterranean and Asia.

13. (B) $p^2 + 2pq + q^2 = 1$
The Hardy-Weinberg principle provides a mathematical model for predicting genotypic frequencies in a population. If allele frequencies are represented by p and q, the frequencies of the three possible genotypes in a diploid population are given by the expansion of the binomial. Specifically, p squared represents the dominant homozygote, $2pq$ the heterozygote, and q squared the recessive homozygote frequency.

14. (C) Random fertilization
In a large, random-mating population, allele frequencies remain constant unless acted upon by specific evolutionary forces. Migration, mutation, and genetic drift are primary factors that shift frequencies over time. Random fertilization, however, is a fundamental component of the Hardy-Weinberg equilibrium that maintains existing allele frequencies by ensuring every gamete has an equal probability of contributing to the next generation.

15. (C) 0.40
Under the Hardy-Weinberg equilibrium, the frequency of the homozygous recessive genotype is represented by q squared. To find the frequency of the recessive allele, q, one must take the square root of the genotypic frequency. In this specific scenario, the square root of zero point one six is zero point four zero, representing the proportion of that allele in the population.

16. (C) Genetic drift
Genetic drift refers to the random fluctuations in allele frequencies that occur in small populations due to chance events. Unlike selection, which is a non-random process, drift can lead to the loss of beneficial alleles or the fixation of harmful ones. This phenomenon is particularly significant in endangered species or small breeding herds where the number of reproductive individuals is limited.

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17. (B) Allele frequency difference between populations
Migration, or gene flow, alters the genetic makeup of a population when individuals move between groups. The magnitude of this change is determined by the rate of migration and the difference in allele frequencies between the native and immigrant populations. If the two populations are genetically identical, migration will have no effect on the allele frequencies of the recipient group.

18. (D) Asymptotic reduction of the frequency toward zero over time
Continuous selection against a recessive allele leads to a steady decrease in its frequency. However, because the allele is hidden in the heterozygous state, it becomes increasingly difficult to eliminate as its frequency drops. This results in an asymptotic reduction toward zero, where the allele persists at very low levels in the population despite intense selection against the recessive phenotype.

19. (A) Increases recessive allele frequency
Mutation serves as the ultimate source of genetic variation by creating new alleles. If a population experiences a high mutation rate from a dominant allele to a recessive one, the frequency

2011

276. A key requirement for an RRS program to be successful is that the two foundational populations must be:
(A) Genetically identical
(B) Genetically divergent
(C) From the exact same farm
(D) Highly inbred to the point of extinction

2018

277. The Livestock Census in India is typically conducted at an interval of:
(A) 2 years
(B) 5 years
(C) 10 years
(D) 15 years

2008

278. The most recent completed national Livestock Census in India (as per the standard cycle referring to 2019) is the:
(A) 18th
(B) 19th
(C) 20th
(D) 21st

2019

279. According to the 20th Livestock Census, the total livestock population in India showed an overall:
(A) Sharp decline
(B) Stagnation
(C) Positive growth (increase)
(D) Fluctuation with no net change

2001

280. The population dynamics of cattle in India over recent censuses reveal a distinct structural shift characterized by:
(A) Growth in crossbreds and decline in indigenous
(B) Significant growth in both cattle population types
(C) Decline in crossbreds and growth in indigenous
(D) Complete replacement of all buffaloes by cattle

2014

281. The buffalo population in India, according to the 20th Livestock Census:
(A) Decreased significantly
(B) Increased slightly
(C) Remained exactly constant
(D) Doubled in five years

2014

282. Which Indian state reported the highest total livestock population in the 20th Census?
(A) Rajasthan
(B) Uttar Pradesh
(C) Madhya Pradesh
(D) West Bengal

2018

283. Which Indian state reported the highest total poultry population?
(A) Andhra Pradesh
(B) Tamil Nadu
(C) Telangana
(D) Maharashtra

2019

284. The overall sheep population in India during the 20th Census showed:
(A) A significant increase
(B) A massive decline
(C) Absolute stagnation
(D) Replacement by alpacas

2001

285. In contrast to sheep and cattle, the total pig population in India during the 20th Census showed:
(A) Rapid growth
(B) A noticeable decline
(C) Stabilization
(D) Complete disappearance

NODIA

2024

286. The first Livestock Census in India was conducted during the period of:
(A) 1899-1900
(B) 1919-1920
(C) 1947-1948
(D) 1951-1952

2003

287. The structural shift towards crossbred cattle is primarily driven by:
(A) Demand for better draft power
(B) The economic demand for higher milk production
(C) Demand for high-quality beef
(D) Religious preferences

2018

288. Which species constitutes the largest percentage of the total livestock population (excluding poultry) in India?
(A) Goat
(B) Buffalo
(C) Cattle

achieved through selection in a single breeding generation.

29. (A) Total genetic variance
Broad-sense heritability is the ratio of the total genetic variance to the phenotypic variance. This includes all genetic components: additive variance, dominance variance, and epistatic variance. While it provides a measure of the total genetic contribution to a trait, it is less useful than narrow-sense heritability for predicting selection response because it includes non-additive effects that are not consistently inherited.

30. (B) I and III
Epistatic variance is a component of non-additive genetic variance that results from interactions between alleles at different loci. This means the effect of a gene at one position depends on the presence of specific genes elsewhere in the genome. Like dominance variance, epistatic effects are not fully transmitted to offspring because the specific gene combinations are broken up during meiosis and recombination.

31. (D) Narrow-sense heritability
Repeatability measures the correlation between multiple records of the same trait on an individual, such as milk yield across different lactations. It accounts for both genetic variance and permanent environmental variance. Because it includes these components, the repeatability of a trait always sets the theoretical upper limit for its narrow-sense heritability, providing a useful indicator of the trait's potential genetic control.

32. (C) Variable performance of genotypes across different environments
Genotype-environment interaction occurs when the relative performance of different genotypes changes depending on the environment in which they are raised. This means that the best-performing breed in a temperate climate might not be the most productive in a tropical setting. Understanding these interactions is essential for selecting animals that are specifically adapted to local conditions and management systems for optimal production.

33. (B) Carcass quality
In livestock populations, different categories of traits exhibit varying levels of heritability. Fertility and survival traits typically have low heritability, while production traits like milk yield are moderately heritable. Carcass quality traits, such as loin eye area or fat thickness, generally show the highest heritability. This high genetic control allows breeders to make rapid progress in improving these traits through simple mass selection.

34. (D) Dominance deviation
The dominance deviation is a genetic term describing the difference between the observed phenotypic value of a heterozygote and the mid-parent value, which is the average of the two homozygotes. This deviation represents the non-additive effect of gene interaction at a single locus. It is a major component of the genetic variance that contributes to phenomena such as heterosis and inbreeding depression.

35. (A) Breeding value
The breeding value of an individual is defined as the sum of the average effects of all the alleles it carries for a specific trait. It represents the value of the individual as a parent. Because only alleles, not entire genotypes, are passed to offspring, the breeding value is twice the expected deviation of the individual's progeny from the population mean.

36. (C) Daily fluctuations in weather
Environmental variance is divided into permanent and temporary components. Permanent effects, like a chronic injury or early nutritional stunting, affect all records of an animal. Temporary environmental variance includes factors that change from one record to the next, such as daily weather fluctuations, short-term illness, or minor management changes. These factors contribute to the variation observed within multiple measurements of the same individual.

37. (A) Sahiwal
Sahiwal is widely considered the premier indigenous dairy cattle breed of India, originating from the Montgomery region of modern Pakistan. Known for its distinct reddish-brown color and heat tolerance, it produces the highest milk yield among all pure Indian zebu breeds. Because of these superior dairy qualities, Sahiwal cattle have been exported globally to improve milk production in various tropical countries.

38. (D) Jersey
Among the major exotic dairy breeds, the Jersey is renowned for producing milk with the

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1. (B) Bos primigenius
The aurochs, scientifically known as Bos primigenius, is recognized as the extinct wild ancestor of all modern domestic taurine cattle. These large, wild bovines once ranged across Europe, Asia, and North Africa. Domestication occurred approximately ten thousand years ago in the Near East, eventually leading to the diverse breeds of cattle seen globally today.

2. (D) Indus Valley
Zebu cattle, classified as Bos indicus, were primarily domesticated in the Indus Valley region of South Asia. Archaeological evidence suggests this event occurred independently from the domestication of taurine cattle in the Fertile Crescent. These animals developed unique adaptations, such as the prominent fatty hump and large dewlap, to thrive in tropical and subtropical environments.

3. (A) Red Junglefowl
Scientific studies indicate that the Red Junglefowl, or Gallus gallus, is the primary ancestor of the domestic chicken. Native to Southeast Asia, this wild bird contributed the majority of the genetic makeup found in modern poultry. Recent research also suggests some genetic contributions from other junglefowl species, but the Red Junglefowl remains the most significant ancestral source.

4. (C) Commensal pathway
The commensal pathway involves animals being drawn to human settlements by food waste or other benefits, leading to a symbiotic relationship. Dogs and pigs are classic examples of this process, as they scavenged around early human camps. Over generations, these animals became increasingly habituated to humans, eventually undergoing the genetic and behavioral changes associated with domestication.

5. (A) Mouflon
The wild ancestor of modern domestic sheep is widely identified as the Asiatic mouflon, Ovis orientalis. Domestication likely occurred in the Fertile Crescent region around eleven thousand years ago. Through selective breeding over millennia, humans transformed these wild ancestors from hair-bearing animals into the wool-producing livestock breeds that are essential for textile and meat production in modern agriculture.

6. (D) Horse
The directed pathway of domestication occurs when humans intentionally capture and tame animals for a specific purpose, such as transport or power. Horses were domesticated through this route long after cattle and sheep, primarily for their utility in mobility, warfare, and agriculture. This deliberate process differs from the commensal or prey pathways followed by other livestock species.

7. (B) India and China
The domestication of the wild water buffalo took place in two distinct geographical regions, leading to two different types. Riverine buffaloes were domesticated in the Indian subcontinent, while swamp buffaloes originated in China and Southeast Asia. These two groups differ in their chromosome numbers and primary utility, representing independent domestication events from the wild progenitor Bubalus arnee.

8. (C) Sheep
Based on extensive archaeological records, sheep were among the first livestock species to be domesticated by humans. This process began roughly eleven thousand years ago in Southwest Asia. In contrast, horses and chickens were domesticated much later in human history. The early domestication of sheep provided Neolithic societies with a reliable source of meat, milk, and eventually wool fibers.

9. (D) It eliminates all natural instincts.
Domestication syndrome refers to a suite of phenotypic and behavioral changes occurring in animals during domestication. Key traits include increased docility, reductions in brain size, and alterations in coat color or ear shape. However, it does not eliminate all natural instincts. Domesticated animals still retain fundamental biological behaviors related to survival and reproduction, although these traits are often significantly modified.

2010

264. A tester line in evaluating combining ability is usually:
(A) A highly heterozygous synthetic population
(B) A well-characterized inbred line or population against which others are crossed
(C) A completely unrelated wild species
(D) A randomly selected unpedigreed group

2009

265. Reciprocal Selection (RS) was primarily designed to improve:
(A) General Combining Ability only
(B) Specific Combining Ability
(C) Additive variance strictly
(D) Purebred appearance

2002

266. Reciprocal Recurrent Selection (RRS) was introduced by:
(A) Sewall Wright
(B) R.A. Fisher
(C) Comstock, Robinson, and Harvey
(D) Jay L. Lush

2005

267. The fundamental objective of RRS is to simultaneously improve:
(A) Environmental variance and repeatability
(B) General Combining Ability and Specific Combining Ability
(C) Mutational load and inbreeding
(D) Pre-zygotic and post-zygotic isolation

2002

268. In an RRS program between two populations A and B, individuals from population A are selected based on:
(A) Their own purebred performance
(B) The performance of their half-sib purebred progeny
(C) The performance of their crossbred progeny when mated to testers from population B
(D) Their phenotypic similarity to population B

2005

269. The theoretical advantage of RRS over simple pure line selection is most prominent when:
(A) Only additive gene action exists
(B) Overdominance is a major source of genetic variation
(C) Heritability is equal to 1.0
(D) Environmental variance is zero

2013

270. One major practical limitation of RRS in large livestock (like cattle) is:
(A) Requirement of very short generation interval cycles
(B) Exceptionally long cycle time for progeny evaluation
(C) Complete elimination of all observed hybrid vigor
(D) Exclusive utility for genetically identical twins

2024

271. Because of its practical limitations, RRS is most extensively and successfully applied in:
(A) Dairy cattle
(B) Beef cattle
(C) Poultry and Swine
(D) Horses

2014

272. In RRS, what is done with the elite purebred individuals of population A after they have been identified by the crossbred progeny test?
(A) They are slaughtered
(B) They are crossed with population B permanently
(C) They are mated inter se within population A to generate the next generation of purebreds
(D) They are discarded

2022

273. Modified Reciprocal Recurrent Selection often incorporates:
(A) Purebred performance data alongside crossbred progeny data
(B) Only phenotypic data from parents
(C) No progeny testing whatsoever
(D) Completely random mating

2013

274. If heterosis is driven entirely by partial dominance rather than overdominance, RRS compared to pure line selection is:
(A) Vastly superior
(B) About equally effective or potentially less efficient due to longer cycle time
(C) Impossible to conduct
(D) Statistically invalid

2004

275. In poultry, RRS has been historically instrumental in the development of superior commercial:
(A) Dual-purpose native birds
(B) White Leghorn layer strains
(C) Fighting cocks
(D) Exhibition bantams

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of the recessive allele will gradually increase over many generations. This process continues until a balance is reached between the mutation rate and other evolutionary forces like selection or drift.

20. (A) P-4, Q-3, R-2, S-1
Evolutionary forces shape the genetic structure of livestock populations through distinct mechanisms. Mutation creates entirely new genetic variants, while migration introduces existing alleles from outside groups. Genetic drift causes random changes in frequencies, particularly in small herds. Selection acts by providing individuals with superior traits a higher reproductive success, ultimately driving the adaptation and improvement of the population over time.

21. (A) Unequal number of breeding males and females
Effective population size is a theoretical measure reflecting the number of individuals contributing to the next generation's genetic diversity. In livestock, this is typically much lower than the actual census size because of unequal sex ratios. Often, a few elite males are mated to many females, which accelerates the rate of inbreeding and reduces the overall genetic variation in the herd.

22. (D) Stabilizing selection
Stabilizing selection is a type of natural or artificial selection that favors individuals with intermediate phenotypes while acting against those with extreme traits. This process reduces phenotypic variation and maintains the status quo within a population. An example in livestock might include selecting for an optimal birth weight that ensures both calf survival and easy parturition for the dam.

23. (B) Its initial frequency
For a newly arisen neutral mutation, the probability that it will eventually become fixed in a population is exactly equal to its initial frequency. In a diploid population of size N, a new mutation has a frequency of one divided by two N. This highlights that most neutral mutations are lost by chance, while only a small fraction ever achieve fixation.

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24. (C) Infinitely large
The Hardy-Weinberg law relies on several key assumptions to ensure that allele and genotypic frequencies remain constant. One fundamental requirement is that the population must be infinitely large. This assumption eliminates the effects of random sampling errors, also known as genetic drift, which would otherwise cause unpredictable changes in the genetic structure of smaller populations over successive breeding generations.

25. (D) V_G and V_E
Phenotypic variance represents the total observable variation for a specific trait within a population. It is fundamentally partitioned into two primary components: genetic variance and environmental variance. Genetic variance reflects the differences caused by the inherited DNA, while environmental variance accounts for all non-genetic factors, such as nutrition, management, and climate, that influence the expression of the trait.

26. (A) Additive variance
Additive genetic variance is the component of genetic variation that results from the cumulative effects of individual alleles. This is the only part of the genetic variance that is directly and predictably transmitted from parents to their offspring. Consequently, it is the most important component for animal breeders, as it determines the narrow-sense heritability and the potential response to selection.

27. (B) The same locus
Dominance variance is a type of non-additive genetic variance that occurs due to interactions between alleles at the same locus. It reflects the degree to which the heterozygote deviates from the average of the two homozygotes. Unlike additive variance, dominance effects are not passed directly to offspring because alleles are segregated and recombined in new combinations during the process of fertilization.

28. (B) Additive genetic variance
Narrow-sense heritability is a critical parameter in animal breeding, defined as the ratio of additive genetic variance to the total phenotypic variance. It measures the extent to which offspring resemble their parents for a specific trait. This value ranges from zero to one and helps breeders predict how much gain can be

48. (C) Prominent hump and large dewlap
Bos indicus cattle, also known as zebu, are distinguished from European Bos taurus cattle by several key morphological features. The most prominent are the large fatty hump over the shoulders and a voluminous, folded dewlap hanging from the neck. These adaptations are essential for survival in hot climates, as they increase the surface area for heat dissipation and provide energy reserves.

49. (B) 50
Riverine buffaloes, which include most of the famous dairy breeds in India like the Murrah and Nili-Ravi, possess a diploid chromosome number of fifty. This distinguishes them from swamp buffaloes, which have forty-eight chromosomes. Despite this difference, the two types can interbreed, although the resulting hybrids have forty-nine chromosomes and may exhibit slightly reduced fertility in subsequent generations.

50. (A) I, II, III and IV
India possesses a diverse range of buffalo breeds, each with unique strengths. The Murrah is the leading dairy breed, while the Bhadawari is famous for the highest milk fat content. Surti buffaloes are recognized by their sickle-shaped horns, and the Jaffarabadi is known for its massive body size. Swamp buffaloes, however, are rare in India and primarily used for work elsewhere.

51. (A) High milk fat content (up to 13%)
The Bhadawari buffalo, native to the Agra and Etawah regions of Uttar Pradesh, is economically significant due to its exceptional milk fat percentage. While its total milk volume is lower than the Murrah, its milk can contain up to thirteen percent fat, the highest among all buffalo breeds. This makes the breed particularly valuable for the production of ghee and other high-fat dairy products.

52. (A) Nili-Ravi
The Nili-Ravi buffalo is a high-yielding dairy breed originating from the banks of the Sutlej and Ravi rivers. A key distinguishing physical feature of this breed is the presence of "wall eyes," which refers to a white or light-colored iris. Additionally, these buffaloes often have white markings on their forehead, face, muzzle, and lower limbs, which are considered characteristic breed marks.

53. (D) Saurashtra (Gujarat)
Jaffarabadi buffaloes are native to the Saurashtra region of Gujarat, particularly the Gir forest and Jamnagar districts. They are one of the heaviest and most massive buffalo breeds in the world. Characterized by their drooping horns and prominent foreheads, these animals are known for producing large quantities of milk with a high fat content, often exceeding eight percent in many individuals.

54. (A) Murrah and Surti
The Mehsana buffalo is a recognized dairy breed from the Mehsana district of Gujarat. It is considered to have evolved from the natural crossing between the Murrah and Surti breeds. This combination has resulted in an animal that possesses the high milk-yielding capacity of the Murrah along with the hardiness and slightly smaller frame of the Surti, making it highly efficient.

55. (A) 48
Swamp buffaloes are primarily found in Southeast Asia and parts of Northeast India. They are characterized by a diploid chromosome number of forty-eight. This differs from the fifty chromosomes found in riverine buffaloes. Swamp buffaloes are mostly used for draft power in paddy fields, and their milk production is generally lower compared to the specialized dairy breeds of the riverine type.

56. (D) Toda
The Toda buffalo is a unique breed reared by the Toda tribe in the high-altitude Nilgiri hills of Tamil Nadu. These animals are well-adapted to the cool, hilly climate and are culturally central to the lives of the tribal pastoralists. They possess a distinct gregarious nature and are known for their thick, crescent-shaped horns and long, coarse hair that protects them from the cold.

57. (B) Draft power in paddy fields
In Southeast Asian countries, swamp buffaloes are the backbone of traditional agriculture, primarily serving as the main source of draft power in wet paddy fields. Their large, splayed hooves allow them to move effectively through deep mud. While they do produce some milk and meat, their economic value is almost entirely derived from their physical labor in rice cultivation and transport.

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highest concentration of butterfat and protein. Originally from the Island of Jersey, these small-framed cows are highly efficient converters of feed into milk solids. Their milk is particularly valued for the production of cheese and butter, making them a popular choice for intensive dairy operations worldwide.

39. (B) Amritmahal
The Amritmahal is a classic example of a specialized draft cattle breed from the Karnataka region of India. Historically bred for military transport and heavy agricultural work, these animals are known for their exceptional stamina, speed, and hardiness. Unlike dairy or dual-purpose breeds, the cows are very poor milkers, as the selection focus has been entirely on the physical strength of the bullocks.

40. (B) I, III and IV
Dual-purpose cattle breeds in India are valued for both the milk production of the cows and the draft power of the bullocks. Prominent examples include the Hariana and Ongole breeds. While these cows are moderate milk yielders, the males are excellent for agricultural tasks. These breeds offer a balanced economic return for smallholder farmers who require both dairy products and farm labor.

41. (D) Gujarat
The Gir cattle breed is native to the Saurashtra region of Gujarat, specifically the Gir forests and surrounding districts. Characterized by their distinctive convex foreheads and long, pendulous ears, they are one of the most important dairy breeds in India. Gir cattle are also highly regarded internationally, especially in Brazil, where they have been extensively used to develop high-yielding tropical dairy strains.

42. (A) Holstein Friesian
The Holstein Friesian breed, originating from the Netherlands and Germany, is the world's highest-producing dairy animal in terms of milk volume. These large, black-and-white cattle dominate the commercial dairy industry globally. While their milk has a lower fat percentage compared to breeds like the Jersey, their sheer volume of production makes them the primary choice for large-scale liquid milk supply.

43. (B) Sahiwal and Brown Swiss
Karan Swiss is a specialized crossbred dairy strain developed at the National Dairy Research Institute in Karnal, India. It was created by crossing the indigenous Sahiwal breed with the exotic Brown Swiss breed. The goal was to combine the high milk production and hardiness of the Brown Swiss with the heat tolerance and disease resistance inherent in the Sahiwal cattle.

44. (B) Lyre-shaped horns
The Kankrej is a powerful dual-purpose cattle breed from the arid regions of Gujarat and Rajasthan. It is easily identified by its majestic, lyre-shaped horns and its unique "sawai chal" or swinging gait. These animals are highly prized for their hardiness and ability to perform heavy draft work under harsh desert conditions, while the cows provide a reasonable amount of milk.

45. (A) Hereford
The Hereford is a world-famous exotic beef cattle breed originally from England. Characterized by its red body and white face, it is highly valued for its efficient growth, excellent meat quality, and adaptability to various grazing conditions. Unlike dairy-focused breeds like the Sahiwal or Brown Swiss, Herefords have been selectively bred for centuries to maximize muscle development and carcass yield.

46. (C) Arid and semi-arid deserts
The Tharparkar is a hardy dual-purpose cattle breed that originated in the Tharparkar district of Sindh and is now common in Rajasthan. These animals are perfectly adapted to arid and semi-arid desert environments, where they can survive on sparse vegetation and limited water. Known for their white or light grey coats, they provide good milk yields and are excellent draft animals.

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47. (D) Sahiwal
The Sahiwal breed is often referred to locally as "Lola" because of its characteristically loose and thin skin. This physical trait is common among high-quality zebu dairy cattle and is thought to play a role in heat dissipation. The breed's docile nature and high milk production make it the cornerstone of many dairy improvement programs in tropical and subtropical regions across the globe.

(D) Sheep

2004

289. India's global rank in total milk production is:
(A) First
(B) Second
(C) Third
(D) Fifth

2004

290. According to recent national data, the per capita availability of milk in India has:
(A) Continuously declined
(B) Stagnated below the ICMR recommendation
(C) Steadily increased, surpassing the ICMR recommendation
(D) Remained constant since 1990

2008

291. Among the top milk-producing states in India, which two frequently alternate for the highest rank?
(A) Punjab and Haryana
(B) Uttar Pradesh and Rajasthan
(C) Gujarat and Maharashtra
(D) Kerala and Tamil Nadu

2024

292. India's global rank in total egg production is approximately:
(A) First
(B) Third
(C) Tenth
(D) Fifteenth

2015

293. The state consistently leading in egg production in India is:
(A) Andhra Pradesh
(B) Punjab
(C) West Bengal
(D) Gujarat

2002

294. India's rank in global meat production is approximately:
(A) First
(B) Second
(C) Eighth
(D) Twentieth

2012

295. Which state is the highest contributor to total meat production in India?
(A) Maharashtra
(B) Uttar Pradesh
(C) West Bengal
(D) Andhra Pradesh

2015

296. The largest single species contributor to India's total meat production is:
(A) Goat
(B) Buffalo
(C) Poultry
(D) Sheep

2025

297. In recent years, the national trend for total wool production in India has been:
(A) Exponentially increasing
(B) Stagnant or slightly declining
(C) Doubling every five years
(D) Shifting entirely to synthetic fibers

2023

298. Which Indian state is the undisputed leader in total wool production?
(A) Jammu & Kashmir
(B) Himachal Pradesh
(C) Rajasthan
(D) Uttarakhand

2010

299. In India's total milk pool, order the major contributing species/categories from highest to lowest share:
(A) Indigenous Cattle > Buffalo > Crossbred Cattle
(B) Buffalo > Crossbred Cattle > Indigenous Cattle
(C) Crossbred Cattle > Buffalo > Indigenous Cattle
(D) Buffalo > Indigenous Cattle > Crossbred Cattle

2008

300. The continuous growth in per capita availability of poultry meat and eggs in India is fundamentally a result of:
(A) Decreased human population
(B) Transition from backyard rearing to intensive commercial farming
(C) Ban on cattle slaughter
(D) Increased import of finished poultry products

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58. (B) Gujarat (Kutch)
The Banni buffalo is native to the Banni grasslands of the Kutch district in Gujarat. This breed is remarkably adapted to the harsh, saline environment of the Rann of Kutch and is known for its "night grazing" habit. Banni buffaloes are high milk yielders and are managed by the local Maldhari community using traditional pastoralist practices that emphasize the animal's natural resilience.

59. (D) Tightly curled, short horns
The Murrah is the most famous dairy buffalo breed in the world, originating from Haryana and Punjab. Its most distinctive physical characteristic is its tightly curled, short horns, which resemble the shape of a spiral. These jet-black animals are exceptionally efficient milk producers and are used extensively in crossbreeding programs to improve the dairy potential of local buffalo populations throughout India and beyond.

60. (A) Murrah, Mehsana, Surti, Bhadawari
In terms of average lactation milk yield, the Murrah stands at the top as the premier dairy buffalo breed. The Mehsana follows closely, having inherited high production from its Murrah ancestors. The Surti is a moderate producer known for efficiency, while the Bhadawari typically has the lowest volume but compensates with the highest fat percentage, making the sequence logically Murrah to Bhadawari.

61. (A) Fine apparel wool
The Merino sheep breed, which originated in Spain, is globally recognized as the finest producer of apparel-grade wool. Its wool fibers are exceptionally soft, thin, and crimped, making them ideal for high-quality clothing. Because of its superior genetic traits for fiber production, the Merino has been used to develop almost all other fine-wool sheep breeds across Australia, South Africa, and the Americas.

62. (D) Nellore
The Nellore is a prominent hair sheep breed from Andhra Pradesh, recognized as the tallest sheep breed in India. It is primarily valued for its superior mutton production and high growth rate. Unlike wool-producing breeds, the Nellore is better suited for meat markets due to its large body frame and efficient feed conversion, making it a favorite among commercial meat producers.

63. (A) Jamunapari
The Jamunapari is a majestic goat breed native to the Etawah district of Uttar Pradesh. It is easily identified by its large size, long pendulous ears, and a distinctively arched "Roman nose." This dual-purpose breed is prized for both its meat and high milk yield, which can exceed two kilograms per day. It has been used extensively to improve other goat breeds worldwide.

64. (A) Changthangi
Pashmina, one of the world's finest and most expensive natural fibers, is harvested from the Changthangi goat of the Ladakh region. These goats produce a thick, warm undercoat to survive the extreme sub-zero temperatures of the high-altitude Himalayas. This delicate undercoat is combed out by hand during the spring and processed into luxurious shawls and garments that are renowned for their incredible warmth.

65. (A) Mohair
The Angora goat, originally from Turkey, is the unique source of the lustrous commercial fiber known as mohair. Mohair is distinct from sheep's wool and cashmere because of its high sheen and durability. These goats are sheared twice a year, providing a valuable agricultural product used in high-end textiles, upholstery, and carpets. It should not be confused with Angora wool, which comes from rabbits.

66. (D) Black Bengal
The Black Bengal goat is a small, highly prolific breed native to West Bengal, Bihar, and Bangladesh. It is famous for its exceptional meat quality and its valuable skin, which is used for high-grade leather products. These goats often produce twins or triplets in a single kidding, making them an ideal choice for poverty alleviation and small-scale farming in humid tropical regions.

67. (B) Pelt (lamb skin)
The Karakul sheep is a specialized breed from Central Asia, primarily kept for the production of pelts from newborn lambs. These pelts, often called Persian lamb or Astrakhan, feature unique tightly curled patterns and are highly valued in the international fur trade. While the adults also provide meat and coarse wool, the primary economic focus of Karakul farming remains the harvest of these high-value skins.

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to survive for longer periods without access to free water compared to temperate breeds.

123. (C) Hemoglobin oxygen affinity and heart size
The Yak is uniquely adapted to the low-oxygen environments of high-altitude regions like the Tibetan Plateau. Genetic adaptations have resulted in yaks having a higher hemoglobin oxygen affinity, allowing their blood to bind oxygen more efficiently at low pressures. They also possess larger hearts and lungs relative to their body size, which facilitates the circulation of oxygen-rich blood to their tissues under extreme conditions.

124. (C) Prevent protein denaturation and assist in cellular repair
Heat Shock Proteins are a group of specialized molecular chaperones produced by cells in response to thermal stress. Their primary role is to stabilize other proteins, preventing them from denaturing or unfolding when body temperature rises. HSPs also assist in the repair of damaged proteins and the removal of irreparable ones. This cellular defense mechanism is crucial for the survival and recovery of livestock during severe heatwaves.

125. (A) Genetic disease resistance
Trypanotolerance is a remarkable example of genetic disease resistance found in certain West African cattle breeds like the N'Dama. These animals can survive and remain productive in areas infested with tsetse flies, which transmit the trypanosome parasite. Unlike other cattle breeds that suffer from severe anemia and death, N'Dama cattle have evolved genetic mechanisms to limit parasite multiplication and control the associated clinical symptoms of the disease.

126. (D) Dense fleece cover
Sheep are well-known for their ability to withstand cold environments, primarily due to their dense fleece cover. The wool fibers trap a layer of still air close to the skin, which acts as a highly effective insulator against heat loss. The quality and density of the fleece determine the animal's level of protection. This morphological adaptation is essential for the survival of sheep in temperate and high-altitude regions globally.

127. (B) Panting (respiratory evaporation)
Because poultry lack sweat glands, they cannot cool themselves through dermal evaporation. Instead, they rely heavily on panting, which is a form of respiratory evaporation. By increasing their breathing rate, birds move air over the moist surfaces of their lungs and air sacs, allowing heat to be carried away in the exhaled water vapor. This process is the primary mechanism for thermoregulation in chickens during periods of high ambient temperature.

128. (B) Reflecting solar radiation
Light-colored hair coats, such as white, grey, or light red, are common in tropical cattle breeds like the Tharparkar or Brahman. These colors are beneficial because they have a high albedo, meaning they reflect a significant portion of incoming solar radiation. By reducing the amount of heat absorbed from the sun, light-colored animals can stay cooler and reduce the physiological burden of thermoregulation in intense tropical sunlight.

129. (D) Seasonal reproduction and estrus cycling
Photoperiodism is the physiological response of an organism to changes in day length. In many temperate sheep breeds, it is the primary regulator of seasonal reproduction. As day length decreases in the autumn, hormonal changes are triggered that initiate estrus cycling in ewes. This ensures that lambs are born in the spring when weather conditions are most favorable and food is abundant, maximizing the chances of offspring survival.

NODIA

130. (A) Both A and R are true and R is the correct explanation of A.
Bos indicus cattle are characterized by several physical features that enhance their heat tolerance, including large dewlaps and pendulous sheaths. These anatomical structures significantly increase the total surface area of the skin relative to the animal's body volume. A larger surface area provides more space for heat exchange with the environment through radiation and convection, directly explaining why these breeds are so well-adapted to hot climates.

131. (A) Ticks
Bos indicus cattle exhibit a natural resistance to external parasites, particularly ticks, compared to Bos taurus breeds. This resistance is due to several factors, including a more sensitive skin that allows the animal to detect and dislodge ticks through muscle twitching. Furthermore, their immune system reacts more effectively to

black meat is highly prized for its unique flavor and purported medicinal properties. This breed is also remarkably hardy and resistant to many common poultry diseases prevalent in tropical regions.

78. (D) Rapid growth rates and efficient feed conversion ratios
The economic success of commercial broiler production depends on the ability of the birds to reach market weight in the shortest possible time. Therefore, breeding programs focus intensively on maximizing rapid growth rates and ensuring efficient feed conversion ratios. These traits allow producers to minimize the cost of feed and labor, while maximizing the total volume of meat produced per housing cycle.

79. (B) Hot and humid tropical climates
The Naked Neck gene causes a significant reduction in feather coverage, particularly around the neck. This morphological trait is highly advantageous in hot and humid tropical climates because it facilitates better heat dissipation through the skin. Birds carrying this gene are more resistant to heat stress, showing better growth and survival rates under high temperatures compared to their fully feathered counterparts in the same environment.

80. (A) P-4, Q-3, R-1, S-2
Poultry breeds are classified based on their primary economic utility. The White Leghorn is the definitive egg-laying type, while the Cornish is the cornerstone of meat-type breeding. The Rhode Island Red serves as a dual-purpose breed, providing both eggs and meat. Finally, the Aseel is a specialized indigenous game bird valued for its stamina and fighting traits rather than for commercial production.

81. (B) Minorca
The Mediterranean class of poultry includes breeds that originated around the Mediterranean Sea, such as the Leghorn, Minorca, and Ancona. These birds are generally characterized by their lightweight bodies, large combs, and white earlobes. They are primarily selected for high egg production and typically lay white-shelled eggs. The Minorca is the largest breed in this class and is known for its stylish black plumage.

82. (A) American
The Plymouth Rock is a well-known breed belonging to the American class of poultry. This class includes breeds developed in the United States, such as the Rhode Island Red and New Hampshire, which were primarily bred for dual-purpose utility. American breeds are characterized by their yellow skin, red earlobes, and the production of brown-shelled eggs, reflecting their development for both meat and egg markets.

83. (B) Sex-linked trait
The characteristic barring pattern of the Plymouth Rock is a classic example of a sex-linked trait. The gene for barring is located on the Z chromosome. Because males are ZZ and females are ZW in birds, this trait can be used for "sexing" chicks at hatch. A barred female passed her Z chromosome only to her sons, while her daughters receive the non-barred Z from their father.

84. (D) Asiatic
The Brahma and Langshan breeds belong to the Asiatic class of poultry. These birds are distinguished by their massive body size, feathered shanks, and relatively slow growth compared to modern commercial strains. Originating in Asia, these breeds were influential in the development of many American dual-purpose breeds. They are known for their calm temperament and are often kept today for exhibition or ornamental purposes.

85. (A) Karnal
The National Bureau of Animal Genetic Resources, abbreviated as NBAGR, is the premier Indian institution for the characterization and conservation of livestock. It is headquartered in Karnal, Haryana. The bureau plays a critical role in identifying new breeds, maintaining the national database of animal genetic resources, and formulating policies for the sustainable management of India's diverse livestock and poultry populations across the country.

86. (D) In situ
In situ conservation involves the preservation of livestock breeds within their original geographic locations and traditional production systems. This strategy allows animals to continue evolving in response to local environmental pressures and management practices. It is often considered

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68. (A) Chokla
The Chokla is a well-known sheep breed from the Shekhawati region of Rajasthan. It is widely considered to produce the finest carpet-quality wool in India. These sheep are relatively small in size but are highly adapted to the arid climate of the desert. Their wool is characterized by good staple length and luster, making it highly desirable for the traditional Indian carpet industry.

69. (D) Garole
The Garole is a small, highly prolific sheep breed found in the Sunderbans region of West Bengal. It is scientifically famous for carrying the FecB or Booroola mutation, which significantly increases the ovulation rate and results in multiple births. This genetic trait was eventually transferred to other sheep breeds, such as the Australian Merino, to enhance their reproductive efficiency and total lamb production.

70. (A) Both A and R are true and R is the correct explanation of A.
The Garole sheep is unique among Indian breeds for its ability to regularly produce multiple offspring, often twins or triplets. This exceptional prolificacy is directly caused by a natural mutation in the BMPR1B gene, also known as the FecB locus. This mutation increases the ovary's sensitivity to hormones, leading to higher ovulation rates. This biological mechanism fully explains the reproductive performance of the breed.

71. (B) Saanen
The Saanen goat, originating from Switzerland, is universally nicknamed the "Queen of Goats" due to its remarkably high and consistent milk production. These large, pure white goats are the most popular dairy goat breed globally. They have been extensively used in commercial dairies and breeding programs to enhance the milk output of local goat populations across various continents, thanks to their genetic potential.

72. (A) Meat
The Boer goat was developed in South Africa specifically for meat production. It is characterized by its large, muscular frame, white body, and brown head. Unlike dairy breeds, the Boer goat has been selected for rapid growth, high carcass yield, and excellent meat quality. It is now the most widely used meat goat breed in the world for crossbreeding to improve local meat-producing flocks.

NODIA

73. (A) White Leghorn
The White Leghorn, originally from the Mediterranean region, is the primary genetic foundation for almost all modern commercial white egg-laying strains. These birds are renowned for their high egg production, small body size, and excellent feed efficiency. Because they direct most of their energy into egg laying rather than meat production, they are the most economically efficient choice for the global egg industry.

74. (D) White Cornish
Modern commercial broilers are complex crosses designed for rapid growth and heavy muscling. The White Cornish breed serves as the essential paternal line in these crosses because of its broad breast and massive meat development. When crossed with maternal lines like the White Plymouth Rock, the resulting offspring exhibit the fast growth rates and high meat yield required for efficient large-scale broiler production.

75. (A) Rhode Island Red
The Rhode Island Red is a classic American dual-purpose poultry breed known for its distinctive dark red plumage. It is valued for its ability to produce a significant number of large, brown-shelled eggs while also providing a reasonable amount of meat. This versatility has made it one of the most popular breeds for backyard flocks and small-scale commercial operations focused on brown egg production.

76. (D) Aseel
The Aseel is a famous indigenous game bird of India, renowned for its incredible fighting prowess, physical strength, and stamina. Historically used for cockfighting, the breed features a powerful, upright carriage and very little flesh on its bones. While it is a poor egg producer, its hardy nature and aggressive personality make it a culturally significant and genetically unique component of India's poultry heritage.

77. (A) Fibromelanosis (black meat and organs)
The Kadaknath is a unique indigenous poultry breed from Madhya Pradesh, characterized by fibromelanosis. This genetic condition causes an intense accumulation of black pigment in the skin, meat, bones, and internal organs. The

distinct environmental conditions and traditional management practices that shaped the breed's evolution. Conservation efforts often prioritize the core breeding tract to ensure that the breed's unique adaptations and cultural heritage are preserved in their original context.

96. (C) Breed Registration Committee (BRC) under ICAR
In India, the registration of new livestock and poultry breeds is the responsibility of the Breed Registration Committee. This committee operates under the Indian Council of Agricultural Research and is assisted by the National Bureau of Animal Genetic Resources. The BRC rigorously reviews scientific data on the breed's uniqueness and stability before granting official recognition and an accession number to the newly identified animal population.

97. (A) Male (XY)
In all domestic mammals, including cattle, sheep, and pigs, sex determination follows the XY system. Males are the heterogametic sex, meaning they possess two different types of sex chromosomes, X and Y. Females are homogametic, possessing two X chromosomes. This system ensures that the sex of the offspring is determined by the sperm cell, which can carry either an X or a Y chromosome during fertilization.

98. (D) Female (ZW)
Unlike mammals, poultry and other birds utilize the ZW sex-determination system. In this system, the female is the heterogametic sex, possessing one Z and one W chromosome. Males are the homogametic sex, with two Z chromosomes. Consequently, in chickens and turkeys, the sex of the offspring is determined by the egg provided by the hen, rather than by the sperm provided by the rooster.

99. (A) SRY
The SRY gene, standing for Sex-determining Region Y, is the master genetic switch located on the Y chromosome of mammals. Its expression in the developing embryo triggers the transformation of undifferentiated gonads into testes. The hormones subsequently produced by the testes then direct the development of male physical characteristics. In the absence of the SRY gene, the embryo naturally develops into a female.

100. (C) III
Sex chromosome aneuploidies involve an abnormal number of X or Y chromosomes. In mammals, individuals with XXY develop Klinefelter's syndrome, while those with a single X chromosome (XO) exhibit Turner's syndrome. Both conditions typically lead to infertility. The statement that XXX causes a fertile male syndrome is incorrect; XXX individuals are female and often fertile, although they may show minor developmental variations but are not male.

101. (B) Early embryonic death or intersex individuals
Triploidy, the condition of having three sets of chromosomes, is a severe genetic abnormality in poultry. Most triploid embryos die early in development. Those that do survive to hatch are usually intersex individuals with abnormal gonadal development and are invariably sterile. This chromosomal imbalance prevents normal meiosis and hormone production, making triploidy a major cause of reproductive failure in various bird species.

102. (B) Gynandromorph
A gynandromorph is an organism that contains both male and female tissues, often divided down the center of the body. This rare condition occurs during early embryonic development when sex chromosomes fail to segregate properly during cell division. While found in many insects, gynandromorphism is also occasionally observed in poultry, where one half of the bird appears male and the other half appears female.

103. (C) Placental vascular anastomosis in heterosexual twin pairs
Freemartinism is a form of infertility occurring in a female calf born as a twin to a male. It happens because the placental blood vessels of the two fetuses fuse together, a process called vascular anastomosis. This allows male hormones and cells from the male twin to enter the female twin's circulation, interfering with her reproductive development and resulting in a sterile female with masculine internal traits.

104. (D) A sterile female chimera
Genetically, a freemartin calf starts as a female but becomes a chimera because it carries some cells from its male twin. These male cells, containing XY chromosomes, persist in her blood and organs. Because the male hormones have permanently stunted the development of

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the most effective way to maintain the genetic diversity and cultural significance of indigenous breeds while supporting the livelihoods of the local pastoralist communities.

87. (B) Ex situ conservation
Ex situ conservation refers to the preservation of genetic material outside the animal's natural environment. Cryopreservation of semen, embryos, and oocytes in liquid nitrogen is a primary method of ex situ in vitro conservation. This technique provides a long-term safety net against the extinction of threatened breeds, allowing for the potential restoration of the population even if the live animals are lost in the wild.

88. (C) Commercial sale of dairy products
The mandate of the National Bureau of Animal Genetic Resources focuses on the scientific management of livestock diversity. This includes the identification, characterization, and registration of new breeds, as well as the implementation of conservation programs for threatened populations. While the bureau supports the improvement of indigenous breeds, it is not involved in the commercial processing or sale of dairy products like milk or ghee.

89. (D) Accession number
When a new livestock or poultry breed is officially recognized and registered by the National Bureau of Animal Genetic Resources, it is assigned a unique accession number. This number serves as a permanent identification code in the national registry, ensuring that the breed is formally documented. This process is essential for the legal protection of animal genetic resources and for tracking the status of different breeds.

90. (A) IV, II, I, III
The formal registration of a new livestock breed in India follows a structured scientific process. First, the population must undergo thorough phenotypic and genetic characterization in its native tract. An application with detailed breed descriptors is then submitted to the bureau. The Breed Registration Committee evaluates the evidence, and if approved, the breed is officially recognized and issued a unique national accession number.

91. (B) Population size and number of active breeding females
The Food and Agriculture Organization categorizes livestock breeds based on their risk of extinction. The primary criteria for the "Endangered" status are the total population size and, more importantly, the number of active breeding females. If the population falls below a critical threshold, genetic diversity is rapidly lost through inbreeding and drift, necessitating urgent conservation interventions to prevent the loss of unique genetics.

92. (B) Morphological traits and biometry
Phenotypic characterization is the first step in documenting a livestock breed. It involves the systematic collection of data on observable morphological traits, such as coat color, horn shape, and ear type. Biometry, or the measurement of physical dimensions like body length, height at withers, and heart girth, is also essential. These details provide a standardized description that allows the breed to be distinguished from other populations.

93. (B) Microsatellite markers and SNPs
Molecular characterization provides a deeper look into the genetic structure and diversity of a breed. Scientists use DNA-based tools, most commonly microsatellite markers and Single Nucleotide Polymorphisms, often abbreviated as SNPs. These markers allow for the estimation of genetic distance between breeds, levels of inbreeding, and the identification of unique genetic signatures that are not visible through simple phenotypic observation of the animals.

NODIA

94. (C) Ex situ in vitro conservation
The preservation of somatic cells, such as skin fibroblasts, for potential future use in cloning via somatic cell nuclear transfer is a specialized form of ex situ in vitro conservation. This approach allows for the storage of the complete genome of an individual. While currently expensive and technically demanding, it provides an additional layer of security for the most critically endangered animal genetic resources.

95. (A) Native geographic area of breed origin and maintenance
The core breeding tract is the specific geographic region where a livestock breed originated and where its purest representatives are still found today. This area is typically characterized by

back together, resulting in the formation of two distinct species.

114. (B) Mule
A mule is the most well-known example of an interspecific hybrid, produced by crossing a male donkey with a female horse. Mules are valued for their strength, endurance, and intelligence. However, because they inherit sixty-four chromosomes from the horse and sixty-two from the donkey, they have sixty-three chromosomes. This odd number prevents normal meiosis, making almost all mules sterile and unable to produce their own offspring.

115. (A) Heterogametic sex
Haldane's rule is a biological principle stating that in species hybrids, if only one sex is sterile, rare, or absent, it is most often the heterogametic sex. In mammals, this means male hybrids are more likely to be sterile than female hybrids. This phenomenon is thought to be caused by genetic incompatibilities involving the sex chromosomes that are more easily expressed in the sex that has two different types of chromosomes.

116. (D) Female (ZW)
According to Haldane's rule, the heterogametic sex in hybrids is more likely to be sterile. Since birds follow the ZW system, where females are the heterogametic sex (ZW) and males are homogametic (ZZ), a sterile hybrid in poultry is most likely to be a female. This is the opposite of the situation in mammals, illustrating how sex-determination systems influence the biological outcomes of interspecific hybridization.

117. (A) Behavioral isolation
Behavioral isolation is a pre-zygotic barrier where different species do not mate because of differences in their courtship rituals or signals. Animals often rely on specific sounds, dances, or pheromones to attract a mate. If a member of one species does not recognize the courtship behavior of another, they will not mate. This mechanism is particularly important in birds and some mammals for maintaining species boundaries.

118. (D) Ecological (habitat) isolation
Ecological or habitat isolation occurs when two species live in the same general geographic area but occupy different ecological niches or habitats. Because they rarely encounter each other during the breeding season, they do not mate. For example, one species might prefer mountainous terrain while a closely related species stays in the valleys. This separation prevents gene flow and supports the maintenance of distinct species.

119. (A) Fertile F1 generation but weak or sterile F2 offspring
Hybrid breakdown is a post-zygotic isolating mechanism that appears in later generations of hybrids. While the first-generation (F1) crossbreds may be healthy and fertile, their offspring (F2) or the results of backcrossing show reduced viability or sterility. This happens because the favorable gene combinations found in the parents are broken up by recombination during the formation of gametes in the F1 individuals, leading to genetic incompatibilities.

120. (A) I, II, III and IV
Pre-zygotic mechanisms prevent the formation of a zygote and include mechanical, gametic, behavioral, and ecological isolation. These barriers act before fertilization. Hybrid sterility, however, is a post-zygotic mechanism because it only becomes apparent after a hybrid individual has been successfully born and reaches reproductive age. Understanding these different stages of isolation is essential for studying the evolutionary relationships between different livestock species and breeds.

121. (A) High density of sweat glands and vascularized skin
Bos indicus cattle are exceptionally heat tolerant because they possess a higher density of larger sweat glands compared to Bos taurus cattle. Furthermore, their skin is highly vascularized and often features a larger surface area due to the presence of a dewlap and pendulous sheath. These physiological adaptations allow for efficient evaporative cooling and heat dissipation, enabling them to maintain productivity in harsh tropical environments.

122. (B) Excretion of highly concentrated urine and dry feces
Sheep breeds native to arid regions have evolved several mechanisms to conserve water. One of the most effective is the ability of their kidneys to produce highly concentrated urine, minimizing fluid loss. Additionally, they can absorb more water from their digestive tract, resulting in very dry feces. These adaptations allow desert sheep

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her uterus and ovaries, she is a sterile female chimera. This condition can be diagnosed early through blood tests for the presence of the Y chromosome.

105. (A) DMRT1
In birds, the DMRT1 gene located on the Z chromosome is the primary factor in sex determination. Unlike the SRY system in mammals, sex in birds appears to depend on a dosage mechanism. Males, having two Z chromosomes, have two copies of DMRT1, which triggers male development. Females, with only one Z chromosome, have a lower dose of DMRT1 expression, which allows for the development of female reproductive organs.

106. (D) Z chromosome
Sex-linked traits in poultry are governed by genes located on the Z chromosome. Because the W chromosome is very small and contains few genes, most traits linked to sex follow the inheritance pattern of the Z chromosome. This allows breeders to create "auto-sexing" crosses where chicks can be sorted by sex immediately after hatching based on visible markers like feather color or rate of feather growth.

107. (A) Sex-influenced inheritance
Sex-influenced inheritance occurs when the expression of an autosomal trait is affected by the sex of the individual, usually due to the influence of sex hormones. The presence of horns in some sheep breeds is a classic example; the horned allele acts as a dominant trait in males but as a recessive trait in females. This results in different phenotypic ratios between the two sexes for the same genotype.

108. (C) Diploid (2n)
Somatic cells, which make up the bulk of the body tissues in normal domestic livestock, are diploid. This means they contain two complete sets of chromosomes, one inherited from each parent. In contrast, gametes like sperm and eggs are haploid, containing only one set. The diploid state is essential for maintaining genetic stability and ensuring that the correct number of chromosomes is restored upon fertilization.

109. (D) Prevent mating or fertilization between species
Pre-zygotic isolating mechanisms are evolutionary barriers that prevent different species from successfully mating or forming a zygote. These mechanisms can be ecological, temporal, behavioral, mechanical, or gametic. By preventing the initial stages of reproduction, these barriers maintain the genetic integrity of species and prevent the wasteful production of hybrid offspring that may be sterile or have reduced fitness in the environment.

110. (A) I, II and IV
Post-zygotic isolation occurs after fertilization has taken place. It includes hybrid inviability, where the hybrid embryo fails to develop, and hybrid sterility, where the resulting offspring cannot reproduce. Hybrid breakdown is another mechanism where the first hybrid generation is fertile, but subsequent generations are weak or sterile. Temporal isolation, however, is a pre-zygotic mechanism because it prevents mating from ever occurring in the first place.

111. (B) Temporal isolation
Temporal isolation is a type of pre-zygotic barrier where species are prevented from interbreeding because they mate at different times of the day, season, or year. For example, if two related species of livestock have non-overlapping breeding seasons, they will never naturally produce hybrids even if they live in the same geographic area. This mechanism is a common way that related species maintain their separate genetic identities.

112. (B) Gametic isolation
Gametic isolation occurs when the sperm of one species cannot successfully fertilize the egg of another species. This can be due to biochemical incompatibilities on the surface of the gametes or a hostile environment in the reproductive tract of the female. Even if mating occurs and sperm reach the egg, no zygote is formed, ensuring that the genetic boundaries between the two different species remain intact.

113. (D) Allopatric speciation
Allopatric speciation is the process by which new species evolve when a population is divided by a geographic barrier, such as a mountain range or ocean. Over time, the isolated populations accumulate genetic differences through mutation, selection, and drift. Eventually, these differences become so great that the two groups can no longer interbreed if they are brought

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tick saliva, limiting the success of the parasite's feeding and reducing the transmission of tick-borne diseases like babesiosis.

132. (B) Oval-shaped red blood cells resistant to osmotic lysis
Camels possess unique physiological adaptations that allow them to survive extreme dehydration. Their red blood cells are oval-shaped rather than circular, which allows them to continue flowing through small blood vessels even when the blood becomes viscous during water scarcity. More importantly, these cells are highly resistant to osmotic lysis, allowing them to swell significantly when the camel finally drinks a large volume of water without bursting.

133. (B) Phenotypically more similar than expected by chance
Positive assortative mating is a non-random mating strategy where a breeder pairs individuals that are phenotypically more similar for a specific trait than would be expected by chance. For example, mating the tallest males to the tallest females is positive assortative mating for height. This practice is used to increase the frequency of extreme phenotypes in a population and to concentrate desirable alleles for the selected trait.

134. (C) Increases homozygosity for the traits involved
The primary genetic consequence of positive assortative mating is an increase in homozygosity at the loci governing the specific traits used for selection. Because similar individuals are more likely to carry similar alleles, their offspring are more likely to be homozygous for those alleles. Unlike inbreeding, this increase in homozygosity is localized to the selected traits and does not affect the entire genome of the animal.

135. (D) Phenotypically opposite or dissimilar
Negative assortative mating, also known as disassortative mating, involves pairing individuals that are phenotypically opposite or very dissimilar for a particular trait. An example would be mating a very large bull to a very small cow. This strategy is often used in corrective mating programs to bring the next generation closer to a desired intermediate phenotype or to rectify specific conformational defects in the herd.

136. (D) Increased uniformity (reduction in phenotypic variance)
Negative assortative mating typically leads to an increase in phenotypic uniformity within the next generation. By mating extreme opposites, the breeder produces offspring that are more likely to have intermediate phenotypes. This process reduces the overall phenotypic variance in the population for the specific trait being selected. It is a powerful tool for stabilizing a herd and eliminating extreme outliers that may be undesirable.

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137. (C) Negative assortative mating (Corrective mating)
When a breeder identifies a specific conformational defect in an animal, such as poor udder attachment or crooked legs, negative assortative mating is the best approach. By mating the defective animal to a partner that is exceptionally strong in that same trait, the breeder hopes to correct the flaw in the resulting offspring. This targeted approach is frequently referred to as "corrective mating" in livestock management.

138. (D) Increasing additive genetic variance
Positive assortative mating increases the additive genetic variance for the specific trait being selected. By concentrating similar alleles in homozygous states, it expands the range of genotypes and phenotypes in the population, moving them toward the extremes. This increased variance can be beneficial because it provides more raw material for selection, potentially leading to faster genetic progress for the trait in subsequent breeding generations.

139. (A) Positive assortative mating
Mating the best-performing males to the best-performing females is a classic example of positive assortative mating. This common practice in animal breeding aims to produce the next generation of superior animals by concentrating favorable alleles from both parents. This strategy is highly effective for traits with moderate to high heritability where the animal's own performance is a good indicator of its underlying breeding value.

140. (A) P-4, Q-3, R-2, S-1
Different mating systems produce distinct genetic results. Positive assortative mating increases homozygosity for specific traits, while

negative assortative mating favors intermediate phenotypes. Inbreeding increases homozygosity across the entire genome, which can expose deleterious alleles. Outcrossing, on the other hand, increases heterozygosity across the genome, often leading to improved fitness and performance through the reduction of inbreeding depression and the exploitation of hybrid vigor.

141. (A) Only at loci affecting the specific trait selected
A key difference between inbreeding and positive assortative mating is the scope of their effect on the genome. Inbreeding is based on ancestry and increases homozygosity across all loci throughout the entire genome. Positive assortative mating is based on phenotype and only increases homozygosity at the specific loci that influence the trait being selected. Consequently, positive assortative mating does not carry the same broad risks of inbreeding depression.

142. (D) Negative assortative mating
When a breeder mates tall bulls with short cows, they are practicing negative assortative mating. The goal of such a pairing is typically to produce offspring of an intermediate size, rather than continuing to increase the height of the animals. This is a common management decision when a breeder feels that their animals have become too extreme in one direction and needs to bring them back toward a functional average.

143. (C) Positive assortative mating
Positive assortative mating, if practiced consistently over many generations without selection, is theoretically expected to yield a bimodal distribution of phenotypes. By repeatedly mating individuals with similar extreme traits (e.g., very large with very large and very small with very small), the population eventually separates into two distinct groups at opposite ends of the phenotypic spectrum. This increases the total phenotypic variance while decreasing the number of intermediate individuals.

144. (D) Exhaustion of additive genetic variance for the trait
The long-term progress of positive assortative mating is eventually limited by the exhaustion of additive genetic variance for the specific trait. As the population becomes increasingly homozygous for the favorable alleles, there are fewer opportunities for further genetic gain. Once all the individuals in the breeding group carry the same homozygous genotypes at the relevant loci, selection based on additive effects will no longer produce any additional phenotypic change.

145. (A) More closely related than the average relationship in the population
Inbreeding is the mating of individuals that are more closely related than the average relationship found within the general population. Common examples include matings between full siblings, half siblings, or parents and their offspring. This practice increases the probability that the resulting offspring will inherit two copies of the same allele from a common ancestor, leading to an increase in homozygosity throughout the entire genome.

146. (D) Inbreeding depression
The most prominent and often detrimental phenotypic result of inbreeding is inbreeding depression. This refers to the reduction in performance and fitness observed in inbred individuals. It occurs because inbreeding increases homozygosity, which allows harmful recessive alleles to be expressed in the phenotype. These recessive alleles, which were previously hidden in the heterozygous state, can lead to reduced growth, lower fertility, and increased susceptibility to diseases.

147. (B) Fitness, reproduction, and survival
Inbreeding depression does not affect all traits equally. Traits that are most closely associated with biological fitness, such as fertility, neonatal survival, and overall vitality, are generally the most susceptible. These traits often have low heritability and are heavily influenced by non-additive gene effects like dominance and epistasis. In contrast, highly heritable traits like carcass measurements or adult body weight tend to be less affected by inbreeding.

148. (A) Identical by descent (IBD)
Wright's coefficient of inbreeding, denoted as F, is a statistical measure of the degree of inbreeding in an individual. It specifically calculates the probability that two alleles at a random locus are identical by descent. This means that both alleles are copies of the same physical DNA sequence that existed in a common ancestor. This differs from being "alike in state," where

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alleles are the same but from different ancestral sources.

149. (B) 0.125 (12.5%)
In a half-sib mating, the two parents share one common grandparent. The probability that an offspring will inherit two identical alleles from that single ancestor is zero point one two five, or twelve point five percent. This is calculated using the formula F equals one-half raised to the power of n, where n is the number of steps in the pedigree path connecting the parents through their common ancestor.

150. (B) 0.25 (25%)
A full-sib mating is one of the most intense forms of inbreeding possible in livestock. In this case, the parents share two common ancestors (both the grandmother and the grandfather). The resulting offspring has a twenty-five percent probability of being homozygous by descent at any given locus. This high level of inbreeding, zero point two five, can lead to significant inbreeding depression and is generally avoided in commercial livestock breeding programs.

151. (B) Genetic prepotency
Genetic prepotency is the ability of an individual to consistently transmit its own characteristics to its offspring, regardless of the qualities of the mate. This phenomenon is often observed in highly inbred individuals. Because inbreeding increases homozygosity, the animal produces gametes that are more uniform. As a result, its offspring are also more uniform and more likely to resemble the inbred parent for many traits, a trait highly valued by some breeders.

152. (C) Homozygosity
The fundamental genetic mechanism of inbreeding is the increase in homozygosity. By mating related individuals, there is a higher chance that the offspring will receive the same recessive allele from both parents. This brings hidden recessive alleles out of the carrier (heterozygous) state into the homozygous state where they can be expressed in the phenotype. This exposure is the direct cause of both inbreeding depression and the appearance of genetic defects.

153. (B) Purging the genetic load
While inbreeding can be harmful, it can also be used as a tool to improve a population through a process called purging the genetic load. By practicing intense inbreeding followed by the strict culling of all individuals showing defects or poor performance, a breeder can effectively eliminate many harmful recessive alleles from the herd. This leaves the remaining population with a cleaner genetic makeup, potentially allowing for higher levels of future productivity.

154. (B) Tabular method
The tabular method is a systematic way to calculate inbreeding coefficients and relationship coefficients for all individuals in a pedigree. It involves constructing a numerator relationship matrix, often called the A-matrix. This method is highly efficient for large populations and is the foundation for modern genetic evaluation techniques like BLUP. It allows breeders to track the accumulation of inbreeding across many generations in a complex breeding program.

155. (C) 0.0
In pedigree analysis, the base population consists of individuals whose parents are unknown. By convention, the inbreeding coefficient for all individuals in the base population is set to zero. This does not mean they have no inbreeding in reality, but it serves as a starting point for measuring all subsequent inbreeding that occurs within the recorded pedigree of the population being studied.

156. (A) The correction for the inbreeding of the common ancestor A
In Wright's path coefficient formula, the term $(1 + F_A)$ is used to adjust the calculation if the common ancestor, A, is itself inbred. This correction is necessary because an inbred ancestor is more likely to pass on identical alleles than a non-inbred one. Including this factor ensures that the final inbreeding coefficient calculated for the descendant is accurate and reflects the total history of inbreeding within the pedigree.

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157. (B) Inbreeding
Linebreeding is a deliberate mating strategy that is fundamentally a specialized form of inbreeding. It involves mating individuals that are related to a specific, highly desirable ancestor in order to concentrate that ancestor's genes in the current population. While it increases homozygosity, linebreeding is usually practiced more mildly than close inbreeding to minimize the risk of severe inbreeding depression while maximizing genetic relationship to the chosen sire.

158. (B) Maintain high relationship to a superior ancestor with low F
The primary goal of a linebreeding program is to maintain a high genetic relationship to an exceptionally superior ancestor, such as a legendary sire, while keeping the overall inbreeding coefficient of the offspring relatively low. By carefully selecting mates that both trace back to the ancestor but are not too closely related to each other, a breeder can concentrate the ancestor's favorable alleles in the herd.

159. (A) Elite herds containing an exceptionally superior sire
Linebreeding is not a strategy for every farm. It is most successfully applied in elite herds where an exceptionally superior individual has been identified. If the ancestor being linebred to is not truly outstanding, the program will merely increase inbreeding without any corresponding genetic benefit. Therefore, it requires a high starting point and very accurate performance data to ensure that the chosen ancestor is worthy of being concentrated.

160. (D) Slow down the rate of inbreeding accumulation
Unlike close inbreeding, which aims for rapid homozygosity, linebreeding is designed to slow down the rate of inbreeding accumulation. By using more distant relatives that all share the same common ancestor, a breeder can maintain genetic continuity over many generations without experiencing the sharp decline in fitness often associated with full-sib or parent-offspring matings. This gradual approach makes linebreeding a more sustainable long-term strategy for many purebred breeders.

161. (B) Pathways of genetic transmission from ancestors to descendants
An arrow diagram is a visual tool used in pedigree analysis to clearly show the pathways of genetic transmission from ancestors to their descendants. Each arrow represents a gamete passing from a parent to its offspring. This diagram makes it much easier to identify common ancestors and calculate the number of generations in each path, which is a necessary step for determining inbreeding and relationship coefficients.

162. (D) Eventual accumulation of inbreeding depression
A major risk of prolonged linebreeding, even when done carefully, is the eventual accumulation of inbreeding depression. Although the rate of inbreeding is slower than in close inbreeding, the inbreeding coefficient still increases over time. If this process is not accompanied by intense selection and culling of inferior animals, the herd may eventually suffer from reduced fertility and other fitness-related problems that can negate the genetic gains.

163. (A) The probable proportion of identical genes shared by two individuals due to common ancestry
The coefficient of relationship, denoted as R , measures the probable proportion of genes that two individuals have in common because they share one or more common ancestors. For example, the relationship between a parent and its offspring is zero point five, as they share fifty percent of their genes. This coefficient is essential for predicting the performance of relatives and for planning mating systems like linebreeding or outcrossing.

164. (A) It halves with each successive generation
If no linebreeding is practiced, the genetic relationship between a descendant and a specific ancestor halves with each successive generation. This happens because only half of an individual's genes are passed to each offspring. Consequently, without a deliberate strategy to bring those genes back together through related matings, the genetic influence of even the most outstanding ancestor will quickly dilute to insignificance over time within a large population.

165. (C) When the herd is of average or poor genetic merit
Linebreeding is strictly not recommended when the herd is of average or poor genetic merit. Because linebreeding is a form of inbreeding, it will inevitably expose some deleterious recessive alleles and cause some level of inbreeding depression. If the ancestors being linebred to are not genetically superior enough to compensate for these negative effects, the overall quality of the herd will decline. It is a tool for improving the best.

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166. (B) 0.125
If an individual is mated to its own grandparent, the resulting offspring has an inbreeding coefficient of zero point one two five, assuming no other common ancestors are present. In this pedigree, there is one path through the grandparent that is two steps long. Using the formula F equals one-half raised to the power of three (one plus two generations minus one), the result is one-eighth, which is twelve point five percent.

167. (B) Accurate and deep pedigree records
Successful linebreeding is impossible without accurate and deep pedigree records. A breeder must be able to trace the ancestry of every animal back many generations to identify the specific common ancestors and calculate the resulting inbreeding levels. Without this detailed information, it is impossible to distinguish between beneficial linebreeding and accidental close inbreeding, which could lead to unexpected genetic problems and the loss of the desired ancestral influence.

168. (B) Strict and intense culling of inferior animals
To successfully mitigate the adverse effects of linebreeding, such as the expression of recessive defects or reduced fitness, a breeder must apply strict and intense culling. Any animal that shows even minor signs of inbreeding depression or fails to meet high performance standards must be removed from the breeding program. This ensures that only the best individuals, who have successfully combined the ancestor's genes with a robust phenotype, are allowed to reproduce.

169. (A) Crossbreeding
Crossbreeding is the mating of animals from two or more distinct breeds. This practice is widely used in commercial livestock production to take advantage of heterosis, or hybrid vigor, and breed complementarity. By combining the strengths of different breeds, producers can create offspring that are more productive, hardy, and efficient than either of the parent breeds. Crossbreeding is a fundamental tool for improving traits with low heritability, such as reproduction.

170. (A) I and II
A three-way cross is a structured breeding system that involves mating an F1 crossbred female to a purebred male of a third, different breed. This system is highly effective because it takes full advantage of both individual heterosis in the offspring and maternal heterosis in the crossbred dam. The offspring are not purebred; they carry a mix of all three breeds, making them ideal for terminal production in sectors like the commercial swine industry.

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171. (B) Retain high levels of heterosis while generating their own replacement females
A major advantage of rotational crossbreeding systems is their ability to maintain high levels of heterosis across generations while allowing the farmer to generate their own replacement females within the herd. This eliminates the need to constantly purchase purebred or F1 females from outside sources. By alternating the breed of the sire in each generation, the herd maintains a balanced mix of genetics from the participating breeds, sustaining hybrid vigor indefinitely.

172. (B) 66.7%
In a continuous two-breed rotational cross, also known as criss-crossing, the amount of heterosis eventually stabilizes after several generations. At this equilibrium, the population retains approximately sixty-six point seven percent, or two-thirds, of the maximum heterosis found in the initial F1 generation. This level of hybrid vigor is sufficient to provide significant improvements in fitness and production traits compared to the average of the two original purebred parent populations.

173. (C) 85.7%
A three-breed rotational crossbreeding system is more complex but retains a higher percentage of the initial F1 heterosis than a two-breed system. At equilibrium, a three-breed rotation maintains approximately eighty-five point seven percent of the maximum possible hybrid vigor. This higher level of heterosis makes the system attractive for producers who want to maximize the benefits of crossbreeding while still maintaining a self-sustaining herd for female replacements.

174. (A) All offspring (both male and female) are marketed/slaughtered.
A terminal crossing system is specifically designed for market production, where all offspring, both males and females, are sold or slaughtered. No offspring are kept as replacements for the breeding herd. This allows the breeder to choose a sire breed based entirely on its growth and carcass qualities, and a dam breed based on its

on Cattle. It was created by combining the high milk production of the Holstein Friesian breed with the heat tolerance and hardiness of the indigenous Sahiwal breed. The target genetic composition for Frieswal is fifty-eight percent Holstein Friesian and forty-two percent Sahiwal inheritance.

226. (D) Sheep
Avikalin and Avivastra are synthetic sheep breeds developed at the Central Sheep and Wool Research Institute in Rajasthan, India. Avikalin was developed for superior carpet wool production by crossing Rambouillet and Malpura sheep. Avivastra was created by crossing Rambouillet and Chokla sheep to produce fine apparel-grade wool. Both breeds represent successful examples of using crossbreeding and selection to create improved livestock populations adapted to specific regional and industrial needs.

227. (C) The sum of the squares of the breed fractions ($\sum p_i^2$)
The amount of heterosis retained in a synthetic breed is determined by the formula one minus the sum of the squares of the breed fractions. Therefore, it is inversely proportional to this sum. This mathematical relationship means that using more foundation breeds in equal proportions will lead to higher levels of retained heterosis. For example, a two-breed synthetic retains fifty percent, while a three-breed synthetic retains sixty-six point seven percent.

228. (A) Mating crossbred animals among themselves
Inter se mating refers to the practice of mating crossbred animals with other crossbred animals of the same genetic composition. This is a crucial step in the stabilization and development of a new synthetic breed. By mating within the crossbred population rather than backcrossing to a parent breed, the breeder allows the genome to stabilize and facilitates the selection of individuals that have the best combination of traits from all the ancestral breeds.

229. (C) All possible crosses among a set of parental lines
A diallel cross is a mating design in which all possible crosses are made among a selected set of parental lines, with or without reciprocal crosses. It is widely used in plant and animal breeding to estimate general combining ability (GCA), specific combining ability (SCA), and genetic effects, helping breeders identify superior parents and promising hybrid combinations.

230. (A) Parents, F1s, and reciprocal F1s are all included
Griffing's Method I is the most comprehensive diallel design. It includes all possible combinations: the original parents, the first-generation hybrids (F1s), and the reciprocal crosses. This design allows for the most detailed partitioning of genetic variance, including the estimation of maternal and sex-linked effects by comparing the performance of reciprocal crosses. However, it also requires the largest number of total mating combinations compared to other simplified Griffing designs.

231. (B) Parents + F1s (no reciprocals)
Griffing's Method 2 diallel design is a simplified version that includes the parental lines and their F1 hybrids, but excludes the reciprocal crosses. This design is often used when reciprocal effects are assumed to be negligible or when resources are limited. While it provides less information than Method I, it still allows for the estimation of general and specific combining abilities and the evaluation of the performance of the parents themselves.

232. (C) Only F1s (no parents, no reciprocals)
Griffing's Method 4 is the most streamlined diallel design, consisting only of the F1 hybrids without the parents or the reciprocal crosses. This design is primarily used when the main objective is to identify the best-performing specific crosses for commercial production. Because it requires the fewest number of mating combinations, it is the most practical design for evaluating a large number of parental lines in a single breeding experiment.

233. (B) Maternal effects and/or sex-linked genes
In a diallel analysis, significant differences in performance between reciprocal crosses typically indicate the presence of maternal effects or sex-linked inheritance. Maternal effects occur when the dam influences the offspring's phenotype through factors like milk production or uterine environment. Sex-linked genes are those located on the sex chromosomes. Identifying these effects is important for determining which breed should be used as the sire or the dam in a commercial cross.

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183. (C) 87.5%
Following two generations of backcrossing to the purebred exotic sire after the F1, the offspring are in the third generation (F3). The F1 has fifty percent exotic blood, the F2 has seventy-five percent, and the F3 has eighty-seven point five percent. In each generation, the remaining native inheritance is halved, as the offspring always receive an additional fifty percent of pure exotic genetics from their sire.

184. (C) 5
To reach approximately ninety-six point eight percent purity in a grading up program, five continuous generations of mating to the purebred sire are required. In the first generation, exotic blood is fifty percent; in the second, seventy-five; in the third, eighty-seven point five; in the fourth, ninety-three point seven five; and by the fifth generation, it reaches ninety-six point eight seven five percent. At this stage, the animal is genetically very close to a purebred.

185. (C) 5-6
Theoretically and practically, an animal is considered a purebred after five to six generations of grading up. At this point, the proportion of the original native genetics has been reduced to less than three percent. For most administrative and registration purposes in livestock breeding, this level of purity is sufficient to classify the animal as a member of the improved breed, provided it also meets the phenotypic standards of that breed.

186. (B) Loss of adaptability, heat tolerance, and disease resistance at higher exotic blood levels
A major practical limitation of grading up indigenous cattle with exotic dairy breeds in tropical regions is the loss of environmental adaptability. While the milk yield increases with higher levels of exotic blood, the animals often lose their natural heat tolerance and resistance to local diseases and parasites. This often results in poor health, high mortality, and reduced fertility when the exotic inheritance exceeds fifty to sixty-two point five percent.

187. (A) $\left(\frac{1}{2}\right)^n$
The proportion of native germplasm remaining in a population after n generations of grading up is calculated using the mathematical formula one-half raised to the power of n. For example, after three generations, the native proportion is one-half cubed, which equals one-eighth, or twelve point five percent. This simple exponential decay formula allows breeders to predict exactly how quickly the original genetic makeup will be replaced by the genes of the sire breed.

188. (C) Low-producing, non-descript animals
Grading up is most economical and effective when it is applied to populations of low-producing, non-descript animals. These animals provide a hardy maternal base that can be quickly improved by the introduction of superior genetics from a well-established breed. This strategy is widely used in developing countries to upgrade the local livestock population for better dairy or meat production without the massive investment required for total herd replacement.

189. (B) Change the purebred sire in every generation
To prevent inbreeding in a continuous grading up program, it is essential to change the purebred sire in every generation. If a breeder uses the same sire to mate with his own daughters and granddaughters, the level of inbreeding will rise rapidly, leading to inbreeding depression. By using different, unrelated purebred sires of the same breed, the breeder can maintain the upgrade in purity without increasing relationship among the animals.

190. (A) Both A and R are true and R is the correct explanation of A.
Widespread and indiscriminate grading up is recognized as a significant threat to livestock biodiversity. This is because the process systematically replaces the unique native genome with that of a few globally dominant exotic breeds. Over time, this can lead to the permanent loss of indigenous breeds and their specific adaptations to local environments. While grading up increases production, it must be balanced with conservation efforts to preserve the genetic heritage.

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191. (B) 50% to 62.5%
In India, national breeding policies for cattle generally recommend maintaining the level of exotic inheritance between fifty percent and sixty-two point five percent. This range is considered the "golden mean" where the animals benefit from the high milk production of the exotic breed while still retaining enough of the indigenous breed's heat tolerance and disease resistance to remain productive and

maternal and reproductive efficiency. All the benefit of heterosis is concentrated in the final market product.

175. (B) Mating a terminal meat-type sire to a highly prolific maternal crossbred dam
Breed complementarity is the principle of mating breeds that have different, but complementary, strengths. The best example is mating a sire from a breed known for rapid growth and carcass quality (a terminal sire) to a dam from a crossbred population known for high fertility and milk production (a maternal dam). This combination produces offspring that excel in meat production while benefiting from the superior maternal environment provided by the mother.

176. (D) It leads to wide fluctuations in breed composition between generations
A fundamental disadvantage of rotational crossbreeding systems is that they lead to significant fluctuations in breed composition and phenotypic appearance between generations. Because the breed of the sire changes each cycle, the offspring will more closely resemble the most recent sire's breed. This can result in a lack of uniformity in the herd, which may be a disadvantage if the market requires a very consistent product or if management needs vary.

177. (A) Nucleus multiplier flocks and commercial flocks
A two-tier breeding system, common in the poultry and swine industries, consists of a nucleus tier and a commercial tier. The nucleus tier focuses on intensive selection within purebred lines to maximize genetic progress. These elite genetics are then multiplied and passed down to the commercial tier, where crossbreeding is used to produce the final animals for meat or egg production, ensuring that high-quality genetics reach the market efficiently and economically.

178. (B) It is zero because all F1 individuals inherit intact gametes from purebred parents
In the F1 generation of a cross between two purebreds, the recombination loss is zero. This is because each F1 individual receives one intact set of chromosomes from a homozygous parent of breed A and another from a homozygous parent of breed B. Recombination loss only begins in the F2 generation and subsequent backcrosses, when the favorable combinations of genes from the original parent breeds are broken up during meiosis in the crossbred individuals.

179. (B) Wright's formula based on the breed fractions
Retained heterosis is formally calculated using a formula developed by Sewall Wright, which is based on the proportion of each breed present in the cross. The amount of heterosis retained is proportional to the probability that two alleles at a locus come from different breeds. Specifically, it is calculated as one minus the sum of the squares of the breed fractions, providing a mathematical way to predict the hybrid vigor of any complex cross.

180. (C) II
Crossbreeding is a powerful tool that increases heterozygosity and utilizes both additive and non-additive gene effects. It is particularly effective for improving traits with low heritability, such as fertility and survival. However, the statement that it is used to fix recessive alleles is incorrect. Fixing an allele means making the entire population homozygous for it, which is the opposite of what crossbreeding achieves through the promotion of heterozygosity.

181. (B) Purebred sires of a single highly productive exotic or improved breed
Grading up is a breeding strategy used to transform a low-producing population into a high-producing one by repeatedly mating native females to purebred sires of a superior breed. In each successive generation, the proportion of "exotic" or improved genetics increases. This is a cost-effective way to improve a large number of animals without the need to purchase an entire new herd of expensive, high-quality purebred females from an external source.

182. (B) 50%
In the first generation (F1) of a grading up program, a native female is mated to a purebred exotic sire. Because the sire provides half of the offspring's genetic material, the resulting F1 individuals will have exactly fifty percent exotic inheritance and fifty percent native inheritance. This initial step provides the maximum possible level of individual heterosis, leading to a significant and immediate improvement in performance compared to the original native population.

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in the cat family. A cama is a recent man-made hybrid between a camel and a llama, created through artificial insemination to combine the traits of these two species.

201. (B) Males are sterile, females are fertile
The Dzo, a hybrid of cattle and yak, perfectly follows Haldane's rule. In this cross, the males are the heterogametic sex and are invariably sterile, while the females remain fertile. This allows farmers to backcross the females to either cattle or yaks to produce subsequent generations. This pattern of unisexual sterility is a common feature of many distant interspecific crosses in the animal kingdom, particularly among mammals.

202. (A) They have identical chromosome numbers and highly homologous chromosomes
The ability of domestic cattle and American bison to produce fertile offspring indicates that they share a very close evolutionary relationship. Specifically, both species have sixty chromosomes that are highly homologous. This similarity allows their chromosomes to pair correctly during meiosis in the hybrid, permitting the production of functional gametes. This level of genetic compatibility is rare between different genera and highlights their shared ancestry within the bovine family.

203. (C) Pre-zygotic and post-zygotic reproductive barriers
In nature, the evolutionary impact of hybridization between distant species is severely limited by a variety of reproductive barriers. Pre-zygotic barriers, such as different mating behaviors or breeding seasons, often prevent hybridization from occurring. If a hybrid is formed, post-zygotic barriers like hybrid inviability or sterility usually prevent the hybrid from passing its genes to future generations. These mechanisms work together to maintain the genetic distinctness and integrity of different animal species.

204. (B) No, they generally face hybrid inviability or early embryonic death
While sheep and goats are closely related, they generally cannot produce fertile hybrids naturally. They have different chromosome numbers; sheep have fifty-four while goats have sixty. Although mating can occur and fertilization may take place, the resulting embryos almost always suffer from severe developmental problems, leading to early embryonic death or miscarriage. Rare "geep" hybrids have been documented, but they are extremely uncommon and typically sterile.

205. (B) The superiority of the crossbred offspring over the average of its purebred parents
Heterosis, commonly known as hybrid vigor, is the phenomenon where the performance of crossbred offspring exceeds the average of its two purebred parents. It is most often observed in traits related to fitness, such as growth rate, fertility, and survival. Heterosis is the primary reason why crossbreeding is so widely used in the commercial livestock and poultry industries to maximize the efficiency and productivity of meat and egg production systems.

206. (C) Dominance hypothesis
The dominance hypothesis is one of the classic explanations for heterosis. It suggests that hybrid vigor occurs because the crossbred individual inherits favorable dominant alleles from both parents. These dominant alleles "mask" the expression of deleterious or less favorable recessive alleles that have become fixed in the homozygous state in the parent purebred lines. By hiding these negative recessive effects, the hybrid achieves a higher level of performance than either parent.

207. (B) The heterozygous genotype (Aa) is fundamentally superior to both homozygous genotypes ($\forall$ and aa)
The overdominance hypothesis proposes that heterosis is caused by the inherent physiological superiority of the heterozygous genotype itself. In this model, an individual with the genotype Aa performs better than those with either the AA or aa genotypes. This might be because the heterozygote possesses two different versions of a protein, allowing it to function effectively across a wider range of environmental conditions compared to the homozygotes.

208. (A) Favorable interactions between alleles at different loci
The epistasis hypothesis attributes heterosis to favorable interactions between alleles located at different loci across the genome. While dominance involves interactions at a single locus, epistasis occurs when the combination of genes at multiple positions produces a superior effect. This model suggests that the mixing of two different genomes in a cross can create new, beneficial gene combinations that were not

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present or were disrupted in the original parent populations.

209. (B) Isolate purebred lines performing equal to F1 hybrids
If the dominance hypothesis were the only cause of heterosis, it should theoretically be possible to isolate a purebred line that contains all the favorable dominant alleles in a homozygous state. Such a line would perform just as well as the F1 hybrid. In practice, however, this has proven to be difficult due to the sheer number of genes involved and the presence of genetic linkage, suggesting that other factors like overdominance play a role.

210. (C) No, because purebreeding increases homozygosity, losing the superior heterozygote advantage
Under the overdominance hypothesis, it is impossible to "fix" heterosis in a true-breeding purebred line. This is because the superior performance is tied directly to the heterozygous state. Any attempt at purebreeding inevitably increases homozygosity, which forces the population away from the beneficial Aa genotype toward the less productive $\forall$ or aa homozygotes. Therefore, if overdominance is significant, the maximum performance can only be achieved by creating new F1 hybrids.

211. (C) Highly heritable traits (e.g., carcass measurements)
In livestock breeding, there is a general inverse relationship between heritability and the degree of heterosis. Lowly heritable traits, such as fertility, neonatal survival, and overall longevity, tend to show the highest levels of heterosis. This is because these traits are heavily influenced by non-additive gene effects. Consequently, crossbreeding is the most effective strategy for improving these fitness traits, which are difficult to change through simple purebred selection.

212. (B) The hybrid performs worse than the average of the parents
Negative heterosis occurs when the crossbred offspring performs worse than the average of its two parent breeds. This is relatively rare in most commercial livestock crosses but can happen when the parent breeds are extremely divergent or have incompatible adaptations. In such cases, the mixing of the two genomes disrupts favorable genetic combinations without providing any offsetting benefit, leading to a hybrid that is less fit or less productive than its parents.

213. (C) Two sides of the same genetic coin (opposite effects on heterozygosity)
Heterosis and inbreeding depression are fundamentally related phenomena that reflect the same genetic principles. Inbreeding depression is the decline in performance caused by an increase in homozygosity, while heterosis is the improvement in performance caused by an increase in heterozygosity. Both are primarily driven by non-additive gene actions like dominance. Essentially, crossing inbred lines or different breeds restores heterozygosity, thereby "canceling out" inbreeding depression and resulting in hybrid vigor.

214. (B) Recombination loss (breakup of favorable epistatic gene combinations)
The decline in performance often seen when mating F1 hybrids to produce an F2 generation is primarily due to recombination loss. In the F1 generation, favorable epistatic combinations of genes from the parent breeds are preserved. However, during the production of gametes in the F1, these combinations are broken apart by recombination. The resulting F2 individuals have a lower probability of carrying these beneficial multi-gene interactions, leading to a decrease in overall hybrid vigor.

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215. (B) The genetic divergence (distance) between the parent breeds
The amount of heterosis achieved in a cross is generally proportional to the genetic divergence between the two parent breeds. Breeds that have been separated for a long time or have evolved in very different environments tend to have different sets of alleles. When these breeds are crossed, the increase in heterozygosity in the offspring is maximized. Therefore, wider crosses typically yield more significant levels of hybrid vigor than crosses between closely related breeds.

216. (C) Accelerated mutation rate
The physiological expression of heterosis is characterized by several benefits, such as increased metabolic efficiency, improved nutrient partitioning, and greater resistance to environmental stressors. These advantages stem from the superior genetic makeup of the hybrid. However, heterosis does not cause or rely on an accelerated mutation rate. Mutation is a

separate process of random genetic change that occurs independently of whether an animal is a purebred or a crossbred hybrid.

217. (A) $\left[\frac{F_1 - \text{Parent Average}}{\text{Parent Average}}\right] \times 100$
The standard formula for calculating percent heterosis involves comparing the performance of the F1 hybrid to the average performance of its two parent breeds. By subtracting the parent average from the F1 performance and then dividing by the parent average, breeders can determine the relative gain achieved through crossing. Multiplying by one hundred expresses this gain as a percentage, providing a clear measure of the economic benefit provided by the cross.

218. (B) Growth rate and survival
Individual heterosis is the hybrid vigor expressed by the crossbred animal itself. It is most easily observed in traits that reflect the animal's own biological vigor, such as its early growth rate, post-weaning gain, and survival to adulthood. These improvements are due to the animal's own heterozygous genotype. Individual heterosis is a key factor in the success of crossbred broilers, feeder calves, and market lambs in the commercial livestock industry.

219. (C) Milk production and weaning weight of the offspring reared by a crossbred dam
Maternal heterosis refers to the advantage provided by a crossbred mother to her offspring, regardless of the offspring's own genetics. It is best observed in maternal traits like milk production, mothering ability, and the resulting weaning weight of the progeny. Because a crossbred dam is typically more fertile and provides a better uterine environment, her offspring often perform better than those raised by purebred dams of the same breeds.

220. (B) I, II, III and IV
Developing a synthetic breed is a systematic process. It begins with selecting divergent foundation breeds and crossing them to create a desired genetic mix. The next critical step is inter se mating, where crossbreds are mated among themselves to stabilize the genome. Throughout this process, rigorous selection for target traits must be applied. The final generation should be a stabilized population, not one that is constantly backcrossed to an exotic purebred.

221. (C) Sire fertility and mating capacity
Paternal heterosis is the hybrid vigor expressed by a crossbred male. Its primary advantages are seen in reproductive traits such as increased libido, higher semen volume, better sperm quality, and overall improved mating capacity. Using a crossbred sire can be beneficial in commercial operations because these males are often more robust and fertile than purebred sires, potentially leading to higher conception rates and a more concentrated calving or lambing season.

222. (B) Stabilized composite population formed by crossbreeding
A synthetic breed, also known as a composite breed, is a stabilized population of animals that was originally created by crossing two or more different breeds. After the initial crosses, the population is maintained through inter se mating and intense selection. The goal is to create a new breed that combines the desirable traits of the foundation breeds and retains a significant portion of the initial heterosis, providing a productive alternative to purebreds.

223. (C) 75%
In a synthetic breed formed from four equally represented foundation breeds, the amount of retained heterosis is theoretically seventy-five percent of the initial maximum. The formula for retained heterosis is one minus the sum of the squares of the breed proportions. In this case, one minus four times (one-fourth squared) equals three-fourths, or seventy-five percent. This high level of retained hybrid vigor makes four-breed composites a very effective choice.

224. (A) Sunandini
Sunandini is a well-known synthetic cattle breed developed in Kerala, India. It was created by crossing local non-descript cattle with exotic dairy breeds like the Brown Swiss, Jersey, and Holstein Friesian. Through systematic inter se mating and selection, a stabilized population was established that is well-adapted to the humid tropical climate of Kerala while providing significantly higher milk yields than the original native cattle of the region.

225. (A) Holstein Friesian and Sahiwal
The Frieswal cattle strain is an important synthetic dairy population in India, developed through a collaboration between the Military Farms and the Central Institute for Research

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healthy under local tropical and subtropical environmental conditions.

192. (C) Inter se mating among the crossbreds
Once a crossbred population reaches the desired optimal level of exotic and indigenous inheritance, the standard strategy is to switch to inter se mating. This involves mating the crossbred animals among themselves rather than backcrossing to either of the parent breeds. The goal is to stabilize the population at that genetic level, eventually leading to the development of a new synthetic or composite breed that is well-adapted and productive.

193. (B) A jack (male donkey) and a mare (female horse)
A mule is a sterile interspecific hybrid produced by crossing a male donkey, known as a jack, with a female horse, known as a mare. Mules are world-renowned for their hybrid vigor, which manifests as superior strength, intelligence, and hardiness compared to their parent species. They have been used for thousands of years as reliable pack and draft animals in diverse terrains, ranging from steep mountains to hot deserts.

194. (A) A stallion and a jennet
A hinny is the reciprocal cross of a mule, produced by mating a male horse, called a stallion, with a female donkey, called a jennet. Hinnies are generally less common than mules and are often slightly smaller and more horse-like in appearance, particularly in the shape of their heads and ears. Like mules, hinnies are interspecific hybrids and are almost always sterile due to chromosomal incompatibilities between the two parent species.

195. (C) 63
The diploid chromosome number of a mule is sixty-three. This unusual number arises because a horse has sixty-four chromosomes and a donkey has sixty-two chromosomes. The resulting hybrid receives thirty-two chromosomes from its horse mother and thirty-one from its donkey father. This total of sixty-three chromosomes cannot form proper homologous pairs during meiosis, which is the fundamental biological reason for the sterility of the mule.

196. (B) Failure of homologous chromosomes to pair correctly during meiosis
The sterility of mules is primarily a result of chromosomal incompatibility. During the first stage of meiosis, homologous chromosomes from each parent must pair up perfectly to exchange genetic material. Because the horse and donkey have different numbers and structures of chromosomes, they cannot pair correctly in the mule. This failure leads to the production of non-functional gametes, preventing the mule from being able to reproduce naturally.

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197. (B) Bos taurus x Bos indicus
The cross between European taurine cattle (Bos taurus) and Asian zebu cattle (Bos indicus) produces fully fertile offspring of both sexes. While they are often classified as different species, they are genetically similar enough to have perfectly homologous chromosomes that pair normally during meiosis. This full fertility has allowed for the development of many productive dairy and beef cattle strains globally, such as the Brangus or Simbrah.

198. (A) Domestic cattle and American Bison
The Beefalo is a fertile hybrid developed in the United States by crossing domestic cattle with the American Bison. The goal was to create an animal with the meat quality and docility of cattle along with the hardiness, forage efficiency, and low-fat meat of the bison. Successful Beefalo must carry exactly three-eighths bison genetics to be officially recognized and to ensure they remain fertile and manageable in a standard farm setting.

199. (A) Dzo
A cross between a domestic cow and a male Yak is called a Dzo if it is male, or a Dzomo if it is female. These hybrids are common in the high-altitude regions of the Himalayas and Central Asia. They are larger and stronger than both yaks and local cattle, making them excellent for plowing and transport. While the females (dzomos) are fertile and provide good milk, the males (dzos) are sterile.

200. (A) P-3, Q-4, R-1, S-2
Interspecific hybrids are named and identified by their parent species. A mule comes from a jack and a mare, while a hinny comes from a stallion and a jennet. A liger is the offspring of a male lion and a female tiger, illustrating hybridization

234. (A) Model I (Fixed effects)
In diallel analysis, if the parental lines are specifically and purposefully chosen by the breeder rather than being a random sample from a larger population, the appropriate statistical model is Model I, also known as the fixed effects model. In this model, the conclusions and estimates of general and specific combining ability apply only to the specific set of parents used in the study and cannot be generalized to a broader population.

235. (B) Model II (Random effects)
Model II in diallel analysis, or the random effects model, is used when the parental lines are considered a random sample from a larger base population. The primary goal of this model is to estimate the components of genetic variance (additive and non-additive) for the entire population. Unlike Model I, the results from a Model II analysis can be generalized, allowing the breeder to make inferences about the genetic potential of the population as a whole.

236. (A) Additive genetic variance
The General Combining Ability variance component, estimated from a diallel cross, fundamentally reflects the additive genetic variance present in the population. GCA measures the average performance of a parental line across all its hybrid combinations. Because additive gene effects are the only ones passed predictably to all offspring, a high GCA indicates that the parent carries many favorable alleles that can be effectively selected for to improve the population through purebreeding.

237. (B) Non-additive genetic variance (Dominance and Epistasis)
The Specific Combining Ability variance component in a diallel analysis corresponds to the non-additive genetic variance, which includes both dominance and epistatic gene effects. SCA measures how much a specific cross deviates from the performance expected based on the GCA of its parents. A high SCA indicates that a particular pair of parents produces offspring with significant heterosis, suggesting that crossbreeding is an effective strategy for improving that specific combination.

238. (B) The number of required crosses increases quadratically with the number of parents
Diallel crosses are highly resource-intensive because the total number of required mating combinations increases quadratically as the number of parental lines (n) increases. For a full diallel, the number of crosses is n^2. For example, evaluating five lines requires twenty-five combinations, but evaluating ten lines requires one hundred. This rapid increase in the size of the experiment often limits the number of breeds or lines that can be included in a study.

239. (C) n^2
For a set of n parental lines, the total number of cross combinations required for a full Griffing's Method I diallel is n squared. This includes n selfings (parents), $\frac{n(n-1)}{2}$ unique F1 hybrids, and another $\frac{n(n-1)}{2}$ reciprocal crosses. This comprehensive design ensures that every possible genetic interaction between the selected lines is accounted for, providing the most complete picture of their breeding value and potential for use in systematic crossbreeding programs.

240. (A) II, IV, I, III
Griffing's diallel analysis follows a logical sequence. First, the crossing design is implemented and phenotypic data is collected. Next, an analysis of variance is performed to test for overall differences between genotypes. If significant, the GCA and SCA variance components are estimated. Finally, the specific genetic effects for each parent and cross are calculated. This structured approach allows breeders to identify the best overall parents and the most promising specific hybrid combinations.

241. (C) Reduce crosses while estimating combining ability
A partial diallel cross is a modified design used to estimate combining ability when dealing with a very large number of parental lines. The primary objective is to reduce the total number of mating combinations required, making the experiment more manageable and less expensive. By carefully selecting a structured subset of all possible crosses, breeders can still obtain reliable estimates of GCA and SCA while significantly decreasing the physical resources and time needed.

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242. (B) Only a structured subset (s) of the other lines
In a partial diallel, each parental line is not mated with every other line in the set. Instead, it is crossed with only a specific, structured subset of s other lines. The selection of these crosses is usually done according to a mathematical design, such as a circulant scheme, to ensure that every line is represented equally and that the resulting data can be analyzed to provide statistically valid estimates of the general combining abilities.

243. (B) A third unrelated inbred line or breed
A triallel cross is a mating design that involves three different parental lines. It is created by mating an F1 hybrid (the cross of parents A and B) to a third, unrelated inbred line or breed (C). This results in an offspring with the pedigree (AxB)xC. Triallel crosses provide information on how three different genomes interact, which is particularly useful for studying maternal effects and complex epistatic interactions that cannot be captured in a simple diallel.

244. (A) Two different F1 hybrids $(A \times B) \times (C \times D)$
A quadriallel cross, more commonly known as a double cross, involves four different parental lines. It is produced by mating two different F1 hybrids, such as (AxB) and (CxD). The resulting offspring carries genetic material from all four ancestors. Double crosses were historically important in the hybrid corn industry and are still used in some poultry and swine breeding programs to maximize the number of crossbred offspring produced from limited purebred parental stock.

245. (B) Epistatic interactions
Triallel and quadriallel crosses are more complex than standard diallels and are particularly useful for estimating epistatic interactions between genes. Because these designs involve three or four different genomes, they allow researchers to partition non-additive genetic variance into more detailed components, such as additive-by-additive or dominance-by-dominance epistasis. This deep genetic analysis provides a better understanding of the complex biological mechanisms that contribute to heterosis and the overall performance of crossbred populations.

246. (C) Partial, triallel, and quadriallel crosses
Kempthorne's designs are specialized statistical frameworks used for the analysis of complex mating systems, including partial diallels, triallel crosses, and quadriallel crosses. Kempthorne developed the mathematical theory for partitioning the genetic variance in these designs into their respective components of GCA, SCA, and various epistatic interactions. His work is fundamental for modern quantitative genetics and the scientific evaluation of sophisticated breeding programs in both livestock and agricultural crops.

247. (B) Extreme time requirement (generation interval) and cost
The primary disadvantage of triallel and quadriallel crosses in large livestock is the extreme requirement for time and financial resources. Because these designs require two or three successive generations of crossing before the final offspring can be evaluated, the total time involved is very long, especially for species with long generation intervals like cattle. This makes these designs much more common in poultry or swine, where rapid reproduction cycles make the process more feasible.

248. (A) AxA, AxD, and DxD interactions
In the statistical analysis of a double cross, the quadriallel design allows for a very detailed partitioning of epistatic interactions. Specifically, researchers can estimate the variance due to additive-by-additive (AxA), additive-by-dominance (AxD), and dominance-by-dominance (DxD) interactions. This level of detail is impossible to achieve with simpler mating designs and provides a comprehensive view of how genes at different loci work together to influence the performance and hybrid vigor of the crossbred offspring.

249. (A) Every parent is involved in exactly the same number of crosses (s)
A circulant partial diallel is a specific mathematical design used to organize the mating in a partial diallel. It ensures that every parental line in the experiment is involved in exactly the same number of cross combinations, denoted as s. This balance is critical for the statistical analysis, as it prevents any one line from having an undue influence on the overall results and allows for the unbiased estimation of GCA for all participating parents.

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250. (A) Both A and R are true and R is the correct explanation of A.
Partial diallels are often preferred over full diallels when a breeder needs to evaluate a very large number of inbred lines or breeds. As the number of lines increases, the number of required crosses in a full diallel grows quadratically, quickly becoming physically and financially impossible to manage. Partial diallels provide a statistically sound way to obtain the necessary information on combining ability while keeping the size of the breeding experiment within practical limits.

251. (C) Both A and B
The statistical efficiency and reliability of a partial diallel cross depend on two main factors: the total number of parental lines sampled from the population and the number of crosses performed for each line. A higher number of lines provides a better representation of the population's genetic diversity, while a higher value of crosses per line increases the accuracy of the GCA and SCA estimates. Breeders must balance these two factors based on resources.

252. (C) Quadriallel cross
Among the various mating designs used in quantitative genetics, the quadriallel or double cross is the most complex. It involves four different parents and multiple generations of crossing. However, this complexity is what allows it to provide the most detailed and comprehensive partitioning of epistatic variance. By comparing the many different combinations possible in a quadriallel, researchers can disentangle the complex interactions between multiple genes that contribute to the performance of elite livestock.

253. (A) Average performance of a line in hybrid combinations
General Combining Ability is a measure of the average performance of a particular line or breed when it is mated with a series of other lines. It reflects the relative value of that line's additive genetic contributions. A parent with a high GCA is one that consistently produces superior offspring, regardless of which other parent it is mated with. Identifying lines with high GCA is a primary goal for breeders focused on long-term population improvement.

254. (B) Overall population mean of the crosses
Mathematically, the General Combining Ability of a line is expressed as the deviation of its average crossbred progeny's performance from the overall mean of all the crosses in the diallel experiment. For example, if a sire's progeny average ten percent more milk than the total population average, his GCA is positive. This standardized approach allows breeders to easily compare different lines and identify those that are significantly better than the average.

255. (B) Cross performance deviating from parent GCA sums
Specific Combining Ability evaluates the performance of a specific pair of parents in a cross, relative to what would be expected based on their individual GCAs. If a particular cross performs much better or worse than the sum of its parents' average abilities, that deviation is the SCA. High SCA indicates that the two parents have "good nick" or high genetic compatibility, resulting in significant heterosis or specific gene interactions that benefit the offspring.

256. (C) Theoretically zero
If a trait is governed entirely by additive gene action, meaning there are no dominance or epistatic effects, then the Specific Combining Ability variance will be theoretically zero. In such a case, the performance of every cross would be exactly equal to the average of its parents' general combining abilities. A non-zero SCA variance is the primary evidence for the existence of non-additive gene interactions like heterosis in a breeding population.

257. (B) Half-sib families
GCA is traditionally and most effectively estimated by evaluating the performance of half-sib families. When a single parent is mated to many different individuals, the average performance of its offspring reflects its own average additive genetic contribution, as the non-additive effects and environmental factors tend to average out across the different mates. This makes the half-sib progeny test the standard method for determining the breeding value and GCA of sires in most livestock.

258. (B) Full-sib families (specific crosses)
SCA is estimated by evaluating the variance between specific full-sib families, which are the offspring of a specific pair of parents. By comparing the performance of many different full-sib groups in a diallel cross, breeders can determine which specific pairs of parents produce

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diminishes. In this case, both methods are selecting for the same favorable dominant alleles. RRS might even be less efficient in terms of genetic gain per year because its selection cycles are typically much longer due to the progeny testing requirement. Therefore, RRS is usually reserved for situations where overdominance is important.

275. (B) White Leghorn layer strains
Historically, Reciprocal Recurrent Selection has been instrumental in the development of superior commercial White Leghorn layer strains. By using RRS, breeders were able to simultaneously improve egg number, egg size, and shell quality, while also maximizing the hybrid vigor that ensures high livability and feed efficiency in large-scale commercial poultry houses. This method remains a cornerstone of the global poultry breeding industry for maintaining the steady increase in egg production seen over recent decades.

276. (B) Genetically divergent
A key requirement for a successful RRS program is that the two foundational populations must be genetically divergent. If the two groups are too similar, there will be very little non-additive genetic variation to exploit, and the crossbred offspring will not show significant heterosis. By choosing populations that are genetically distant or have different ancestral origins, breeders can maximize the potential for identifying superior specific combining abilities and creating highly productive commercial hybrids.

277. (B) 5 years
The national Livestock Census in India is an essential statistical exercise conducted every five years. It is a comprehensive door-to-door survey that collects detailed data on the number, species, age, sex, and breed of all livestock and poultry across the country. This regular monitoring is vital for formulating government policies, planning animal health services, and assessing the overall contribution of the livestock sector to the national economy and food security.

278. (C) 20th
The 20th Livestock Census, conducted in 2019, is the most recent complete national census of India's animal genetic resources. It was a landmark exercise as it utilized digital technologies for real-time data collection and processing. The results provided a detailed snapshot of the status of various livestock species and marked important trends, such as the increasing importance of crossbred cattle and the steady growth of the buffalo and poultry populations.

279. (C) Positive growth (increase)
According to the 20th Livestock Census, the total livestock population in India was approximately five hundred thirty-five point seven eight million, showing a positive growth of four point six percent compared to the previous census in 2012. This overall increase reflects the resilience and growing economic importance of the livestock sector in rural India. The growth was observed across most major species, including cattle, buffaloes, sheep, and goats.

280. (A) Growth in crossbreds and decline in indigenous
The population dynamics of cattle in India revealed a significant structural shift in the 20th Census. While the total cattle population increased slightly, there was a dramatic twenty-seven percent growth in the number of crossbred and exotic cattle. At the same time, the population of indigenous cattle showed a decline of about six percent. This trend highlights the increasing preference among farmers for high-yielding crossbred animals to meet the rising demand for commercial milk production.

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281. (B) Increased slightly
The buffalo population in India continued its steady upward trend in the 20th Livestock Census, reaching approximately one hundred nine point eight five million. This represents a slight increase of about one percent since the 2012 census. Buffaloes remain a cornerstone of India's dairy industry, contributing more than half of the total milk produced in the country. Their ability to thrive on low-quality roughage and provide high-fat milk makes them essential for smallholder farmers.

282. (B) Uttar Pradesh
Uttar Pradesh reported the highest total livestock population among all Indian states in the 20th Livestock Census. It is home to a massive number of cattle, buffaloes, and goats, reflecting its large geographic size and the central role of animal husbandry in its agricultural economy. Rajasthan and Madhya Pradesh followed Uttar Pradesh in the rankings, highlighting the concentration of

exploit both additive and non-additive gene effects, particularly overdominance, to achieve maximum genetic progress in commercial livestock and poultry.

267. (B) General Combining Ability and Specific Combining Ability
The fundamental objective of Reciprocal Recurrent Selection is to simultaneously improve both the General Combining Ability and the Specific Combining Ability within and between two breeding populations. By selecting individuals based on their crossbred progeny's performance, RRS enhances the additive genetic value for purebred traits while also maximizing the non-additive effects that drive heterosis in the commercial hybrid. This dual focus makes it one of the most powerful tools in modern breeding.

268. (C) The performance of their crossbred progeny when mated to testers from population B
In an RRS program involving two populations, A and B, individuals in population A are not selected based on their own appearance or their purebred offspring. Instead, they are selected based on the performance of their crossbred progeny produced by mating them with "tester" individuals from population B. This ensures that the animals kept for breeding in population A are those that carry the best genes for creating high-performing hybrids with the other population.

269. (B) Overdominance is a major source of genetic variation
The theoretical advantage of RRS over traditional pure line selection is most significant when overdominance is a major source of genetic variation for the target trait. In an overdominance scenario, the heterozygote is superior to both homozygotes. Because RRS selects for crossbred performance, it is more effective at identifying and increasing the frequency of the specific allele combinations that result in superior heterozygous hybrids, something that pure line selection cannot do as effectively.

270. (B) Exceptionally long cycle time for progeny evaluation
A major practical limitation of applying RRS in large livestock species like cattle or horses is the exceptionally long cycle time required for progeny evaluation. In each selection cycle, a generation of crossbred progeny must be produced, raised, and their performance measured before the superior purebred parents can be identified and mated to start the next cycle. For species with long generation intervals, this process can take many years, making it difficult to implement.

271. (C) Poultry and Swine
Because of its requirement for multiple generations and many progeny, RRS is most extensively and successfully applied in the poultry and swine industries. These species have relatively short generation intervals and high reproductive rates, which allows breeders to complete the selection cycles much faster and more economically than with larger livestock. Most modern commercial egg-laying and broiler strains have been developed using some form of RRS to maximize their productivity and efficiency.

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272. (C) They are mated inter se within population A to generate the next generation of purebreds
In a Reciprocal Recurrent Selection program, once the elite individuals from population A have been identified through the crossbred progeny test, they are mated inter se within their own purebred group. This step is essential for creating the next generation of improved purebreds for population A. By repeating this process in both populations A and B, the breeder systematically improves both lines so that their subsequent crosses continue to reach higher levels of performance.

273. (A) Purebred performance data alongside crossbred progeny data
Modified Reciprocal Recurrent Selection is a variation of the standard RRS method that incorporates purebred performance data alongside the data from crossbred progeny tests. By using information from both sources, breeders can improve the accuracy of their selections and potentially achieve faster genetic gain. This approach is particularly useful for traits that have moderate heritability in the purebreds but also show significant heterosis in the crossbred hybrids, balancing additive and non-additive improvement.

274. (B) About equally effective or potentially less efficient due to longer cycle time
If heterosis is driven entirely by partial dominance rather than overdominance, the theoretical advantage of RRS over simple pure line selection

2. Sum of average effects of genes carried by an individual
3. Interaction between alleles at the same locus
4. Total genetic value of an individual

(A) P-2, Q-3, R-1, S-4
(B) P-4, Q-1, R-3, S-2
(C) P-3, Q-2, R-4, S-1
(D) P-1, Q-4, R-2, S-3

2002

9. Non-additive genetic deviations include which of the following components?
(A) Only the additive variance component.
(B) Dominance and epistatic deviations.
(C) Genotype-environment interaction only.
(D) Permanent environmental variance effects.

2005

10. The phenotypic variance (V_P) of a trait is primarily partitioned into which components?
(A) $V_A + V_D + V_I$
(B) $V_G + V_E + V_{\{GE\}}$
(C) $V_E + V_{\{Et\}} + V_{\{Ep\}}$
(D) $V_{\{PHSC\}} + V_{\{ANOVA\}}$

2009

11. Which component of genetic variance is chiefly responsible for the resemblance between parents and their offspring?
(A) Additive genetic variance (V_A)
(B) Dominance variance (V_D)
(C) Epistatic variance (V_I)
(D) Genotype-environment variance ($V_{\{GE\}}$)

2001

12. A lactating cow loses a quarter of her udder due to mastitis. This causes a reduction in milk yield for all her subsequent lactations. This effect is classified under:
(A) Additive genetic variance component.
(B) Temporary environmental variance effect.
(C) Permanent environmental variance.
(D) Epistatic genetic variance deviation.

2013

13. Evaluate the following statements regarding the resemblance between relatives:
I. The covariance between half-sibs estimates $\frac{1}{4}V_A$.
II. The covariance between full-sibs estimates $\frac{1}{2}V_A + \frac{1}{4}V_D$.
III. The covariance between parent and offspring estimates $\frac{1}{2}V_A$.

Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I, II and III

2010

14. Heritability in the narrow sense (h^2) is mathematically defined as:
(A) $\frac{V_G}{V_P}$
(B) $\frac{V_D}{V_P}$
(C) $\frac{V_A}{V_P}$
(D) $\frac{V_A}{V_G}$

2022

15. In a paternal half-sib correlation analysis for estimating heritability, the expected mean square for sires (between sires) typically contains which variance components?
(A) σ^2_w
(B) $\sigma^2_w + k\sigma^2_s$
(C) σ^2_s
(D) $k\sigma^2_w + \sigma^2_s$

2015

16. When estimating heritability via parent-offspring regression, what is the expectation of the regression coefficient (b) if the regression is computed on the mid-parent value?
(A) $\frac{1}{2}h^2$
(B) $2h^2$
(C) $\frac{1}{4}h^2$
(D) h^2

2012

17. Repeatability (r) sets the upper limit for which genetic parameter?
(A) Broad sense heritability
(B) Degree of dominance
(C) Inbreeding coefficient
(D) Mutation rate

2002

18. Determine the correct combination of statements regarding Most Probable Producing Ability (MPPA):
I. MPPA is used to rank individuals for culling based on repeated records.

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India's livestock resources in the northern and central regions of the country.

283. (B) Tamil Nadu
Tamil Nadu emerged as the leader in total poultry population according to the 20th Livestock Census. The state has a highly developed and intensive commercial poultry sector, particularly in regions like Namakkal. This growth is driven by advanced breeding, efficient management, and a strong market for both eggs and broiler meat. Other major poultry-producing states include Andhra Pradesh and Telangana, which also show significant populations due to their extensive commercial operations.

284. (A) A significant increase
The 20th Livestock Census recorded a significant increase in the total sheep population in India, which grew by approximately fourteen percent to reach over seventy-four million. This growth was particularly notable in states like Telangana and Andhra Pradesh. The increase reflects the growing economic value of sheep for mutton production and the success of various state and national level programs aimed at improving the livelihoods of traditional shepherd communities across the country.

285. (B) A noticeable decline
In contrast to the growth seen in cattle, buffaloes, and sheep, the total pig population in India showed a noticeable decline of over twelve percent in the 20th Livestock Census. The population fell to approximately nine point zero six million. This decline may be attributed to various factors, including outbreaks of diseases like African Swine Fever, changing socio-economic conditions in traditional pig-rearing regions, and a shift in farming priorities among small-scale livestock producers.

286. (B) 1919–1920
The first Livestock Census in India was conducted during 1919–1920 to obtain reliable information on the country's livestock resources. Since then, livestock censuses have been carried out periodically to assess changes in animal population, distribution, and composition. The data support planning, policy formulation, and development programs for the livestock sector.

287. (B) The economic demand for higher milk production
The increasing proportion of crossbred cattle in India is mainly driven by the demand for higher milk production. Crossbred cattle combine the high milk yield of exotic breeds with the adaptability of indigenous breeds, improving dairy productivity. This shift has contributed significantly to increasing national milk production and farmers' income.

288. (C) Cattle
Cattle constitute the largest share of India's livestock population (excluding poultry). They are widely distributed across the country and play a vital role in milk production, draught power, manure production, and rural livelihoods. Their numerical dominance makes them the most important livestock species in India's agricultural economy.

289. (A) First
India ranks first in the world in total milk production, reflecting the success of dairy development initiatives such as Operation Flood and the expansion of cooperative milk marketing. Continuous improvements in breeding, feeding, veterinary care, and dairy infrastructure have enabled India to maintain its leading position globally.

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290. (C) Steadily increased, surpassing the ICMR recommendation
The per capita availability of milk in India has steadily increased over the years due to sustained growth in milk production. It has surpassed the recommended dietary intake suggested by the ICMR, indicating improved dairy availability. This growth reflects advances in animal husbandry, cooperative marketing, and enhanced productivity.

291. (B) Uttar Pradesh and Rajasthan
Uttar Pradesh and Rajasthan are the leading milk-producing states in India and frequently alternate for the highest rank depending on annual production. Their large bovine populations, strong dairy infrastructure, and widespread milk cooperative networks contribute substantially to India's overall milk production.

292. (B) Third
India ranks approximately third in global egg production, supported by a rapidly expanding

commercial poultry industry. Improved breeding, nutrition, disease control, and modern management practices have significantly increased egg output, making poultry one of the fastest-growing sectors of Indian agriculture.

293. (A) Andhra Pradesh
Andhra Pradesh consistently leads India in egg production because of its well-developed commercial poultry industry, modern layer farms, and efficient production systems. The state's favorable climate, feed availability, and strong marketing infrastructure have helped maintain its leading position in the poultry sector.

294. (C) Eighth
India ranks approximately eighth in global meat production, with poultry contributing the largest share of total meat output. Growth in commercial livestock farming, improved breeds, better nutrition, and modern processing facilities have steadily increased the country's meat production over recent decades.

295. (B) Uttar Pradesh
Uttar Pradesh is the highest contributor to meat production in India, owing to its large livestock population and extensive meat processing industry. The state contributes significantly through buffalo, cattle, goat, and poultry production, making it a major center for both domestic consumption and meat exports.

296. (C) Poultry
Poultry is the largest single contributor to India's total meat production due to its rapid growth rate, high feed efficiency, and short production cycle. Expansion of intensive commercial poultry farming and increasing consumer demand for affordable animal protein have made poultry the dominant source of meat in the country.

297. (B) Stagnant or slightly declining
India's wool production has remained stagnant or shown a slight decline in recent years. Factors such as reduced sheep populations in some regions, lower profitability, competition from synthetic fibers, and changing production systems have contributed to this trend despite continued demand for quality wool.

298. (C) Rajasthan
Rajasthan is the leading wool-producing state in India, accounting for the largest share of national wool production. The state supports large populations of hardy sheep breeds such as Marwari and Magra, which are well adapted to the arid climate and contribute significantly to carpet-grade wool production.

299. (B) Buffalo > Crossbred Cattle > Indigenous Cattle
In India's total milk production, the major contributors are Buffalo, followed by Crossbred Cattle, and then Indigenous Cattle. Buffaloes produce a large proportion of India's milk because of their high milk fat content and widespread distribution, while crossbred cattle contribute through their superior milk yield compared to indigenous breeds.

300. (B) Transition from backyard rearing to intensive commercial farming
The steady increase in per capita availability of poultry meat and eggs is mainly due to the transition from traditional backyard rearing to intensive commercial poultry farming. Improved genetics, balanced nutrition, disease control, automation, and efficient production systems have greatly enhanced productivity, making poultry products more affordable and widely available.

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CHAPTER 04

Genetic Properties of Population

2022

1. Under the Hardy-Weinberg law, which of the following is an essential assumption for a population to remain in genotypic equilibrium?
(A) Random mating
(B) Assortative mating
(C) High mutation rate
(D) Overlapping generations

2006

2. Which concept correctly distinguishes the transmission mechanism between individuals and populations?
(A) Individuals transmit genotypes, while populations transmit alleles.
(B) Both levels transmit intact genotypes across successive generations.
(C) Individuals transmit genes; populations show genotype frequencies.
(D) Both levels transmit specific allelic combinations without change.

2015

3. Given the Assertion (A) and Reason (R):
Assertion (A): The effective population size (N_e) is always equal to the census population size in natural livestock herds.
Reason (R): Unequal sex ratios and fluctuating population sizes reduce the effective population size.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2007

4. What is the mathematical relationship between effective population size (N_e) and the rate of inbreeding (ΔF)?
(A) $\Delta F = \frac{1}{N_e}$
(B) $\Delta F = \frac{2N_e}{1}$
(C) $\Delta F = \frac{N_e}{2}$
(D) $\Delta F = \frac{1}{2N_e}$

2005

5. In the algebraic formulation of population mean for metric characters, what does the value 'd' represent on the genotypic value scale?
(A) The additive value of the superior homozygote class.
(B) Genotypic value of the heterozygote relative to the mid-parent.
(C) Total epistatic interaction deviation across multiple distinct loci.
(D) Average effect of gene substitution within a random mating population.

2018

6. The average effect of a gene is defined as the mean deviation from the population mean of individuals which received that gene from one parent, provided that the other parent is chosen:
(A) From a highly inbred line
(B) Based on positive assortative mating
(C) At random from the population
(D) From a different distinct breed

2011

7. How does the average effect of gene substitution (α) differ conceptually from the average effect of a gene?
(A) α is exclusively applicable to epistatic interactions.
(B) α measures the permanent environmental variance.
(C) α measures dominance deviation only.
(D) α is the mean change when one allele replaces another.

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2008

8. Match the concepts in List I with their definitions in List II.
List I: (Concept)
P. Breeding Value
Q. Dominance Deviation
R. Epistatic Deviation
S. Genotypic Value
List II: (Definition)
1. Interaction between alleles at different loci

offspring that deviate from their expected GCA-based average. This variance between specific crosses is the mathematical basis for determining the importance of non-additive gene effects like dominance in the population.

259. (B) Selection (purebreeding)
A high ratio of GCA variance to SCA variance indicates that most of the genetic variation for a trait is due to additive gene effects. In this situation, the best strategy for long-term improvement is purebred selection. By identifying and breeding the individuals with the highest breeding values, the breeder can consistently increase the frequency of favorable alleles in the population. Crossbreeding to exploit SCA would be less effective because non-additive effects are relatively small.

260. (A) P-1, Q-2, R-3, S-4
The choice of a breeding strategy depends on the underlying genetic architecture of the target traits. High GCA variance suggests that pure line selection is the most effective approach. Conversely, high SCA variance indicates that crossbreeding should be used to exploit heterosis and non-additive effects. Traits with low heritability are best improved through inter-family selection, while highly heritable traits can be successfully improved through mass selection based on individual performance.

261. (B) Exploiting SCA through systematic crossbreeding
In advanced poultry breeding, purebred selection within elite lines eventually reaches a genetic plateau once most of the additive genetic variance has been exhausted. To achieve further improvements in commercial performance, breeders must shift their focus to exploiting Specific Combining Ability. This is done through systematic crossbreeding of divergent lines to find combinations that produce the maximum amount of heterosis, resulting in superior commercial layers and broilers that exceed any purebred.

262. (C) $\sigma^2_{GCA} = \frac{1}{4}\sigma^2_A$
In a population where there are no inbreeding or epistatic effects, the variance of the General Combining Ability is mathematically equal to one-fourth of the additive genetic variance. This relationship arises because GCA reflects the contribution of half-sibs, and half-sibs share one-quarter of their additive genetic variance. This formula is essential for researchers to convert GCA estimates from diallel crosses into standard estimates of the population's total additive genetic variance.

263. (C) σ^2_D
The variance of the Specific Combining Ability fundamentally represents the non-additive genetic variance in a cross. Under certain simplifying assumptions, the SCA variance is considered equal to the total dominance variance of the population. This direct relationship allows breeders to use the results of diallel experiments to estimate the magnitude of dominance effects, providing a scientific basis for predicting the amount of heterosis that can be achieved through crossbreeding.

264. (B) A well-characterized inbred line or population against which others are crossed
A tester line is a well-characterized genetic group, such as an inbred line or a specific population, used in a topcross or diallel design to evaluate the combining ability of other unknown lines. By mating multiple unknown lines to the same common tester, any differences in the performance of the resulting offspring can be attributed to the genetic differences between the lines being tested. This approach is highly effective for screening large numbers.

265. (B) Specific Combining Ability
Reciprocal Selection is a breeding method specifically designed to improve the Specific Combining Ability between two different populations. Instead of selecting within each population based on its own performance, selection is based on how well members of one population cross with members of the other. The goal is to maximize the performance of the crossbred offspring by identifying and selecting the individuals that produce the most significant heterosis when crossed.

266. (C) Comstock, Robinson, and Harvey
Reciprocal Recurrent Selection, a sophisticated breeding strategy, was first introduced in 1949 by the scientists Comstock, Robinson, and Harvey. Their goal was to provide a method that could simultaneously improve both the purebred lines and their crossbred performance. This approach addressed the limitations of simple purebred selection and allowed breeders to systematically

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II. MPPA calculations do not require the repeatability of the trait.
III. MPPA incorporates the number of records an individual has.
IV. MPPA ignores the population mean.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and IV
(C) I and III
(D) III and IV

2022

19. A genetic correlation between two traits is primarily caused by which biological phenomenon?
(A) Pleiotropy and linkage effects.
(B) Random genetic drift events.
(C) Positive assortative mating.
(D) Uniform environmental effects.

2003

20. When using Analysis of Covariance (ANCOVA) on paternal half-sib data to estimate genetic correlation, which component is isolated to represent the additive genetic covariance?
(A) Dam component of covariance
(B) Within-progeny environmental covariance
(C) Permanent environmental covariance
(D) Sire component of covariance

2005

21. What happens to the standard error of heritability estimates when the sample size increases significantly?
(A) It remains unaffected.
(B) It decreases for higher precision.
(C) It increases proportionally.
(D) It fluctuates unpredictably.

2007

22. Polymorphism Information Content (PIC) is a metric primarily used to assess:
(A) The breeding value of a sire
(B) The temporary environmental variance
(C) The informativeness of a genetic marker
(D) The rate of genetic drift

2005

23. Given the Assertion (A) and Reason (R):
Assertion (A): Wright's $F_{\{ST\}}$ measures the amount of genetic differentiation among subpopulations.
Reason (R): $F_{\{ST\}}$ is calculated entirely based on phenotypic variance across different environments.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2006

24. Which technique is most appropriately used to estimate the extent of recent genetic admixture and gene flow between livestock breeds?
(A) Analysis using microsatellite or SNP marker panels.
(B) Paternal half-sib Analysis of Variance (ANOVA).
(C) Estimation of the temporary environmental variance.
(D) Calculating the repeatability of milk yield traits.

2014

25. A 'breed signature' in livestock genetics refers to:
(A) The physical brand mark placed on the animal's hide.
(B) Allelic patterns unique to a specific breed.
(C) The average phenotypic measurement of the breed.
(D) The total number of chromosomes in the breed.

2012

26. Which scenario results in a deviation from Hardy-Weinberg equilibrium?
(A) Large population size
(B) Directional selection
(C) No migration
(D) Random mating

2013

27. The concept that 'transmission of genes' governs population genetics while 'transmission of genotypes' dictates individual genetics implies that:
(A) Meiosis breaks parental genotypes into alleles.
(B) Mitosis ensures offspring inherit complete parental genomes.
(C) Populations maintain fixed genotypes regardless of systems.
(D) Allele frequencies are irrelevant at the population level.

2010

28. Select the correct sequence of steps for calculating effective population size (N_e) under fluctuating population sizes over generations:
(A) Determine sizes per generation → Calculate

NODIA

harmonic mean of sizes → Derive N_e
(B) Determine sizes per generation → Calculate arithmetic mean of sizes → Derive N_e
(C) Derive N_e directly from the final generation census → Calculate harmonic mean
(D) Calculate standard deviation of sizes → Apply to base generation → Derive N_e

2003

29. If a population experiences a severe bottleneck, what is the immediate effect on the rate of inbreeding (ΔF) and genetic drift?
(A) Both decrease
(B) ΔF increases, but drift decreases
(C) ΔF decreases, but drift increases
(D) Both increase

2007

30. In the $a, d, -a$ scale for a metric character, the midpoint between the two homozygote values is designated as:
(A) a
(B) d
(C) 0
(D) $-a$

2012

31. The average effect of a gene depends on:
(A) Only the genotypic value of the homozygotes.
(B) Population gene frequency and genotypic values.
(C) The permanent environmental effect components.
(D) The mutation rate observed at the specific locus.

2008

32. In a single-locus two-allele model, if 'p' and 'q' are allele frequencies, the average effect of gene substitution (α) is defined algebraically as:
(A) $a - d(q - p)$
(B) $a + d(p - q)$
(C) $d + a(q - p)$
(D) $a + d(q - p)$

2003

33. Arrange the following genetic measures in order from the most inclusive of genetic effects to the least inclusive (focusing solely on additive effects):
(A) Genotypic Value, Breeding Value, Average Effect of a Gene
(B) Breeding Value, Genotypic Value, Average Effect of a Gene
(C) Average Effect of a Gene, Breeding Value, Genotypic Value
(D) Genotypic Value, Average Effect of a Gene, Breeding Value

2008

34. Epistatic deviation (I) arises due to:
(A) Dominance interactions at a single locus.
(B) Environmental variations affecting genotypes.
(C) Inter-allelic interactions across different loci.
(D) Maternal effects exerted on the offspring.

2023

35. The term $V_{\{GE\}}$ in phenotypic variance partitioning stands for:
(A) Genotype-Environment Interaction Variance.
(B) General Environmental Variance components.
(C) Genomic Epistatic Variance interactions.
(D) Genetic-Epigenetic Variance deviations.

2010

36. Which component of genetic variance is strictly defined as the variance of breeding values?
(A) V_D
(B) V_I
(C) V_G
(D) V_A

2022

37. Which of the following is considered a temporary environmental effect ($V_{\{Et\}}$) rather than a permanent one ($V_{\{Ep\}}$)?
(A) Loss of a teat.
(B) Minor climatic fluctuation during one season.
(C) Chronic localized infection.
(D) Severe stunting during early calfhood.

2007

38. Given the Assertion (A) and Reason (R):
Assertion (A): The covariance between full-sibs is generally larger than the covariance between half-sibs.
Reason (R): Full-sibs share a quarter of the dominance variance (V_D) in addition to half of the additive variance (V_A), whereas half-sibs share only a quarter of V_A.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

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2021

39. Broad sense heritability (H^2) is most useful for traits that will be propagated via:
(A) Random mating
(B) Outcrossing
(C) Sire-evaluation breeding programs
(D) Clonal or vegetative propagation

2021

40. In estimating heritability by paternal half-sib correlation, the correlation (t) is equal to:
(A) $\frac{1}{4}h^2$
(B) h^2
(C) $\frac{1}{2}h^2$
(D) $2h^2$

2023

41. When conducting intra-sire regression of offspring on dam to estimate heritability, the major advantage is that it:
(A) Eliminates the sire component of variance.
(B) Removes bias from non-random mating of sires.
(C) Eliminates environmental correlation in sires.
(D) Doubles the estimated heritability automatically.

2021

42. Repeatability (r) reflects the correlation between:
(A) Repeated records of different traits in the same animal
(B) Repeated records of the same trait on the same individual
(C) Single records of a trait on different individuals
(D) Single records of different traits on different individuals

2005

43. Match the parameter in List I with its primary application in List II.
List I: (Parameter)
P. Heritability (narrow sense)
Q. Repeatability
R. Genetic Correlation
S. Inbreeding Coefficient
List II: (Application)
1. Predicting correlated response to selection
2. Predicting breeding value from own phenotype
3. Estimating probability of identical-by-descent alleles
4. Predicting future records of an individual (MPPA)
(A) P-2, Q-4, R-1, S-3
(B) P-1, Q-2, R-3, S-4
(C) P-3, Q-1, R-4, S-2
(D) P-4, Q-3, R-2, S-1

2006

44. The MPPA is calculated using the formula: Population Mean + $\frac{nr}{1+(n-1)r}$ multiplied by:
(A) (Individual's best record - Population Mean)
(B) Population Variance
(C) (Individual's average - Population Mean)
(D) Repeatability squared

2015

45. A negative genetic correlation between milk yield and fat percentage implies that:
(A) Traits are controlled by unlinked genes.
(B) Environmental factors lower both traits.
(C) The heritability of both traits is zero.
(D) Selecting for milk yield decreases fat percentage.

2025

46. Analysis of Covariance (ANCOVA) estimates genetic correlation by analyzing:
(A) Variance of a single track.
(B) Only the environmental variances.
(C) Covariances between traits on related individuals.
(D) Epistatic deviations exclusively.

2009

47. Assortative mating affects the precision of parameter estimates by primarily:
(A) Decreasing additive genetic variance.
(B) Inflating genetic variance and relative resemblance.
(C) Increasing the frequency of heterozygotes.
(D) Randomizing environmental effects.

2021

48. Identify the INCORRECT combination of statements regarding genetic diversity assessment:
I. Heterozygosity measures the proportion of heterozygous individuals at a locus.
II. Expected heterozygosity under Hardy-Weinberg is calculated as $1 - \sum p_i^2$.
III. Allelic richness solely depends on the mutation rate and ignores sample size.
Which of the above statement(s) is/are INCORRECT?
(A) I and II

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(D) Convert additive variance into epistatic variance

2024

93. Match the heritability estimation method in List I with its key characteristic in List II.
List I: (Method)
P. Parent-Offspring Regression
Q. Paternal Half-Sib Correlation
R. Intra-sire Regression of Offspring on Dam
S. Mid-Parent Offspring Regression
List II: (Characteristic)
1. Eliminates environmental covariance shared by sire and offspring
2. Standard error of h^2 is often lowest with balanced extensive data
3. Regression coefficient directly estimates h^2
4. Coefficient needs to be multiplied by 2 to estimate h^2
(A) P-4, Q-2, R-1, S-3
(B) P-3, Q-1, R-4, S-2
(C) P-1, Q-4, R-2, S-3
(D) P-2, Q-3, R-1, S-4

2022

94. If repeatability is 0.4 and heritability is 0.25, the permanent environmental variance as a proportion of phenotypic variance is:
(A) 0.65
(B) 0.15
(C) 0.40
(D) 0.25

2003

95. The MPPA is most practically applied in livestock management for:
(A) Estimating mutation rates.
(B) Determining the sex ratio.
(C) Culling females based on early lactations.
(D) Selecting carcass traits at slaughter.

2007

96. Phenotypic correlation encompasses both:
(A) Dominance and epistatic correlations
(B) Genetic and environmental correlations
(C) Additive and mutational correlations
(D) Drift and inbreeding correlations

2024

97. If a genetic correlation between two traits is due to linkage rather than pleiotropy, what is expected over many generations of random mating?
(A) The correlation will permanently increase.
(B) The correlation will remain constant.
(C) Pleiotropy will eventually replace linkage.
(D) Correlation decays due to recombination.

2018

98. Select the correct sequence for obtaining the sire component of variance in an ANOVA:
(A) Calculate Total Mean Square → Subtract Error Mean Square → Divide by k
(B) Calculate Between Sires Mean Square → Subtract Error Mean Square → Divide by k
(C) Calculate Error Mean Square → Add Between Sires Mean Square → Divide by k
(D) Divide Between Sires Sum of Squares by Total Sum of Squares → Multiply by k

2003

99. Allelic richness in conservation genetics is particularly sensitive to:
(A) Temporary environmental fluctuations
(B) Assortative mating within large herds
(C) Population bottlenecks
(D) Age of the individuals

2018

100. In Wright's statistics, the total inbreeding coefficient of an individual ($F_{\{IT\}}$) is related to $F_{\{IS\}}$ and $F_{\{ST\}}$ by the formula:
(A) $(1 - F_{\{IT\}}) = (1 - F_{\{IS\}})(1 - F_{\{ST\}})$
(B) $F_{\{IT\}} = F_{\{IS\}} + F_{\{ST\}}$
(C) $F_{IT} = F_{IS} \times F_{ST}$
(D) $(1 - F_{\{ST\}}) = (1 - F_{\{IT\}})(1 - F_{\{IS\}})$

NODIA

2013

101. Admixture analysis using programs like STRUCTURE relies on:
(A) Assuming all individuals are in one population.
(B) Measuring permanent environmental marks.
(C) Assessing single-locus dominance deviations.
(D) Multi-locus genotype data clustering.

2015

102. A 'breed signature' is critically useful for:
(A) Determining efficiency precisely.
(B) Authenticating purity and origin of products.
(C) Measuring temporary deviations in milk yield.
(D) Calculating standard errors of ANOVA.

2002

103. Arrange the following steps to map a quantitative trait locus (QTL) using breed signatures:
(A) Identify breed specific markers → Genotype segregating populations → Conduct association analysis → Locate QTL
(B) Conduct association analysis → Locate

2010

59. An individual's Breeding Value (A) is defined mathematically as the sum of:
(A) Average effects of the genes it carries
(B) Dominance deviations of all its genes
(C) Epistatic deviations of all its genes
(D) Permanent environmental effects

2019

60. Dominance deviation (D) occurs because:
(A) Heterozygote value is not at the midpoint.
(B) Alleles at different loci interact.
(C) Environment permanently alters phenotype.
(D) Genetic drift fixes one allele.

2007

61. In variance partitioning, the total phenotypic variance cannot be less than:
(A) V_A
(B) $V_P + V_E$
(C) Zero
(D) $V_G \times V_E$

2017

62. Which variance component is heavily utilized by breeders to improve quantitative traits via mass selection?
(A) Epistatic variance (V_I)
(B) Dominance variance (V_D)
(C) Additive genetic variance (V_A)
(D) Temporary environmental variance ($V_{\{Et\}}$)

2022

63. Given the Assertion (A) and Reason (R):
Assertion (A): Permanent environmental variance ($V_{\{Ep\}}$) contributes to the repeatability of a trait.
Reason (R): $V_{\{Ep\}}$ affects the individual's performance identically across all its repeated records.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2010

64. The additive genetic coefficient of relationship between half-sibs is:
(A) $\frac{1}{2}$
(B) $\frac{1}{4}$
(C) $\frac{1}{8}$
(D) 1

2011

65. The biological significance of narrow sense herizability is that it indicates the proportion of phenotypic variation that is:
(A) Transmissible from parents to offspring.
(B) Fixed by random genetic drift events.
(C) Due to temporary environmental changes.
(D) Caused strictly by dominance effects.

2019

66. In the ANOVA for paternal half-sibs, the term k in the expected mean square represents:
(A) The number of sires
(B) The total population size
(C) The number of progeny per sire
(D) The heritability estimate

2017

67. To correct for bias due to assortative mating in parent-offspring regression estimates of herizability, one should:
(A) Use intra-sire regression of offspring on dam.
(B) Ignore the dam's phenotype entirely.
(C) Multiply the regression coefficient by 4.
(D) Subtract the mean environmental variance.

2013

68. Match the parameter in List I with its theoretical range in List II.
List I: (Parameter)
P. Heritability (h^2)
Q. Repeatability (r)
R. Genetic Correlation (r_g)
S. Inbreeding Coefficient (F)
List II: (Range)
1. -1.0 to +1.0
2. 0.0 to 1.0 (proportion of identical-by-descent alleles)
3. 0.0 to 1.0 (proportion of phenotypic variance)
4. 0.0 to 1.0 (correlation between repeated records)
(A) P-3, Q-4, R-1, S-2
(B) P-2, Q-3, R-4, S-1
(C) P-1, Q-2, R-3, S-4
(D) P-4, Q-1, R-2, S-3

2014

69. High repeatability in a trait implies that:
(A) First records are poor indicators of performance.
(B) Culling on early records will be effective.
(C) Environmental variance dominates the trait.
(D) Heritability must strictly equal 1.0.

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(B) II and III
(C) Only I
(D) Only III

2015

49. In Wright's F-statistics, $F_{\{IS\}}$ represents:
(A) Inbreeding of individuals relative to their subpopulation
(B) Inbreeding of individuals relative to the total population
(C) Inbreeding of subpopulations relative to the total population
(D) Total genetic variance

2014

50. Estimation of migration rates and gene flow helps breeders understand:
(A) The exact breeding value of a single sire.
(B) The permanent environmental effects on herds.
(C) The extent of isolation or admixture in populations.
(D) Dominance deviation within an individual.

2024

51. The use of SNP chips in identifying a 'breed signature' is based on the principle of:
(A) Finding unique frequencies or haplotypes.
(B) Detecting identical temporary variations.
(C) Measuring the total cellular DNA content.
(D) Identifying non-heritable epigenetic marks.

2011

52. Hardy-Weinberg equilibrium frequencies for a two-allele system (p and q) are represented by:
(A) $p + 2pq + q = 1$
(B) $p^2 + pq + q^2 = 1$
(C) $2p + 2pq + 2q = 1$
(D) $p^2 + 2pq + q^2 = 1$

2010

53. Evaluate the following statements about individual vs population genetic architecture:
I. Populations can maintain stable allele frequencies over time.
II. Individual genotypes are perfectly replicated in offspring through sexual reproduction.
III. Transmission of genotypes is characteristic of asexual reproduction or cloning.
IV. Evolutionary changes occur at the population level, not within a single organism's lifespan.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) I, III and IV
(C) II, III and IV
(D) I, II and III

2025

54. If a population consists of 10 breeding males and 90 breeding females, the effective population size (N_e) is approximately:
(A) 100
(B) 50
(C) 36
(D) 10

2009

55. Genetic drift is most pronounced in populations with:
(A) High effective population size (N_e)
(B) Extremely high mutation rates
(C) Strict negative assortative mating
(D) Low effective population size (N_e)

2006

56. The genotypic value scale assigns the value of $-a$ to which class in a single-locus two-allele trait?
(A) Favorable homozygote.
(B) Unfavorable homozygote.
(C) Heterozygote class.
(D) Mid-parent point.

2014

57. The average effect of a gene is a property of:
(A) The individual allele only.
(B) Population and gene frequency.
(C) Epistatic interactions exclusively.
(D) The temporary environment.

2015

58. Identify the correct combination of statements concerning the average effect of gene substitution (α):
I. It is equivalent to the difference between the average effects of the two alleles.
II. It dictates the response to directional selection.
III. It assumes epistasis is the only source of variance.
IV. It remains constant regardless of allele frequency changes.
V. It is a linear function of the additive genetic value.
Which of the above statements are correct?
(A) I, II and V
(B) II, III and IV
(C) I, III and V
(D) II, IV and V

NODIA

(A) Increased heterozygosity
(B) Hardy-Weinberg equilibrium
(C) Increased additive variance
(D) Fixation or loss of alleles

2011

82. For a metric trait, the population mean depends upon:
(A) Allele frequencies and genotypic values.
(B) Only the genotypic values $(a, d, -a)$.
(C) Only the allele frequencies.
(D) The temporary environment exclusively.

2017

83. Identify the INCORRECT combination of statements regarding the average effect of a gene:
I. It is independent of allele frequencies in the population.
II. It defines the regression of genotypic value on the number of favorable alleles.
III. It applies strictly to clonal populations.
IV. It determines the breeding value.
V. It accounts for all non-additive effects perfectly.
Which of the above statement(s) is/are INCORRECT?
(A) I, III and V
(B) II, IV and V
(C) I, II and III
(D) III, IV and V

2003

84. The average effect of gene substitution (α) is crucial for predicting:
(A) Response to selection
(B) Inbreeding depression limits
(C) Expected specific combining ability
(D) Temporary environmental fluctuations

2004

85. Breeding value (A) represents:
(A) The phenotype of an individual
(B) The interaction between dominance and environment
(C) The temporary environmental advantage of a dam
(D) Value judged by the mean of its progeny.

2015

86. Which deviation describes the non-linear interaction between alleles at the same locus?
(A) Epistatic deviation
(B) Dominance deviation
(C) Breeding value deviation
(D) Environmental deviation

2001

87. The equation $V_P = V_G + V_E + V_{\{GE\}}$ assumes that:
(A) Genotype and environment are correlated.
(B) Variance components are multiplicative.
(C) Genotypic values and deviations are additive.
(D) Heritability is always 1.0.

2016

88. Given the Assertion (A) and Reason (R):
Assertion (A): Narrow-sense heritability is the ratio of additive genetic variance to phenotypic variance.
Reason (R): Additive genetic variance is the only component of genetic variance transmitted predictably to progeny.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2008

89. Permanent environmental variance ($V_{\{Ep\}}$) differs from temporary environmental variance ($V_{\{Et\}}$) in that $V_{\{Ep\}}$:
(A) Influences all repeated measurements.
(B) Affects only a single record.
(C) Is inherited by the offspring.
(D) Constitutes dominance variance.

2009

90. The covariance between parent and offspring is mathematically expected to be:
(A) V_A
(B) $\frac{1}{2} V_A$
(C) $\frac{1}{4} V_A + \frac{1}{4} V_D$
(D) $\frac{1}{2} V_A + \frac{1}{4} V_D$

2025

91. A broad sense heritability near 1.0 implies that:
(A) The trait cannot be selected for.
(B) Most variation is due to genetic differences.
(C) The environment is highly variable.
(D) The additive variance is zero.

2001

92. In estimating heritability from half-sib data, the presence of maternal effects may:
(A) Inflate the estimate if dam components are used
(B) Decrease the estimate of h^2
(C) Have no effect on the estimate

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2015

70. When utilizing MPPA, as the number of records (n) increases, the weighting factor $\frac{nr}{1+(n-1)r}$ approaches:
(A) 0
(B) r
(C) 1
(D) infinity

2001

71. Pleiotropy refers to:
(A) Multiple genes affecting a single trait.
(B) Linkage of multiple genes on one chromosome.
(C) Interaction between genotype and environment.
(D) A single gene affecting multiple traits.

2010

72. In calculating genetic correlation using ANCOVA, the formula is:
(A) $\frac{\text{cov}_G(X,Y)}{\sqrt{var_G(X) \times var_G(Y)}}$
(B) $\frac{\text{cov}(X,Y)}{var(X)+var(Y)}$
(C) $\frac{var_G(X)}{\text{cov}_G(X,Y)}$
(D) $\text{cov}_G(X,Y) \times var_G(X)$

2012

73. Identify the correct combination of factors that decrease the precision (increase standard error) of heritability estimates:
I. Small sample size
II. Very large number of progeny per sire
III. Unbalanced data structure
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I, II and III

2019

74. Which diversity metric utilizes allele frequencies to calculate the probability that two alleles chosen at random from a population are different?
(A) Wright's $F_{\{IT\}}$
(B) Expected Heterozygosity (H_e)
(C) Narrow-sense heritability
(D) Average effect of gene substitution

2014

75. In population structure analysis, an $F_{\{ST\}}$ value of 0.25 among breeds indicates:
(A) Complete panmixia across all breeds.
(B) Significant genetic differentiation in breeds.
(C) No genetic differentiation.
(D) Complete fixation of identical alleles.

2024

76. Introgression or genetic admixture in native livestock populations is often detected using:
(A) Analysis using genomic marker panels.
(B) Pedigree depth analysis only.
(C) Evaluation of permanent environments.
(D) Heritability of body weight.

NODIA

2004

77. Conservation genetics prioritizes breed signatures because they:
(A) Ensure the breed is phenotypically uniform.
(B) Indicate the exact economic value.
(C) Define evolutionary heritage and identity.
(D) Eliminate all recessive alleles.

2019

78. Select the correct sequence of steps to test a population for Hardy-Weinberg equilibrium:
(A) Calculate observed genotype counts → Estimate allele frequencies → Calculate expected counts → Perform Chi-square test
(B) Perform Chi-square test → Estimate allele frequencies → Calculate expected counts → Observe genotypes
(C) Estimate allele frequencies → Perform Chi-square test → Calculate observed genotype counts → Calculate expected counts
(D) Calculate expected counts → Perform Chi-square test → Estimate allele frequencies → Calculate observed counts

2014

79. The transmission of genes rather than genotypes from generation to generation forms the foundation of:
(A) Clonal expansion
(B) Epigenetic inheritance
(C) Mendelian population genetics
(D) Permanent environmental variance

2008

80. Unequal sex ratios in breeding herds dramatically reduce N_e because:
(A) Males and females mutate at different rates.
(B) The rarer sex contributes half the genetic material.
(C) Females always possess more genetic variance.
(D) Epistatic interactions are sex-linked.

2004

81. The continuous action of genetic drift in a finite, closed population eventually leads to:

QTL → Identify breed specific markers → Genotype segregating populations
(C) Genotype segregating populations → Identify breed specific markers → Locate QTL → Conduct association analysis
(D) Locate QTL → Genotype segregating populations → Conduct association analysis → Identify breed specific markers

2012

104. The Hardy-Weinberg law states that allele and genotype frequencies remain constant given certain assumptions. Which assumption implies no differential reproductive success?
(A) No mutation.
(B) Random mating.
(C) Infinite population size.
(D) Absence of natural or artificial selection.

2006

105. Transmission of genes implies that individuals:
(A) Act merely as temporary holding vehicles for alleles.
(B) Pass down their exact genotype intact to the next generation.
(C) Can alter their genetic code through use and disuse.
(D) Reproduce strictly by clonal division.

2006

106. The effective population size (N_e) calculation for a population with 1 male and 100 females is roughly:
(A) 4
(B) 50
(C) 100
(D) 101

2025

107. An increase in the rate of inbreeding (ΔF) directly corresponds to:
(A) A decrease in heterozygosity
(B) An increase in effective population size
(C) A decrease in fixed alleles
(D) An increase in population census size

2015

108. Given the Assertion (A) and Reason (R):
Assertion (A): The value a on the metric character scale represents the genotypic value of one homozygote.
Reason (R): The metric scale is defined such that the midpoint between the two homozygotes is zero.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2018

109. The mathematical formulation of the average effect of a gene focuses on:
(A) Non-additive interactions only.
(B) Inbreeding depression limits.
(C) Expected differences from random matings.
(D) Environmental variance components.

2018

110. In quantitative genetics, α (average effect of gene substitution) becomes zero when:
(A) The population is fixed for an allele
(B) The heterozygote is exactly intermediate
(C) Genetic variance is maximum
(D) The population is at a stable equilibrium under overdominance

2010

111. The sum of the average effects of genes carried by an individual is strictly equivalent to its:
(A) Phenotypic value
(B) Epistatic value
(C) Breeding value
(D) Dominance value

2003

112. Interaction deviation (I) is another term for:
(A) Genotype-environment interaction
(B) Epistatic deviation
(C) Dominance deviation
(D) Additive deviation

2006

113. Match the variance component in List I with its description in List II.
List I: (Component)
P. V_A
Q. V_D
R. V_I
S. $V_{\{GE\}}$
List II: (Description)
1. Non-linear interaction between loci
2. Chief cause of resemblance between relatives
3. Differential response of genotypes across environments
4. Interaction between alleles at a single locus
(A) P-2, Q-4, R-1, S-3
(B) P-4, Q-2, R-3, S-1
(C) P-1, Q-3, R-4, S-2
(D) P-3, Q-1, R-2, S-4

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2010

114. If a genotype performs exceptionally well in a temperate climate but very poorly in a tropical climate compared to other genotypes, this is an example of:
(A) Genotype-environment interaction ($V_{\{GE\}}$).
(B) Dominance variance component.
(C) Epistatic variance deviation.
(D) Temporary environmental variance.

2018

115. Sub-partitioning of genetic variance separates V_G into:
(A) V_E, $V_{\{Et\}}$, $V_{\{Ep\}}$
(B) V_P, V_E, $V_{\{GE\}}$
(C) V_A, V_D, V_I
(D) $V_{\{PHSC\}} + V_{\{ANOVA\}} + V_{\{REML\}}$

2004

116. A permanent environmental effect ($V_{\{Ep\}}$) differs from a genetic effect because:
(A) It is not transmitted to progeny.
(B) It influences all repeated records.
(C) It affects the phenotype.
(D) It causes variation in the herd.

2007

117. The genetic covariance between a parent and its offspring is determined by:
(A) Epistatic variance only
(B) Dominance variance only
(C) Temporary environmental variance
(D) $\frac{1}{2}$ of Additive genetic variance

2019

118. Which statement best defines broad-sense herizability?
(A) Phenotypic variance due to additive genetic variance.
(B) Phenotypic variance due to total genetic variance.
(C) Ratio of dominance to total genetic variance.
(D) Ratio of temporary to permanent environmental variance.

2006

119. In half-sib ANOVA estimation of h^2, the formula used is:
(A) $\frac{2\sigma_s^2}{\sigma_s^2 + \sigma_w^2}$
(B) $\frac{\sigma_s^2}{\sigma_w^2}$
(C) $\frac{4\sigma_s^2}{\sigma_s^2 + \sigma_w^2}$
(D) $\frac{\sigma_w^2}{\sigma_s^2 + \sigma_w^2}$

2010

120. A negative estimate of herizability from sire components is biologically impossible but statistically possible due to:
(A) High genetic variance
(B) Assortative mating
(C) Pleiotropy
(D) Sampling error or extensive environmental variation

2021

121. The upper limit of broad-sense herizability is set by:
(A) Repeatability
(B) Breeding value
(C) Genetic drift
(D) Dominance deviation

2022

122. If the MPPA is computed for a cow, a trait with very low repeatability will cause the MPPA to:
(A) Heavily rely on the cow's records.
(B) Shrink closer to the population mean.
(C) Disregard the population mean.
(D) Approach an infinite value.

2004

123. A genetic correlation indicates that:
(A) Environments for both traits are identical.
(B) Traits share genetic control or linkage.
(C) Phenotypic variance equals genotypic variance.
(D) Mutation rate is synchronized across loci.

2021

124. When conducting parent-offspring regression to estimate heritability, a smaller standard error is achieved primarily by:
(A) Increasing the number of parent-offspring pairs
(B) Decreasing the number of parent-offspring pairs
(C) Using traits with very low heritability
(D) Restricting the environmental variance

NODIA

2016

125. Assortative mating affects genetic parameter estimation by:
(A) Decreasing homozgosity.
(B) Eliminating genetic drift.
(C) Inflating additive genetic variance.
(D) Decreasing temporary variance.

2025

126. Heterozygosity serves as an essential metric because it directly indicates:

(A) The exact number of chromosomes.
(B) The permanent environmental variation.
(C) The average age of the population.
(D) Genetic diversity within a population.

2010

127. Which F-statistic measures the reduction in heterozygosity in a subpopulation due to non-random mating within that subpopulation?
(A) $F_{\{ST\}}$
(B) $F_{\{IT\}}$
(C) $F_{\{IS\}}$
(D) $F_{\{XY\}}$

2004

128. Gene flow between livestock populations acts to:
(A) Increase genetic divergence among them.
(B) Reduce genetic differentiation among them.
(C) Fix different alleles in each population.
(D) Eliminate all additive genetic variance.

2002

129. Microsatellite markers are highly suitable for detecting genetic admixture because they:
(A) Code for major morphological traits.
(B) Exhibit zero mutation rates.
(C) Reflect permanent environment differences.
(D) Are highly polymorphic at every locus.

2022

130. A breed signature established via a dense SNP chip can be used for:
(A) Genomic selection and purebred status.
(B) Detecting identical temporary variations.
(C) Measuring the total cellular DNA content.
(D) Identifying non-heritable epigenetic marks.

2003

131. In a randomly mating population, if the frequency of allele 'A' is 0.6, the expected frequency of heterozygotes 'Aa' is:
(A) 0.36
(B) 0.16
(C) 0.48
(D) 0.24

2003

132. The distinction between the transmission of genes and genotypes underscores the mechanism of:
(A) Independent assortment and recombination.
(B) Mitotic segregation processes.
(C) Asexual reproduction methods.
(D) Environmental induction of mutations.

NODIA

2005

133. When population sizes fluctuate over generations, N_e is dominated by:
(A) The largest population size
(B) The arithmetic mean size
(C) The final population size
(D) The smallest population size (bottleneck)

2008

134. Genetic drift causes allele frequencies to:
(A) Move towards 0.5 deterministically
(B) Remain perfectly constant
(C) Shift strictly via selection pressures
(D) Fluctuate randomly across generations

2018

135. On the genotypic value scale $a, d, -a$, the degree of dominance is given by:
(A) $\frac{a}{d}$
(B) $\frac{d}{a}$
(C) $a - d$
(D) $d - a$

2018

136. The average effect of a gene is expressed as a deviation from:
(A) The genotypic value of the heterozygote
(B) The mean phenotypic value of the offspring
(C) Zero
(D) The population mean

2002

137. Which term represents the effect of replacing one allele with another in a randomly mating population?
(A) Average effect of gene substitution (α).
(B) Epistatic substitution component.
(C) Dominance deviation deviation.
(D) Inbreeding coefficient measure.

2013

138. The breeding value of an offspring is theoretically expected to be:
(A) The sum of the parents' breeding values
(B) The geometric mean of the parents' breeding values
(C) The difference of the parents' breeding values
(D) The arithmetic mean of the parents' breeding values

(C) Alleles at the same locus
(D) The genotype and the environment

2018

190. Phenotypic variance (V_P) is calculated by adding V_G, V_E, and $V_{\{GE\}}$. When is $V_{\{GE\}}$ typically considered negligible?
(A) In uniform, controlled environments.
(B) When heritability is zero.
(C) When mutations are frequent.
(D) Between wildly different climate zones.

2008

191. Sub-partitioning of genetic variance shows that the resemblance between a clone and its parent is governed by:
(A) V_A only
(B) V_A and V_D only
(C) Total V_G ($V_A + V_D + V_I$)
(D) V_E only

2003

192. Which variance component causes an animal's repeated records (e.g., successive lactations) to differ from one another?
(A) V_A
(B) $V_{\{Et\}}$ (Temporary environmental variance)
(C) V_D
(D) Within-individual temporary effects.

2008

193. The genetic covariance between an uncle and nephew is mathematically equivalent to the covariance between:
(A) Full-sibs
(B) Parent and offspring
(C) Half-sibs
(D) Identical twins

2013

194. A trait with a narrow-sense heritability of 0.05 is generally improved most effectively by:
(A) Family selection or progeny testing
(B) Mass selection
(C) Random mating
(D) Eliminating all permanent environmental variance

2019

195. In the ANOVA for estimating heritability from half-sibs, the "Between Sires" variance component (σ_s^2) estimates:
(A) $\frac{1}{2} V_A$
(B) V_A
(C) $\frac{1}{4} V_A$
(D) V_D

2010

196. When estimating heritability via parent-offspring regression, why is the regression coefficient on a single parent multiplied by 2?
(A) Because parents are diploid organisms.
(B) Parent transmits only half additive variance.
(C) Because it accounts for dominance effects.
(D) Environmental variance is doubled.

2001

197. Repeatability analysis using ANOVA partitions phenotypic variance into:
(A) Sire variance and dam variance
(B) Additive variance and dominance variance
(C) Epistatic variance and mutational variance
(D) Between-individual variance and within-individual variance

2013

198. The primary purpose of calculating Most Probable Producing Ability (MPPA) is to:
(A) Predict the genetic worth of offspring.
(B) Estimate the narrow-sense heritability.
(C) Compare animals with different record counts.
(D) Determine the Hardy-Weinberg equilibrium.

2011

199. Linkage causes genetic correlation between traits when:
(A) A gene affects multiple traits simultaneously.
(B) Traits are strictly controlled by environment.
(C) Genes are close on the same chromosome.
(D) Assortative mating is absent.

2009

200. ANCOVA on paternal half-sib data estimates genetic correlation by analyzing the:
(A) Ratio of temporary to permanent environmental variance.
(B) Sum total of all epistatic genetic interactions.
(C) Differences in allele frequencies observed across breeds.
(D) Sire variances and sire covariance.

2025

201. Which condition introduces significant bias in the estimation of heritability by parent-offspring regression?
(A) Common environment shared by dam and offspring.
(B) Utilizing very large population sample sizes.

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(A) The number of loci
(B) The degree of dominance
(C) The square root of the sample size
(D) The trait's mutation rate

2021

152. Polymorphism Information Content (PIC) calculates marker usefulness by considering:
(A) Allele number and their frequencies.
(B) Chromosomal physical location.
(C) Permanent environmental variance.
(D) The non-additive genetic variance.

2008

153. Wright's F-statistics ($F_{\{IS\}}$, $F_{\{IT\}}$, $F_{\{ST\}}$) primarily describe:
(A) Population structure H-W deviations.
(B) Phenotypic variation components.
(C) Heritability partitions.
(D) Linkage disequilibrium between genes.

2003

154. A high estimated migration rate (gene flow) into a local livestock population suggests:
(A) Rapid speciation.
(B) Loss of architecture due to admixture.
(C) Fixation of all local alleles.
(D) Complete isolation.

2007

155. Breed signatures detected by SNP chips are invaluable for:
(A) Altering the coat color permanently.
(B) Identifying cryptic admixture or fraud.
(C) Measuring effects on carcass weight.
(D) Calculating the phenotypic mean.

2025

156. The Hardy-Weinberg principle is a null model because it:
(A) Describes a population where no evolutionary forces are acting
(B) Represents the worst possible breeding scenario
(C) Requires a completely homozygous population
(D) Eliminates random mating

2008

157. Population genetic architecture is typically characterized by:
(A) Individual breeding values
(B) Exact pedigree records of every animal
(C) Allele and genotype frequencies
(D) Dominance deviations of single animals

2024

158. If the sex ratio in a breeding population is highly skewed towards one sex (e.g., heavily managed dairy cattle), the effective population size is:
(A) Close to the total census size.
(B) Dictated largely by the number of females.
(C) Completely unaffected by sex ratio changes.
(D) Dictated by the number of the rarer sex.

2016

2011

159. The relationship between rate of inbreeding (ΔF) and effective population size (N_e) means that to minimize inbreeding, breeders must:
(A) Minimize N_e
(B) Select aggressively for a single sire
(C) Maximize N_e
(D) Increase temporary environmental variance

2019

160. A metric character displays partial dominance when:
(A) $a = d$
(B) $d > a$
(C) $0 < d < a$
(D) $d = 0$

2013

161. The average effect of a gene is a concept rooted in:
(A) Single individual deterministic effects.
(B) Controlled inbreeding experiments only.
(C) Clonal reproduction models.
(D) Random mating population mean contexts.

NODIA

2003

162. The average effect of gene substitution (α) equals the average effect of the favorable allele minus:
(A) The average effect of the unfavorable allele.
(B) The dominance deviation component.
(C) The population mean value.
(D) The epistatic deviation.

2022

163. A sire's expected progeny difference (EPD) or predicted transmitting ability (PTA) is theoretically equal to:
(A) His breeding value
(B) His full genotypic value
(C) One-half of his breeding value
(D) One-quarter of his dominance deviation

(A) Determines the animal's interaction with the environment.
(B) Is purely due to dominance variance effects.
(C) Arises from epistatic interactions between alleles.
(D) Can be transmitted to progeny.

2007

214. Epistatic/interaction deviation (I) becomes zero when:
(A) The environment perfectly controls the phenotype
(B) Genes at different loci act perfectly independently (additively) across loci
(C) Dominance is complete at all loci
(D) Allele frequencies are 0.5

2005

215. The partitioning of phenotypic variance into V_G and V_E is a fundamental premise. What does a large V_E indicate about a trait?
(A) It is highly heritable.
(B) It has no genetic basis whatsoever.
(C) Strong influence by non-genetic factors.
(D) The population is strictly inbred.

2008

216. Genetic variance is sub-partitioned to isolate V_A because V_A is:
(A) The variance of epistatic interactions.
(B) Variance altered by the environment.
(C) Variance fixed by temporary fluctuations.
(D) Variance of breeding values.

2017

217. A temporary environmental variance ($V_{\{Et\}}$) affects:
(A) Only the specific record taken at that time
(B) The permanent anatomy of the animal
(C) Every record of the animal throughout its life equally
(D) The genetic transmission to the progeny

2002

218. The expected genetic covariance between parent and offspring is strictly limited to:
(A) $\frac{1}{2} V_A$ and $\frac{1}{4} V_D$
(B) $\frac{1}{2} V_A$ and no V_D or V_I.
(C) $\frac{1}{4} V_A$ and $\frac{1}{2} V_D$
(D) V_A and V_D

2019

219. Narrow-sense herizability (h^2) is always:
(A) Greater than broad-sense herizability
(B) Less than or equal to broad-sense herizability (H^2)
(C) Greater than repeatability
(D) Equal to the mutation rate

2005

220. The Expectation of Mean Squares (EMS) in paternal half-sib ANOVA provides the theoretical basis for equating the sire variance component to:
(A) $\frac{1}{4} V_A$
(B) V_P
(C) $\frac{1}{2} V_A$
(D) V_E

2018

221. Parent-offspring regression is advantageous over paternal half-sib correlation for estimating h^2 because it:
(A) Eliminates all environmental variance entirely
(B) Requires much smaller sample sizes
(C) Is generally less subject to confounding by dominance variance
(D) Is perfectly unaffected by assortative mating

2017

222. Repeatability (r) represents the correlation between repeated records on the same individual. It is formulated as:
(A) $\frac{V_G + V_{Ep}}{V_P}$
(B) $\frac{V_G}{V_P + V_{Ep}}$
(C) $\frac{V_{Et}}{V_P}$
(D) $\frac{V_A}{V_G}$

2008

223. Calculating MPPA is most critical when selecting:
(A) Sires based on progeny performance.
(B) Slaughter animals for meat quality.
(C) Dams based on record counts.
(D) Clones for a controlled environment.

2025

224. A genetic correlation of -0.80 between trait X and trait Y implies that:

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(A) One allele is completely fixed
(B) Migration is zero
(C) Mutation rate is zero
(D) Allele frequencies are perfectly equal

2010

178. $F_{\{ST\}}$ values range from 0 to 1. A value of 0 indicates:
(A) Complete differentiation between subpopulations
(B) Complete lack of genetic differentiation between subpopulations
(C) Perfect inbreeding within the subpopulation
(D) Complete fixation of a single allele

2002

179. Detecting genetic admixture involves evaluating an animal's genome to find:
(A) The total number of genes it expresses.
(B) Its breeding value for milk yield traits.
(C) Proportions from ancestral populations.
(D) Temporary environmental effects.

2006

180. A major application of breed signatures in livestock conservation is:
(A) Selecting exclusively for high production.
(B) Prioritizing funding for native herds.
(C) Increasing the temporary variance.
(D) Genomic definition of purebreds.

2022

181. Under the Hardy-Weinberg law, if genotype frequencies in a population are altered by a single generation of non-random mating, how many generations of random mating are required to restore equilibrium for an autosomal locus?
(A) Ten generations
(B) One generation
(C) Five generations
(D) It can never be restored

2001

182. The distinction between transmission of genes and genotypes means that in sexually reproducing livestock:
(A) Genotypes are passed on identically.
(B) Genotypes are broken down and reassembled.
(C) Genes are broken down and reassembled.
(D) Genes mutate at a constant rate.

2002

183. If a population of cattle size fluctuates as 10, 100, and 1000 over three generations, the effective population size (N_e) will be closest to:
(A) 1000
(B) 370
(C) 27
(D) 10

2017

184. In a closed herd, the rate of inbreeding (ΔF) is determined primarily by:
(A) The selection intensity on females
(B) The phenotypic variance (V_P)
(C) The amount of temporary environmental variance
(D) The effective population size (N_e)

2017

185. In algebraic formulation, if a metric character shows overdominance, the value of d relative to a is:
(A) $d = 0$
(B) $d < a$
(C) $d = a$
(D) $d > a$

NODIA

2009

186. The concept of average effect of a gene is fundamental because it connects individual allele effects to:
(A) Mendelian exact crosses
(B) Statistical properties of the population
(C) Clonal propagation rates
(D) Environmental temperature fluctuations

2015

187. The average effect of gene substitution (α) essentially measures the change in population mean if:
(A) The environment is permanently altered.
(B) One allele is substituted for another.
(C) A dominant allele mutates to recessive.
(D) An individual is replaced by its clone.

2025

188. An individual's breeding value (A) can be accurately estimated by:
(A) Evaluating the mean of its progeny.
(B) Squaring its genotypic value.
(C) Measuring its single phenotype.
(D) Determining its epistatic deviations.

2019

189. Dominance deviation (D) is an intra-locus interaction, meaning it occurs between:
(A) Alleles at different loci on the same chromosome
(B) Alleles at different loci on different chromosomes

2007

139. Dominance deviation reflects the fact that the effects of alleles at a locus are:
(A) Strictly additive.
(B) Non-additive in nature.
(C) Independent of each other.
(D) Caused by the environment.

2023

140. Phenotypic variance partitioning is most fundamentally represented as $V_P = V_G + V_E$. The inclusion of $V_{\{GE\}}$ is necessary when:
(A) Genotypes respond differently to environments.
(B) All genotypes perform poorly in harsh environments.
(C) Environmental variation is entirely zero.
(D) Breeding values are completely fixed.

2025

141. The additive genetic variance is specifically the variance of:
(A) Dominance deviations
(B) Genotypic values
(C) Breeding values
(D) Environmental deviations

2009

142. If a permanent environmental effect ($V_{\{Ep\}}$) acts favorably on a dairy cow, her subsequent lactations will:
(A) Fluctuate randomly.
(B) Drop to the population mean.
(C) Exhibit negative repeatability.
(D) Show a consistent upward deviation.

2015

143. The genetic covariance between a sire and his offspring is composed of:
(A) V_A
(B) $\frac{1}{2} V_D$
(C) $\frac{1}{4} V_A$
(D) $\frac{1}{2} V_A$

2019

144. Heritability in the narrow sense (h^2) predicts:
(A) Similarity of environmental effects.
(B) Parental-offspring additive resemblance.
(C) Permanent environmental changes.
(D) The exact genotype of offspring.

2024

145. In estimating heritability using paternal half-sib design, a major assumption is that:
(A) Sires and dams have equal permanent effects.
(B) All epistatic variance is transmitted directly.
(C) Dominance variance constitutes 50% resemblance.
(D) Offspring share $\frac{1}{4}$ additive genetic variance.

2004

146. A parent-offspring regression coefficient (b) of 0.15 for a single parent implies a heritability of:
(A) 0.15
(B) 0.075
(C) 0.30
(D) 0.60

2024

147. Repeatability is considered the upper limit of heritability because:
(A) r is measured exclusively in clones.
(B) h^2 is measured only on a single record.
(C) r includes permanent and non-additive effects.
(D) h^2 includes all environmental variance.

2003

148. MPPA effectively shrinks an individual's phenotypic average towards the population mean if:
(A) Repeatability is low
(B) Repeatability is 1.0
(C) The individual has only a single record
(D) The population mean is zero

2005

149. Phenotypic correlation (r_P) between two traits is a function of:
(A) Only their genetic correlation
(B) Only their environmental correlation
(C) Additive variance only
(D) Weighted genetic and environmental components.

2002

150. Analysis of Covariance (ANCOVA) for half-sibs yields the sire component of covariance, which estimates:
(A) $\frac{1}{2}$ of the environmental covariance
(B) $\frac{1}{4}$ of the additive genetic covariance
(C) 100% of the phenotypic covariance
(D) $\frac{1}{2}$ of the dominance covariance

2004

151. Estimating parameter precisions requires calculating standard errors. The standard error of a correlation estimate is inversely proportional to:

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(C) Relying strictly on random mating populations.
(D) Maintaining a zero mutation rate at the locus.

2001

202. Allelic richness is an important diversity metric because it indicates:
(A) The average age of individuals
(B) The number of distinct alleles present at a locus in a population
(C) The proportion of heterozygotes relative to homozygotes
(D) The precise mutation rate of a locus

2001

203. The fixation index $F_{\{ST\}}$ specifically evaluates:
(A) Inbreeding depression
(B) The reduction in heterozygosity due to population subdivision
(C) The individual's breeding value
(D) Temporary environmental fluctuations

2025

204. Gene flow and migration rates are often estimated in modern livestock using:
(A) Neutral genomic markers (microsatellites/ SNPs).
(B) Only phenotypic measurements like body weight.
(C) Calculation of temporary environmental variance.
(D) Dominance variance partitioning methods.

2025

205. The effective number of alleles (n_e) in a population is calculated as the reciprocal of:
(A) The narrow-sense heritability.
(B) The sum of squared allele frequencies.
(C) The population mean.
(D) The dominance deviation.

2015

206. If the frequency of a recessive disease allele is 0.01 in a Hardy-Weinberg population, the frequency of affected individuals is:
(A) 0.01
(B) 0.02
(C) 0.0001
(D) 0.99

2018

207. Individual genetic architecture is best defined by:
(A) The frequencies of alleles in the whole population.
(B) The mutation rate across the entire species.
(C) The specific allele pairing at all loci.
(D) The effective population size.

2010

208. When calculating effective population size (N_e) with unequal sex ratio, the formula is:
(A) $N_e = \frac{4 \times N_m \times N_f}{N_m + N_f}$
(B) $N_e = N_m + N_f$
(C) $N_e = \frac{N_m \times N_f}{4}$
(D) $N_e = \frac{4}{N_m + N_f}$

2013

209. The probability that two alleles chosen at random are identical by descent describes the:
(A) Narrow-sense heritability
(B) Broad-sense heritability
(C) Polymorphism information content
(D) Inbreeding coefficient (F)

2004

210. In evaluating metric characters, the algebraic difference between the genotypic value of a heterozygote and the mid-parent value is termed:
(A) Dominance deviation
(B) Average effect
(C) Breeding value
(D) Additive variance

NODIA

2023

211. The average effect of an allele approaches zero when its frequency in the population approaches:
(A) 0.5
(B) 1.0
(C) 0.0
(D) 0.25

2024

212. The mathematical formulation of the average effect of gene substitution (α) for a locus with alleles A_1 (frequency p) and A_2 (frequency q) is defined as:
(A) $\alpha = a + d(q - p)$
(B) $\alpha = a - d(q - p)$
(C) $\alpha = d + a(q - p)$
(D) $\alpha = a(p + q)$

2001

213. A breeding value (A) represents the sum of average effects of an individual's genes, implying that it is the portion of genotypic value that:

2017

164. Epistasis is defined as non-additive interaction between alleles at:
(A) Different loci
(B) The same locus
(C) Different chromosomes only
(D) Sex-linked loci only

2008

165. The variance component that represents the non-transmissible genetic variation due to allelic interactions at the same locus is:
(A) V_A
(B) V_I
(C) $V_{\{Ep\}}$
(D) V_D

2016

166. A critical reason for sub-partitioning V_G is to identify:
(A) V_E, to control the environment.
(B) V_A, to determine selection response.
(C) $V_{\{GE\}}$, to eliminate all mutations.
(D) V_D, to strictly limit genetic drift.

2007

167. An example of temporary environmental variance ($V_{\{Et\}}$) is:
(A) Permanent injury to the reproductive tract
(B) Genetic mutation in the germline
(C) Daily fluctuation in ambient temperature
(D) A fixed chromosomal translocation

2014

168. Resemblance between full-sibs is higher than between half-sibs because full-sibs share:
(A) A common permanent environment.
(B) All their epistatic variance.
(C) Only temporary environmental variance.
(D) Half V_A and one-quarter V_D.

2003

169. Narrow-sense heritability estimates the proportion of phenotypic variance that is:
(A) Readily transmissible to offspring.
(B) Due strictly to the environment.
(C) Influenced by epistatic deviations.
(D) Due to permanent environmental effects.

2012

170. When utilizing the paternal half-sib ANOVA method, the resulting heritability estimate may be biased upward if:
(A) The trait is purely environmentally determined.
(B) Mutation rates are zero.
(C) Sires are heavily inbred.
(D) Full-sibs are included as half-sibs.

2018

171. In parent-offspring regression, utilizing the mid-parent value instead of a single parent value:
(A) Halves the standard error of the estimate
(B) Provides a regression coefficient that equals h^2 directly
(C) Requires multiplying the regression coefficient by 2
(D) Eliminates additive genetic variance

2021

172. Repeatability analysis using ANOVA partitions phenotypic variance into:
(A) Between-individual and within-individual.
(B) Sire variance and dam variance components.
(C) Additive and dominance variance.
(D) Epistatic and mutational variance.

2002

173. MPPA is a highly effective tool for:
(A) Identifying newly emerged mutations.
(B) Estimating the overall population size.
(C) Deciding culling for future production.
(D) Establishing purebred genomic signatures.

2010

174. Pleiotropy creates genetic correlation because:
(A) Closely linked genes co-segregate.
(B) Environmental effects are non-random.
(C) Assortative mating is applied.
(D) A single gene affects multiple traits.

2006

175. When performing ANCOVA to estimate genetic correlation, a negative cross-product between traits indicates:
(A) The traits are perfectly independent.
(B) The traits share no additive variance.
(C) Genetic increase in one decreases the other.
(D) Heritability for both traits must be zero.

2010

176. The precision of heritability estimates improves (standard error decreases) as:
(A) Genetic drift becomes the dominant force.
(B) Family size and progeny are optimized.
(C) The temporary environmental variance increases.
(D) Assortative mating replaces random mating.

2008

177. Expected heterozygosity under the Hardy-Weinberg equilibrium is maximum when:

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(A) Selection to increase trait X will strongly increase trait Y.
(B) Selection to increase trait X will strongly decrease trait Y.
(C) The two traits are genetically independent.
(D) Both traits are perfectly controlled by the environment.

2009

225. Estimation of genetic correlation by ANCOVA involves:
(A) Calculating the standard error of a single trait.
(B) Measuring identical temporary environmental effects.
(C) Finding the mutation rate of a pleiotropic gene.
(D) Partitioning cross-products between traits.

2011

226. Standard errors of heritability estimates dictate the precision of the parameter. A very large standard error indicates:
(A) Unreliable estimate from small samples.
(B) High confidence in the exact estimate.
(C) That heritability is exactly zero.
(D) That genetic variance is exceptionally high.

2025

227. Genetic diversity metrics like expected heterozygosity provide insights into:
(A) The age structure of the population.
(B) The number of permanent variations.
(C) Evolutionary potential and inbreeding.
(D) The temporary environmental variance.

2006

228. In a subdivided population, $F_{\{IT\}}$ represents:
(A) Total heterozygosity loss in populations.
(B) Correlation of genes within individuals.
(C) Correlation of genes between random individuals.
(D) The environmental correlation between traits.

2010

229. Estimating gene flow between two isolated herds usually reveals whether:
(A) Extinction is imminent
(B) The herds have identical environmental variances
(C) Dominance variance is zero
(D) Recent crossbreeding or migration has occurred

2017

230. A breed signature derived from a 50K SNP chip is characterized by:
(A) The exact sequence of mitochondrial DNA.
(B) Distinct allele frequency combinations.
(C) The number of chromosomes.
(D) The temporary environmental conditions.

2015

231. The Hardy-Weinberg testing is fundamentally a statistical evaluation (typically Chi-square) comparing:
(A) Expected allele frequencies against observed allele frequencies
(B) Expected genotype counts against observed genotype counts
(C) Expected environment against observed environment
(D) Expected mutation rates against observed mutation rates

2010

232. At the population level, genetic architecture is characterized by 'transmission of genes' because:
(A) Genes mutate during every cell division.
(B) Individuals do not possess genotypes.
(C) Populations replicate clonally.
(D) Recombination breaks genotypes each generation.

2021

233. The effective population size (N_e) determines the magnitude of:
(A) Random genetic drift
(B) Additive variance
(C) Epistatic interactions
(D) Temporary environmental fluctuations

2003

234. The mathematical relationship $\Delta F = \frac{1}{2N_e}$ indicates that:
(A) Inbreeding rate is independent of population size
(B) Inbreeding rate decreases as effective population size increases
(C) Inbreeding rate increases as effective population size increases
(D) Drift and inbreeding are completely unrelated

2022

235. The population mean for a metric trait is algebraically represented as:
(A) $a(p-q)+2pqd$
(B) $a(p+q)-2pqd$

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(C) $d(p-q)+2pqa$

(D) a^2+d^2

2007

236. The average effect of an allele is mathematically expressed as the product of:

(A) The frequency of the other allele and the average effect of gene substitution (α)

(B) Its frequency and the dominance deviation

(C) The mutation rate and allele frequency

(D) The environmental variance and allele frequency

2001

237. The average effect of gene substitution (α) is most practically defined as the difference in:

(A) Average effects of the two alleles.

(B) Permanent and temporary effects.

(C) Favorable and unfavorable phenotypes.

(D) Drift between two subpopulations.

2015

238. Breeding value is often represented as an expected progeny difference (EPD) or predicted transmitting ability (PTA) multiplied by:

(A) 1

(B) 2

(C) 0.5

(D) 4

2004

239. Non-additive genetic deviations (dominance and epistasis) are critical because they:

(A) Are perfectly transmitted from parent to offspring.

(B) Determine the narrow-sense heritability.

(C) Form the basis of heterosis utilized.

(D) Are determined by temporary environment.

2019

240. Phenotypic variance (V_P) partitioning allows quantitative geneticists to calculate:

(A) The exact number of genes affecting a trait.

(B) Importance of heredity vs environment.

(C) Precise location of a gene on a chromosome.

(D) Mutation rate of a specific allele.

2018

2012

241. Sub-partitioning of genetic variance into V_A, V_D, and V_I indicates that V_I (epistatic variance) is:

(A) Easily utilized in simple mass selection

(B) Transmitted perfectly from parent to offspring

(C) Responsible for temporary environmental changes

(D) The variance of interaction deviations between loci

2025

242. A permanent environmental effect ($V_{\{Ep\}}$) differs fundamentally from V_G because $V_{\{Ep\}}$:

(A) Cannot be inherited by offspring.

(B) Alters the DNA sequence.

(C) Does not influence the phenotype.

(D) Is caused by random genetic drift.

NODIA

2005

243. The resemblance between half-sibs provides an estimate of:

(A) Total genetic variance

(B) $\frac{1}{2}$ of the additive genetic variance

(C) $\frac{1}{4}$ of the additive genetic variance

(D) $\frac{1}{4}$ of the epistatic variance

2001

244. Narrow sense herizability (h^2) is practically defined as the ratio of:

(A) Additive genetic variance to phenotypic variance

(B) Dominance variance to total variance

(C) Total genetic variance to phenotypic variance

(D) Phenotypic variance to additive genetic variance

2006

245. In estimating heritability from a paternal half-sib design, a large environmental variance within families (σ_w^2) will result in:

(A) A higher heritability estimate

(B) A negative variance component

(C) Zero dominance variance

(D) A lower heritability estimate

2003

246. To obtain an unbiased estimate of heritability using intra-sire regression of offspring on dam, one must:

(A) Double the regression coefficient

(B) Quadruple the regression coefficient

(C) Ignore the dam records entirely

(D) Halve the regression coefficient

2007

247. Repeatability analysis is essential for traits like:

(A) Slaughter weight

(B) Coat color

(C) Milk yield across multiple lactations

(D) Presence of horns

2016

248. The Most Probable Producing Ability (MPPA) heavily weights the individual's own average performance when:
(A) The trait has very low repeatability
(B) The individual has only a single record
(C) The population mean is very low
(D) The trait has high repeatability.

2019

249. A positive genetic correlation but a negative environmental correlation between two traits means that:
(A) Phenotypic correlation varies by magnitude.
(B) Correlation will always be exactly zero.
(C) Pleiotropy is absent from the traits.
(D) Linkage is impossible in this scenario.

2002

250. Estimation of genetic correlation requires obtaining the sire covariance component (cov_s), which equates to:
(A) $\frac{1}{4}\text{cov}_A$
(B) $\frac{1}{2}\text{cov}_A$
(C) cov_A
(D) $\frac{1}{4}\text{cov}_E$

2014

251. The precision of heritability estimates by paternal half-sib correlation is typically maximized when:
(A) The number of progeny per sire (k) is 1
(B) An optimal balance between the number of sires and progeny per sire is achieved
(C) The number of sires is 1
(D) Heritability is completely unknown

2010

252. The selection differential (S) is mathematically defined as the difference between the:
(A) Mean of the selected parents and the population mean.
(B) Highest and lowest records in the herd.
(C) Breeding value and the genotypic value.
(D) Additive variance and the dominance variance.

2023

253. Wright's $F_{\{ST\}}$ statistic is fundamentally a measure of:
(A) Mutation rates across species.
(B) Inbreeding within a single clone.
(C) Subpopulation genetic differentiation.
(D) Permanent environmental deviations.

2024

254. Detecting hybridization or admixture in livestock relies on assigning the probability of an individual's genome originating from:
(A) A single parent
(B) A completely unrelated species
(C) The temporary environment
(D) Putative ancestral gene pools

2011

255. In a population where an autosomal locus has two alleles (A and a) with frequencies p and q, and a sex-linked locus has the same allele frequencies, the time to reach HWE for the sex-linked locus is:
(A) One generation of random mating.
(B) Immediate.
(C) Attained gradually over several generations.
(D) Never achieved if $p \neq q$.

2003

256. Hardy-Weinberg equilibrium is disrupted by all of the following EXCEPT:
(A) Mutation
(B) Random mating
(C) Selection
(D) Migration

2024

257. The conceptual difference between population and individual genetic architecture implies that genetic improvement programs must focus on:
(A) Cloning specific individuals indefinitely.
(B) Ignoring population frequencies entirely.
(C) Fixing heterozygosity at all loci.
(D) Altering population allele frequencies.

2010

258. Fluctuating population sizes reduce effective population size (N_e) because N_e is mathematically derived using the:
(A) Harmonic mean
(B) Arithmetic mean
(C) Geometric mean
(D) Median

2016

259. A highly intense selection program using very few sires will directly cause:
(A) A decrease in the rate of inbreeding (ΔF)
(B) An increase in the effective population size (N_e)
(C) An increase in the rate of inbreeding (ΔF) and genetic drift

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ANSWERS

1. (A) Random mating
The Hardy-Weinberg law describes a theoretical population where allele frequencies remain constant across generations. For genotypic equilibrium to be maintained, individuals must pair without preference for specific traits or genetic similarity. This random mating ensures the union of gametes is accidental, allowing mathematical predictions of genotype frequencies based solely on allele proportions within the gene pool.

2. (C) Individuals transmit genes; populations show genotype frequencies.
At the level of the individual, specific alleles are segregated and passed to offspring through gametes rather than intact genotypes. However, the genetic structure of a whole population is defined by the overall frequencies of these alleles and the resulting genotype distributions. While organisms provide genes, the collective population maintains the proportional distribution of varying genetic combinations.

3. (D) A is false but R is true.
Effective population size rarely equals the census size in real livestock herds. Natural populations often deviate from idealized conditions due to unequal numbers of breeding males and females or periodic fluctuations in total numbers. These factors typically reduce the effective size, meaning the population behaves genetically as though it contains fewer breeding individuals than the actual census count.

4. (D) $\Delta F = \frac{1}{2N_e}$
The rate of inbreeding reflects the increase in homozygosity within a finite population per generation. It is inversely proportional to twice the effective population size. This mathematical relationship highlights that smaller breeding groups experience more rapid genetic drift and faster accumulation of inbreeding, whereas larger effective populations maintain higher levels of genetic diversity and slower inbreeding rates.

5. (B) Genotypic value of the heterozygote relative to the mid-parent.
In the algebraic representation of quantitative traits, the value d quantifies the degree of dominance exhibited at a specific locus. It represents the deviation of the heterozygote's genotypic value from the arithmetic mean of the two homozygous classes. If the heterozygote aligns perfectly with the mid-parent value, dominance is absent and the value of d becomes zero.

6. (C) At random from the population
The average effect of a gene measures the mean deviation from the population average when a specific allele is inherited. This calculation assumes the second allele is provided by a mate chosen randomly from the entire gene pool. This approach accounts for all possible genetic combinations based on existing allele frequencies, reflecting the gene's impact across the whole population.

NODIA

7. (D) α is the mean change when one allele replaces another.
The average effect of gene substitution represents the expected change in the population mean when one allele replaces an alternative one at a specific locus. It integrates the individual average effects of the alleles and considers their frequencies within the population. This parameter is fundamental for predicting genetic progress and the expected response to selection in breeding programs.

8. (A) P-2, Q-3, R-1, S-4
Breeding value is the sum of average effects of genes, while genotypic value represents the total genetic merit of an individual. Dominance deviation results from interactions between alleles at the same locus, whereas epistatic deviation involves interactions between alleles at different loci. These components help scientists partition phenotypic variance into predictable genetic effects and non-additive interactions.

9. (B) Dominance and epistatic deviations.
Non-additive genetic effects encompass interactions that do not follow a simple cumulative

2004

271. When employing parent-offspring regression, utilizing intra-sire regression is preferred over simple regression to avoid:
(A) Eliminates additive variance.
(B) Doubling the dominance variance.
(C) Bias from mating and environment.
(D) Overestimating temporary variance.

2017

272. A repeatability estimate of 0.8 for wool yield suggests that:
(A) A sheep's first shearing is an excellent predictor of its lifetime wool production.
(B) A sheep's first shearing is a terrible predictor of its lifetime wool production.
(C) Environmental variance constitutes 80% of the phenotypic variance.
(D) Additive genetic variance is exactly zero.

2014

273. The MPPA is calculated mathematically to help breeders:
(A) Predict the gene sequence of offspring.
(B) Determine the mutation rate of genes.
(C) Increase the environmental variance.
(D) Avoid culling based on bad records.

2002

274. A genetic correlation exists when:
(A) The expression of two traits is controlled in part by the same genes
(B) Two traits are influenced independently by completely different sets of genes
(C) Environmental effects are perfectly randomized
(D) Dominance deviation is zero for both traits

2004

275. Estimation of genetic correlation requires evaluating the covariance between two traits. In paternal half-sib ANCOVA, this relies on calculating the:
(A) Dam component of temporary variance
(B) Total permanent environmental variance
(C) Sire component of covariance
(D) Dominance covariance exclusively

2004

276. The standard error of a heritability estimate decreases significantly when:
(A) The sample size of families and progeny is large and well-balanced
(B) The number of traits evaluated is reduced
(C) The population is strictly inbred
(D) The mutation rate is artificially increased

2006

277. Polymorphism Information Content (PIC) values range from:
(A) 0 to 1
(B) -1 to +1
(C) 0 to infinity
(D) -infinity to 0

2004

278. In Wright's F-statistics, the equation relating $F_{\{IT\}}$, $F_{\{IS\}}$, and $F_{\{ST\}}$ implies that total inbreeding ($F_{\{IT\}}$) is driven by:
(A) Only non-random mating in subpopulations.
(B) Mating within groups and subdivision.
(C) Only population subdivision effects.
(D) Temporary environmental differences.

2003

279. Estimation of gene flow using genetic markers involves determining the proportion of alleles in a population that:
(A) Mutated in the last generation
(B) Are completely fixed
(C) Originated from immigrants of another population
(D) Are subject to overdominance

2011

280. The generation interval (L) is defined as the average age of the parents when:
(A) They first reach sexual maturity.
(B) Their first offspring is born.
(C) Their progeny are born that will eventually replace them.
(D) They are culled from the herd.

2006

281. In testing equilibrium under the Hardy-Weinberg law, a significant Chi-square value indicates that:
(A) The observed frequencies differ significantly from expected frequencies.
(B) The population is in perfect Hardy-Weinberg equilibrium.
(C) Mutation rates are perfectly balanced.
(D) The effective population size is infinite.

2010

282. The conceptual difference between population and individual genetic architecture highlights that:
(A) Evolution alters an individual's lifetime.
(B) Frequencies change, not genotypes.
(C) Both levels transmit identical genotypes.
(D) Population genetics ignores frequencies.

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(D) A strict return to Hardy-Weinberg equilibrium

2016

260. On the genotypic value scale, if $d = a$, the gene action is strictly described as:
(A) Complete dominance
(B) Overdominance
(C) Partial dominance
(D) No dominance (additive)

2025

261. The average effect of an allele tells a breeder:
(A) The exact phenotype of an offspring.
(B) The complete sequence of the gene.
(C) The permanent environmental variance.
(D) Expected mean change from the allele.

2016

262. The average effect of gene substitution (α) is most directly applicable in calculating:
(A) Epistatic interactions
(B) Breeding values
(C) Environmental deviations
(D) Genetic drift

2009

263. The breeding value (A) of an individual represents its genetic worth as a parent. It is theoretically formulated as:
(A) The sum of all its dominance deviations
(B) The sum of all its epistatic interactions
(C) The sum of average effects of all its alleles
(D) Its phenotypic value minus its genotypic value

2013

264. Dominance deviation (D) limits the effectiveness of simple mass selection because it:
(A) Is perfectly predictable.
(B) Constitutes the total variance.
(C) Is caused by the environment.
(D) Is not transmissible intact to progeny.

2016

265. Phenotypic variance (V_P) is calculated directly by:
(A) Measuring the spread of phenotypic values around the population mean
(B) Measuring the exact breeding value of each animal
(C) Identifying the temporary environmental deviations only
(D) Counting the number of alleles at a single locus

2018

2015

2018

266. Sub-partitioning of genetic variance into V_A, V_D, and V_I indicates that narrow sense herizability (h^2) only considers:
(A) V_D
(B) V_A
(C) V_I
(D) $V_A + V_D$

2011

267. Permanent environmental variance ($V_{\{Ep\}}$) differs from temporary environmental variance ($V_{\{Et\}}$) mainly in its:
(A) Origin (genetic vs environmental).
(B) Duration and consistency of effect.
(C) Impact on the DNA sequence.
(D) Detectability via dense SNP chips.

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2022

268. The genetic covariance between full-sibs differs from half-sibs because full-sibs share:
(A) $\frac{1}{4} V_D$
(B) $\frac{1}{2} V_D$
(C) $\frac{1}{4} V_A$
(D) V_I exclusively

2005

269. A heritability of 0.40 for a trait signifies that 40% of the:
(A) Total variance is due to temporary environmental effects
(B) Dominance variance is transmitted to offspring
(C) Phenotypic variance is due to differences in breeding values
(D) Population has exactly the same genotype

2007

270. Realized herizability (h^2) is calculated in selection experiments as the ratio of:
(A) Selection differential to generation interval.
(B) Genetic response to selection differential.
(C) Phenotypic variance to additive variance.
(D) Total genetic variance to environmental variance.

2008

295. Inbreeding depression is defined as the reduction in the mean phenotypic value of a trait, primarily observed in traits:
(A) With high narrow-sense heritability.
(B) Influenced by dominance gene action.
(C) Unaffected by the environment.
(D) In large panmictic populations.

2024

296. Bias in heritability estimation via parent-offspring regression due to maternal effects is typically circumvented by using:
(A) Dam-offspring regression exclusively
(B) Clonal replication
(C) Total phenotypic variance
(D) Sire-offspring regression

2023

297. Repeatability evaluates the consistency of repeated records. A trait with low repeatability indicates that:
(A) Temporary environmental effects ($V_{\{Et\}}$) are highly influential on single records.
(B) Genetic effects and permanent environmental effects are very large.
(C) The individual is perfectly homozygous.
(D) Heritability is exactly 1.0.

2024

298. Utilizing MPPA in selection decisions is superior to using a single unadjusted record because MPPA:
(A) Ignores the individual's records entirely.
(B) Corrects the average based on record count.
(C) Assumes all variance is additive.
(D) Predicts exactly the permanent environmental effect.

2001

299. Biological causes of genetic correlation include pleiotropy and linkage. Linkage usually creates a genetic correlation that is:
(A) Permanent and unchanging.
(B) Transient and breaks via recombination.
(C) Always exactly 1.0 in value.
(D) Perfectly equal to the phenotypic.

2016

300. The correlated response to selection (CR_Y) in trait Y when selection is applied to trait X depends on the:
(A) Heritability of X, heritability of Y, and the genetic correlation between X and Y.
(B) Temporary environmental variance only.
(C) Number of alleles at the locus for trait Y.
(D) Population mean of trait X.

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2022

283. Effective population size (N_e) is most dramatically reduced by:
(A) Bottlenecks and skewed sex ratios.
(B) Equal numbers of breeding sexes.
(C) Large, constant population sizes.
(D) Zero mutation rates at the locus.

2023

284. The formula $\Delta F = \frac{1}{2N_e}$ shows that an N_e of 50 results in an inbreeding rate per generation of:
(A) 1%
(B) 2%
(C) 5%
(D) 10%

2012

285. In assigning metric values to genotypes on the $a, d, -a$ scale, d equals 0 when:
(A) The heterozygote is exactly intermediate between the two homozygotes.
(B) The heterozygote is equal to the superior homozygote.
(C) Overdominance is present.
(D) The alleles are fixed.

2015

286. The average effect of a gene focuses on its specific contribution to the phenotype:
(A) Assuming it only pairs with an identical allele
(B) Assuming the environment is completely removed
(C) Without considering population allele frequencies
(D) Regardless of its paired allele in the population.

2012

287. Average effect of gene substitution (α) directs the expected response to selection because it measures:
(A) The magnitude of epistatic interactions.
(B) The effect of permanent environment.
(C) Linear, additive effect of replacement.
(D) The precise mutation rate observed.

2006

288. A sire's breeding value (A) indicates his genetic potential to transmit favorable traits. If his $A = +400$ kg for milk yield, his expected progeny difference (EPD) is:
(A) +400 kg
(B) +200 kg
(C) +800 kg
(D) 0 kg

2025

289. Dominance deviation (D) is essentially the difference between:
(A) The individual's breeding value and the population mean
(B) Phenotypic value and environmental deviation
(C) Additive genetic variance and epistatic variance
(D) The genotypic value and breeding value.

2013

290. The variance component $V_{\{GE\}}$ represents genotype-environment interaction. This occurs when:
(A) Relative performance changes with environment.
(B) All genotypes perform equally well in all environments.
(C) Environment has absolutely no effect on phenotype.
(D) Heritability is exactly 1.0.

2021

291. Partitioning of V_G reveals that V_A is the chief determinant of:
(A) Permanent environmental deviations
(B) Non-additive epistatic interactions
(C) The resemblance between relatives and response to selection
(D) Temporary physiological states

2024

292. A localized infection causing a slight drop in a cow's single test-day milk yield is an example of:
(A) $V_{\{Et\}}$
(B) $V_{\{Ep\}}$
(C) V_A
(D) V_D

2002

293. The genetic covariance between a parent and its offspring is generally unaffected by:
(A) Additive genetic variance (V_A)
(B) Allele frequencies
(C) The presence of genes
(D) Dominance variance (V_D)

2009

294. A trait with a narrow-sense heritability of 0.60 is considered:
(A) Lowly heritable
(B) Highly heritable
(C) Moderately heritable
(D) Completely environmentally determined

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pattern across alleles or loci. Dominance involves relationships between alleles at the same locus, while epistasis refers to interactions between alleles at different loci. Unlike additive effects, these deviations are not directly transmissible to offspring because specific gene combinations are disrupted during meiosis and recombination.

10. (B) $V_G + V_E + V_{\{GE\}}$
Total phenotypic variation observed in a population results from genetic differences, environmental influences, and the interaction between these two components. Genetic variance represents the hereditary portion, while environmental variance accounts for non-genetic factors. The interaction variance describes how different genotypes respond uniquely to varying environments, reflecting the complex nature of quantitative trait expression in various livestock.

11. (A) Additive genetic variance (V_A)
Additive genetic variance represents the portion of total genetic variation resulting from the cumulative effects of individual alleles. Because these effects are passed directly to progeny without being disrupted by dominance or epistasis, this component is primarily responsible for the resemblance between parents and offspring. It forms the theoretical basis for estimating herizability and predicting responses to selection.

12. (C) Permanent environmental variance.
When an environmental factor, such as a localized infection or injury, affects an individual consistently throughout its productive life, it is classified as permanent environmental variance. Unlike temporary effects that fluctuate between measurements, these impacts influence all repeated records of the animal. However, because the cause is environmental rather than genetic, these deviations are not transmitted to offspring.

13. (D) I, II and III
The degree of resemblance between relatives is determined by the proportion of genetic variance they share. Half-sibs share one-quarter of the additive variance, while full-sibs share half of the additive variance plus one-quarter of the dominance variance. Parent-offspring pairs share exactly half of the additive variance. All three statements accurately reflect these fundamental quantitative genetic covariance expectations.

14. (C) $\frac{V_A}{V_P}$
Narrow-sense herizability is mathematically defined as the ratio of additive genetic variance to the total phenotypic variance. This parameter is crucial because it measures the proportion of variation that is predictable and transmissible to the next generation. It allows breeders to estimate the breeding values of individuals and predict the genetic gain expected from specific selection programs.

15. (B) $\sigma_w^2 + k\sigma_s^2$
In the analysis of variance for paternal half-sibs, the expected mean square for the sire component includes both the within-family variance and the sire variance multiplied by the number of progeny per sire. This statistical structure allows researchers to isolate the sire variance component. This isolated component is then used to estimate the additive genetic variance and heritability.

16. (D) h^2
When performing a regression of offspring performance on the average value of both parents, known as the mid-parent value, the resulting regression coefficient provides a direct estimate of narrow-sense herizability. This occurs because the mid-parent value represents the total additive genetic contribution from both parents. Consequently, the slope of the regression line directly reflects the trait's heritability.

17. (A) Broad sense herizability
Repeatability measures the correlation between repeated records of the same trait on an individual. It accounts for the total genetic variance and the permanent environmental variance. Because it includes non-additive genetic effects and permanent environmental impacts, it serves as the upper limit for heritability. Heritability only considers genetic components, making it inherently smaller or equal to repeatability.

18. (C) I and III
Most Probable Producing Ability is a tool used to rank animals for culling based on multiple performance records. It incorporates the population mean, the number of records available for the individual, and the trait's repeatability. By adjusting for the number of observations, it provides a more accurate prediction of future

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performance than a simple average of past records.

19. (A) Pleiotropy and linkage effects.
Genetic correlation between two traits occurs primarily because they are influenced by the same genes or genes located closely on the same chromosome. Pleiotropy describes a single gene affecting multiple traits, creating a permanent correlation. Linkage involves different genes that tend to be inherited together, though this correlation can eventually decay over generations through the process of recombination.

20. (D) Sire component of covariance
Analysis of covariance on paternal half-sib data allows for the partitioning of phenotypic covariance into sire and within-family components. The sire component of covariance represents one-quarter of the additive genetic covariance between the two traits. By isolating this component, breeders can calculate the genetic correlation, which describes the extent to which two traits are genetically linked or related.

21. (B) It decreases for higher precision.
The standard error of any genetic parameter, including herizability, is an indicator of its statistical precision. As the total sample size or the number of families increases, the impact of sampling error is reduced. Consequently, the standard error decreases, providing a more reliable and precise estimate of the true population parameter, which is essential for accurate breeding decisions.

22. (C) The informativeness of a genetic marker
Polymorphism Information Content is a metric used to evaluate how useful a genetic marker is for linkage analysis and diversity studies. It considers the number of alleles at a locus and their respective frequencies within the population. A higher PIC value indicates that the marker is highly polymorphic and effective for distinguishing between individuals or tracking genetic inheritance.

23. (C) A is true but R is false.
Wright's F-statistics, specifically $F_{\{ST\}}$, are used to quantify genetic differentiation among subpopulations by measuring the reduction in heterozygosity. However, these statistics are based on allele frequencies and molecular data rather than phenotypic variance across environments. While the assertion correctly identifies $F_{\{ST\}}$ as a measure of genetic differentiation, the reason is incorrect regarding its underlying mathematical calculation.

24. (A) Analysis using microsatellite or SNP marker panels.
Modern genomic techniques, such as microsatellite or Single Nucleotide Polymorphism marker panels, are the most effective tools for detecting genetic admixture and gene flow. These markers provide high-resolution data on allele frequencies across different populations. By comparing these patterns, scientists can estimate the proportions of an individual's genome that originate from distinct ancestral groups or livestock breeds.

25. (B) Allelic patterns unique to a specific breed.
A breed signature refers to a distinct set of genetic markers or allele frequencies that are characteristic of a particular livestock breed. These genomic patterns are used to identify breed purity, authenticate products, and distinguish between different populations. They represent the unique evolutionary history and selection pressures that have shaped the genetic architecture of the breed over time.

26. (B) Directional selection
Hardy-Weinberg equilibrium is maintained only when evolutionary forces are absent. Directional selection favors specific phenotypes, which alters allele frequencies over time and shifts the genotype distribution away from expected equilibrium proportions. Other factors such as mutation, migration, and genetic drift also cause deviations, whereas random mating and large population sizes are necessary conditions to maintain stable equilibrium.

27. (A) Meiosis breaks parental genotypes into alleles.
In sexually reproducing populations, individual genotypes are not passed intact to the next generation. Instead, the process of meiosis segregates allele pairs, ensuring that only individual genes are transmitted via gametes. These alleles then recombine in the offspring to form new genotypes. Therefore, while genotypes define individuals, the transmission and frequency of genes govern the population's genetic structure.

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28. (A) Determine sizes per generation → Calculate harmonic mean of sizes → Derive N_e
When population size varies over time, the effective population size is not simply the average of census counts. It is calculated using the harmonic mean of the sizes across generations. This mathematical approach gives more weight to generations with smaller populations, correctly reflecting how bottlenecks and periods of low numbers disproportionately increase genetic drift and reduce overall diversity.

29. (D) Both increase
A severe population bottleneck significantly reduces the number of breeding individuals, which leads to a dramatic increase in genetic drift. Because there are fewer individuals, the probability of mating between relatives rises, causing the rate of inbreeding to increase. Both phenomena occur simultaneously as the population's genetic base narrows, leading to a loss of heterozygosity and diversity.

30. (C) 0
In quantitative genetics, the genotypic values of the two homozygous classes are often designated as a and $-a$. By defining the scale in this manner, the midpoint between these two homozygotes is mathematically set to zero. This allows the value of the heterozygote, d, to be easily interpreted as the degree of dominance relative to that midpoint.

31. (B) Population gene frequency and genotypic values.
The average effect of a gene is not a fixed property of the allele itself but depends on the context of the population. It is calculated based on the genotypic values of all possible combinations and the frequencies of the alleles with which it might pair. Therefore, the same allele can have different average effects in populations with different gene frequencies.

32. (D) $a + d(q - p)$
The average effect of gene substitution represents the difference between the average effects of two alternative alleles. In a two-allele system, it is algebraically defined by the additive value and the dominance deviation weighted by the difference in allele frequencies. This formula specifically captures how the population mean changes when one allele is replaced by another across all possible genotypes.

33. (A) Genotypic Value, Breeding Value, Average Effect of a Gene
Genotypic value is the most inclusive as it contains all genetic effects, including additive, dominance, and epistatic components. Breeding value is more specific, representing only the sum of additive effects that can be passed to offspring. The average effect of a gene is the most basic unit, describing the mean deviation caused by a single allele in a population.

34. (C) Inter-allelic interactions across different loci.
Epistatic deviation refers to the non-additive genetic effects that occur when alleles at one locus influence the expression of alleles at a different locus. This interaction across distinct parts of the genome adds complexity to the total genotypic value. Because these specific multi-locus combinations are broken up during gamete formation, epistatic effects are generally not transmissible in a predictable manner.

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35. (A) Genotype-Environment Interaction Variance.
The term $V_{\{GE\}}$ represents the variance resulting from the interaction between an individual's genotype and its environment. It occurs when different genotypes do not respond in the same way to environmental changes. For example, one breed might thrive in heat while another suffers, demonstrating that the environmental effect on phenotype depends specifically on the genetic makeup of the individual.

36. (D) V_A
Additive genetic variance is formally defined as the variance of the breeding values of individuals within a population. Since breeding values represent the part of the genotype that is transmitted to offspring, V_A measures the variation in these transmissible effects. This component is the primary determinant of the resemblance between relatives and the population's potential for genetic improvement.

37. (B) Minor climatic fluctuation during one season.
Temporary environmental effects are non-genetic factors that influence an animal's performance during a specific measurement or short period but do not have a lasting impact. A minor seasonal change in weather is a classic example, as it may affect one lactation or shearing record without altering the animal's performance in subsequent years, unlike permanent injuries or chronic conditions.

38. (A) Both A and R are true and R is the correct explanation of A.
Full-sibs share a higher degree of genetic similarity than half-sibs because they have both parents in common. They share half of the additive genetic variance and one-quarter of the dominance variance. In contrast, half-sibs only share one-quarter of the additive variance. This additional shared genetic component explains why full-sibs typically show a greater phenotypic resemblance than half-sibs.

39. (D) Clonal or vegetative propagation
Broad-sense heritability considers the total genetic variance, including additive, dominance, and epistatic effects. These non-additive components are usually lost during sexual reproduction due to segregation and recombination. However, in clonal or vegetative propagation, the entire genotype is passed intact to the next generation. Therefore, broad-sense heritability is the most relevant parameter for predicting performance in such systems.

40. (A) $\frac{1}{4}h^2$
In a paternal half-sib analysis, the intraclass correlation coefficient represents the proportion of total variance attributed to the sire. Since paternal half-sibs share one-quarter of their additive genetic variance, the correlation between them is expected to be one-quarter of the narrow-sense heritability. This relationship allows researchers to estimate herizability by multiplying the observed correlation by four.

41. (B) Removes bias from non-random mating of sires.
Intra-sire regression involves comparing offspring to their dams within the groups created by each sire. This technique is valuable because it effectively controls for the genetic contribution of the sire. By analyzing the relationship between dams and offspring within these groups, breeders can obtain a heritability estimate that is less biased by non-random mating or environmental differences between sires.

42. (B) Repeated records of the same trait on the same individual
Repeatability is a statistical parameter that measures the consistency of an individual's performance for a specific trait over time. It is calculated as the correlation between multiple records, such as milk yield in successive lactations. It indicates the proportion of variation due to total genetic effects and permanent environmental factors, helping to predict future performance based on early records.

43. (A) P-2, Q-4, R-1, S-3
Heritability is used to predict breeding values from phenotypes, while repeatability is the basis for calculating Most Probable Producing Ability. Genetic correlation is essential for predicting how selection for one trait affects another through correlated response. The inbreeding coefficient estimates the probability that two alleles are identical by descent, reflecting the level of genetic relatedness within an individual's pedigree.

44. (C) (Individual's average - Population Mean)
The Most Probable Producing Ability calculation adjusts an individual's average performance by a weighting factor that depends on the trait's repeatability and the number of records. This factor is multiplied by the deviation of the individual's average from the population mean. Adding this adjusted deviation to the population mean provides a reliable estimate of the animal's future productivity for that trait.

45. (D) Selecting for milk yield decreases fat percentage.
A negative genetic correlation between two traits indicates that the genes influencing them have opposing effects. In dairy cattle, milk yield and fat percentage often show this relationship. Consequently, when breeders select for higher milk production, the correlated genetic response typically leads to a reduction in fat concentration. This trade-off must be managed carefully during the selection process.

46. (C) Covariances between traits on related individuals.
Analysis of covariance is a statistical technique used to estimate genetic correlations by examining how two different traits vary together among related animals, such as half-sibs. By partitioning the total covariance into genetic and environmental components, researchers can determine the degree to which traits are influenced by the same sets of genes, independent of shared environmental factors.

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47. (B) Inflating genetic variance and relative resemblance.
Assortative mating occurs when individuals with similar phenotypes mate more frequently than expected by chance. This practice tends to increase the frequency of homozygotes and group similar alleles together, which inflates the additive genetic variance within the population. It also increases the correlation between relatives, which can lead to biased overestimates of herizability if not properly accounted for.

48. (D) Only III
Allelic richness is a measure of genetic diversity that counts the number of distinct alleles at a locus. Unlike simple counts, it is highly sensitive to the size of the sample being analyzed. Researchers must use rarefaction techniques to correct for sample size differences when comparing populations. Therefore, the statement that it ignores sample size is incorrect in a scientific context.

49. (A) Inbreeding of individuals relative to their subpopulation
In Wright's system of F-statistics, $F_{\{IS\}}$ is known as the inbreeding coefficient or the fixation index within subpopulations. It measures the deviation of observed heterozygosity from the expected heterozygosity under random mating within that specific group. A positive value suggests that individuals are more inbred or related than would be expected by chance within their own subpopulation.

50. (C) The extent of isolation or admixture in populations.
Understanding gene flow and migration rates is essential for livestock breeders to assess the degree of genetic exchange between different herds or breeds. These metrics reveal whether populations are remaining genetically distinct or if they are becoming mixed through crossbreeding. This information is vital for conservation efforts and for managing the genetic health and diversity of local animal populations.

51. (A) Finding unique frequencies or haplotypes.
SNP chips allow for the high-throughput genotyping of thousands of markers across the genome. A 'breed signature' is identified by analyzing specific allele frequencies or combinations of linked markers, known as haplotypes, that are unique to a particular breed. This molecular fingerprint enables precise identification of breed origin and helps detect even low levels of genetic crossbreeding or admixture.

52. (D) $p^2 + 2pq + q^2 = 1$
The Hardy-Weinberg principle provides a mathematical model for predicting genotype frequencies from allele frequencies in a large, randomly mating population. For a locus with two alleles, p and q, the frequencies of the three possible genotypes are given by the expansion of the binomial $(p + q)$ squared. This results in the classic equation representing the equilibrium state of the population's genetic structure.

53. (B) I, III and IV
Population genetics focuses on allele frequencies and evolutionary changes that occur over generations at the group level. While individuals transmit genes, their specific genotypes are broken apart by recombination in sexual reproduction. Stable genotypes are only replicated in asexual or clonal systems. Therefore, populations can maintain stability in allele frequencies even as individual genotypes change constantly through the reproductive cycle.

54. (C) 36
Effective population size is heavily influenced by the ratio of breeding males to females. Using the formula $\frac{4 \times N_m \times N_f}{N_m + N_f}$, where N_m is 10 and N_f is 90, the calculation $\frac{4 \times 900}{100}$ equals 36. This demonstrates that a skewed sex ratio significantly reduces the effective population size, making the population genetically equivalent to a much smaller balanced group.

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55. (D) Low effective population size (Ne)
Genetic drift refers to random fluctuations in allele frequencies that occur due to chance sampling in finite populations. These effects are most pronounced in populations with a low effective size (N_e). In small groups, chance events can lead to large shifts in frequencies, potentially resulting in the loss of beneficial alleles or the fixation of harmful ones, regardless of selection pressures.

56. (B) Unfavorable homozygote.
In the quantitative genetic scale used to model metric characters, the three genotypes are assigned values relative to a central point. The favorable homozygote is designated as a, while

the unfavorable homozygote is designated as $-a$. This symmetric scale places the midpoint at zero, allowing the heterozygote value, d, to clearly indicate the presence and direction of dominance.

57. (B) Population and gene frequency.
The average effect of a gene is not an intrinsic property of the allele itself. Instead, it is a statistical property that depends on the frequency of all alleles at that locus within the population. It reflects the mean deviation caused by the allele when it pairs with other alleles according to their existing frequencies, making it a context-dependent measure of genetic impact.

58. (A) I, II and V
The average effect of gene substitution is the difference between the average effects of two alleles and is a linear function of additive genetic value. It is the key parameter that determines how a population will respond to selection pressures. While it changes with allele frequencies, it serves as a crucial bridge between individual gene action and the cumulative response observed in breeding.

59. (A) Average effects of the genes it carries
Breeding value represents the genetic worth of an individual that can be passed to its offspring. It is mathematically defined as the sum of the average effects of the individual alleles an organism possesses at all relevant loci. Since alleles are the units of inheritance, this additive component is the only part of the genotype that is predictably transmitted across generations.

60. (A) Heterozygote value is not at the midpoint.
Dominance deviation occurs when the phenotypic expression of a heterozygote does not equal the average of the two homozygous classes. On the metric scale, if the heterozygote's value deviates from zero, it indicates that the alleles at that locus are interacting non-additively. This intra-locus interaction creates genetic variation that is not directly passed to offspring in a predictable, additive manner.

61. (C) Zero
Variance is a statistical measure of spread and is calculated by squaring deviations from a mean. By definition, squared values and their sums cannot be negative. Therefore, phenotypic variance, which represents the total observed variation in a trait, must always be a non-negative value. A variance of zero would indicate that all individuals in the population have identical phenotypic measurements.

62. (C) Additive genetic variance (V_A)
Additive genetic variance represents the portion of total genetic variation resulting from the cumulative effects of individual alleles. Because these effects are passed directly to progeny without being disrupted by dominance or epistasis, this component is primarily responsible for the resemblance between parents and offspring. It forms the theoretical basis for estimating heritability and predicting responses to selection.

63. (A) Both A and R are true and R is the correct explanation of A.
Repeatability measures the correlation between multiple records of an individual. This correlation is high when factors affecting performance remain constant over time. Permanent environmental variance includes non-genetic impacts that persist throughout an animal's life, such as early developmental effects or permanent injuries. Because these factors influence every record an individual produces, they contribute significantly to the consistency or repeatability of the trait.

64. (B) $\frac{1}{4}$
The coefficient of relationship measures the expected proportion of genes that two individuals share by descent. Half-sibs have only one parent in common, meaning they each inherit half of their genetic material from that shared parent. On average, they will share one-quarter of their additive genetic variance. This value is used to calculate the genetic covariance and phenotypic resemblance between half-siblings.

65. (A) Transmissible from parents to offspring.
Narrow-sense heritability is the ratio of additive genetic variance to phenotypic variance. Biologically, it represents the degree to which offspring will resemble their parents for a specific trait. Because additive effects are the only genetic components that are transmitted directly through gametes, this parameter indicates how much of the observed variation can be exploited by breeders to produce permanent genetic change.

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66. (C) The number of progeny per sire
In a balanced paternal half-sib analysis of variance, k represents the constant number of offspring evaluated for each sire. This value is a critical part of the expected mean square for the sire component. It allows researchers to calculate the variance between sires by adjusting the mean squares. If the data is unbalanced, an average or weighted k value must be used.

67. (A) Use intra-sire regression of offspring on dam.
Assortative mating, where similar individuals mate, can lead to overestimates of heritability in parent-offspring studies. To correct for this bias, breeders use intra-sire regression. By comparing offspring to their dams within the groups sired by a single male, the genetic contribution and non-random mating effects of the sire are controlled. This provides a more accurate estimate of the trait's true heritability.

68. (A) P-3, Q-4, R-1, S-2
Heritability and repeatability are proportions of variance or correlations that range from zero to one. Genetic correlation describes the relationship between two traits and can range from negative to positive one. The inbreeding coefficient also ranges from zero to one, representing the probability of identity by descent. These standardized ranges allow for the comparison of genetic parameters across different traits and populations.

69. (B) Culling on early records will be effective.
High repeatability indicates that an individual's first performance record is a very reliable indicator of its future production. This consistency means that animals with poor initial records are unlikely to improve significantly in later years. Therefore, breeders can confidently cull underperforming individuals based on their early records, which speeds up the selection process and improves the overall productivity of the herd.

70. (C) 1
The weighting factor used in the Most Probable Producing Ability formula adjusts the individual's deviation based on the reliability of the data. As the number of records increases, the influence of temporary environmental fluctuations is minimized. Mathematically, the formula approaches one as n goes to infinity. This means that with many records, the individual's observed average becomes a nearly perfect predictor of its true producing ability.

71. (D) A single gene affecting multiple traits.
Pleiotropy is a biological phenomenon where a single gene or locus influences two or more seemingly unrelated phenotypic traits. This occurs because the gene's product is involved in biochemical pathways that affect multiple physiological processes. Pleiotropy is a major cause of permanent genetic correlation between traits, as selection for one trait will inevitably lead to a genetic change in the other.

72. (A) $\frac{\text{cov}_G(X, Y)}{\sqrt{var_G(X) \times var_G(Y)}}$
Genetic correlation measures the strength and direction of the genetic relationship between two traits. It is calculated by dividing the genetic covariance between the traits by the geometric mean of their individual genetic variances. This formula results in a standardized value between negative one and positive one, allowing breeders to understand how traits will change together in response to selection pressure.

73. (C) I and III
The precision of heritability estimates is measured by their standard error. Small sample sizes lead to high sampling error, reducing precision. Unbalanced data, where some sires have many progeny and others very few, also increases the standard error and reduces the reliability of the estimate. Optimal precision is achieved with large, balanced datasets that provide a thorough representation of the population's genetic diversity.

74. (B) Expected Heterozygosity (H_e)
Expected heterozygosity is a fundamental measure of genetic diversity within a population. It is calculated from allele frequencies and represents the probability that two alleles drawn at random from the gene pool will be different. This metric is used to monitor genetic health and inbreeding levels. A higher value indicates greater genetic variation, which is essential for a population's ability to adapt to changes.

75. (B) Significant genetic differentiation in breeds.
$F_{\{ST\}}$ is a measure of population structure that quantifies the genetic difference between subpopulations or breeds. A value of 0.25 indicates that 25% of the total genetic variation is found between the groups, while the remainder

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112. (B) Epistatic deviation
Interaction deviation, commonly known as epistatic deviation, refers to the non-additive genetic variation that results from genes at different loci influencing each other. These complex interactions mean that the total genetic value is not just the sum of individual gene effects. Because these specific multi-gene combinations are rearranged during reproduction, interaction deviations contribute to the total genotype but not to the transmissible breeding value.

113. (A) P-2, Q-4, R-1, S-3
Additive variance is the primary cause of resemblance between relatives, while dominance variance involves interactions between alleles at the same locus. Epistatic variance refers to non-linear interactions between genes at different loci. Genotype-environment interaction variance describes how different genotypes respond uniquely across varying environments. Each component plays a specific role in determining the total phenotypic variation observed in a livestock population.

114. (A) Genotype-environment interaction ($V_{\{GE\}}$).
Genotype-environment interaction occurs when the relative performance of different genotypes changes depending on the environmental conditions. If one animal performs best in cold weather while another excels in heat, their phenotypic rankings swap as the environment changes. This variance component is important for breeders to consider, as it may mean that selection for performance in one environment does not transfer to another.

115. (C) V_A, V_D, V_I
Total genetic variance is sub-partitioned into three main components based on the nature of the gene action. Additive variance represents the cumulative effects of individual alleles. Dominance variance accounts for interactions between alleles at the same locus. Epistatic variance includes interactions between alleles at different loci. This partitioning allows quantitative geneticists to identify the transmissible portion of genetic merit, which is essential for breeding.

116. (A) It is not transmitted to progeny.
Permanent environmental effects consist of non-genetic factors that influence an individual's performance consistently throughout its life. While these effects cause an animal to consistently deviate from the population average, they do not involve changes to the DNA that can be inherited. Therefore, unlike genetic effects, these permanent environmental deviations are not passed on to the animal's offspring, making them irrelevant for long-term genetic improvement.

117. (D) $\frac{1}{2}$ of Additive genetic variance
The genetic resemblance between a parent and its offspring is based on the fact that each parent contributes exactly half of its genes to the next generation. Therefore, the covariance between them is expected to be one-half of the additive genetic variance. Dominance and epistatic interactions are not shared because the parent's specific gene combinations are broken up and rearranged during the formation of gametes.

118. (B) Phenotypic variance due to total genetic variance.
Broad-sense herizability is the proportion of total phenotypic variation that is caused by all genetic differences among individuals. It includes additive, dominance, and epistatic variance components. This parameter provides an estimate of the overall importance of genetics compared to the environment for a particular trait. While useful for clonal populations, it is less informative for selective breeding programs than narrow-sense herizability.

119. (C) $4\ \sigma^2s\ /\ (\sigma^2s + \sigma^2w)$
In a paternal half-sib design, the variance between sires represents one-quarter of the additive genetic variance. To estimate herizability, the sire variance component is divided by the total phenotypic variance and then multiplied by four. This calculation assumes that there are no shared environmental effects among half-siblings and that the sire variance accurately reflects the additive genetic variation present in the whole population.

120. (D) Sampling error or extensive environmental variation
Variance components are mathematically expected to be positive, but statistical estimations can sometimes yield negative values. This usually happens in small datasets where sampling error is high or when environmental variation within groups is much larger than the variation between them. These negative results are biologically impossible and indicate that

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predict how much a trait will improve in the next generation following a selection program.

85. (D) Value judged by the mean of its progeny.
An individual's breeding value is defined by the average performance of its offspring compared to the population mean. Since each parent transmits only a sample of its genes, the progeny's mean performance reflects the cumulative average effects of those genes. This practical definition allows breeders to estimate an animal's genetic worth as a parent, which is the most important factor in selective breeding.

86. (B) Dominance deviation
Dominance deviation is the component of genetic variation that arises from non-additive interactions between alleles at the same locus. It describes how the effect of one allele depends on the presence of the other allele in a diploid genotype. Because this specific interaction is broken up during the formation of gametes, dominance deviation is not passed directly from parents to their offspring.

87. (C) Genotypic values and deviations are additive.
The basic model for partitioning phenotypic variance assumes that the total variation is the sum of independent components from genetics and the environment. This linear model implies that genetic and environmental effects do not influence each other and that there is no correlation between them. While this is a simplification, it provides a functional framework for estimating heritability and other essential genetic parameters in livestock populations.

88. (A) Both A and R are true and R is the correct explanation of A.
Narrow-sense heritability focuses exclusively on the additive genetic variance because this is the only component that follows a predictable pattern of inheritance. Additive effects are the result of individual genes that act independently, allowing them to be passed from parent to offspring. Dominance and epistatic effects depend on specific combinations that are lost during reproduction, making them irrelevant for predicting selection response.

89. (A) Influences all repeated measurements.
Permanent environmental variance consists of non-genetic factors that affect an animal's performance consistently across its entire life. For example, a chronic health condition or an early nutritional deficit may permanently limit a cow's milk production in every lactation. This differs from temporary effects, which vary randomly from one record to the next. These permanent impacts increase the correlation between an individual's repeated performance records.

90. (B) $\frac{1}{2} V_A$
In sexual reproduction, each parent transmits exactly one allele at each locus to its offspring, which represents half of its breeding value. Consequently, the expected genetic covariance between a parent and its progeny is equal to one-half of the additive genetic variance. Dominance and epistatic deviations are not included because the specific gene combinations of the parent are rearranged during the process of meiosis and recombination.

91. (B) Most variation is due to genetic differences.
Broad-sense heritability measures the proportion of total phenotypic variation that is caused by all genetic factors, including additive and non-additive effects. A value near 1.0 indicates that almost all of the differences observed between individuals are due to their genetic makeup, with very little influence from the environment. This suggests that the trait is highly stable and strongly determined by the individual's genotype.

92. (A) Inflate the estimate if dam components are used
Maternal effects are non-genetic influences provided by the mother, such as milk supply or uterine environment, that affect the offspring's phenotype. When estimating heritability, if these effects are not separated from the genetic components, they can lead to an upward bias in the results. This is especially true when using dam-offspring resemblance, as the shared environment makes the relatives appear more genetically similar.

93. (A) P-4, Q-2, R-1, S-3
Parent-offspring regression often requires multiplying the coefficient by two to estimate heritability, while mid-parent regression estimates it directly. Paternal half-sib correlations provide low standard errors in large datasets. Intra-sire regression of offspring on dam is a specialized technique designed to eliminate environmental correlations shared between the sire and its

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offspring, providing a more refined estimate of the true additive genetic variance.

94. (B) 0.15
Repeatability is the sum of total genetic variance and permanent environmental variance as a proportion of total variance. Heritability (narrow-sense) represents the additive genetic portion. By subtracting heritability from repeatability, we can estimate the proportion of variance due to permanent environmental factors and non-additive genetic effects. In this case, 0.4 minus 0.25 equals 0.15, representing the non-transmissible consistent portion of phenotypic variation.

95. (C) Culling females based on early lactations.
Most Probable Producing Ability is a practical management tool used to identify the most productive animals in a herd. By adjusting an animal's average performance for the number of records and the trait's repeatability, it provides a more reliable prediction of future performance. This allows dairy farmers to make informed decisions about which cows to keep and which to cull after their early lactations.

96. (B) Genetic and environmental correlations
The phenotypic correlation between two traits is the observed relationship that results from both genetic and environmental factors. It reflects how much the traits vary together due to shared genes, such as pleiotropy, as well as shared environmental influences. Understanding this total correlation is important for breeders, as it describes the actual relationship they see in the animals, regardless of the underlying causes.

97. (D) Correlation decays due to recombination.
Genetic correlation caused by linkage occurs because genes for different traits are physically close on the same chromosome and tend to be inherited together. However, over many generations of random mating, crossing over during meiosis will eventually separate these genes. This leads to a gradual reduction or decay in the correlation between the traits, unlike correlation caused by pleiotropy, which remains permanent.

98. (B) Calculate Between Sires Mean Square → Subtract Error Mean Square → Divide by k
In a nested analysis of variance, the sire variance component is isolated by comparing the variation between groups sired by different males with the variation within those groups. The within-group variation, or error mean square, is subtracted from the between-sire mean square. The result is then divided by the number of offspring per sire, k, to yield the true sire component of variance.

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99. (C) Population bottlenecks
Allelic richness measures the total number of different alleles present in a population. It is much more sensitive to population bottlenecks than measures like heterozygosity. During a severe reduction in population size, rare alleles are frequently lost by chance, even if the overall levels of heterozygosity remain relatively stable. Therefore, allelic richness is a critical indicator of a population's long-term genetic health and diversity.

100. (A) $(1 - F_{\{IT\}}) = (1 - F_{\{IS\}})(1 - F_{\{ST\}})$
Wright's F-statistics are mathematically linked to describe the hierarchy of genetic variation. The total inbreeding coefficient of an individual, $F_{\{IT\}}$, accounts for both the non-random mating within its own subpopulation ($F_{\{IS\}}$) and the genetic differentiation of that subpopulation from the total population ($F_{\{ST\}}$). This multiplicative relationship allows researchers to partition the sources of inbreeding and understand the genetic structure of subdivided populations.

101. (D) Multi-locus genotype data clustering.
Admixture analysis uses complex statistical programs like STRUCTURE to analyze genotype data from many markers simultaneously. These programs look for clusters of alleles that are typically found in different ancestral populations. By assigning parts of an individual's genome to these theoretical clusters, scientists can determine the degree of mixing or admixture between different breeds or groups of animals without requiring pedigree records.

102. (B) Authenticating purity and origin of products.
Breed signatures provide a genomic benchmark for identifying purebred animals and their products. In the food industry, these signatures are used to authenticate high-value products, such as specific regional cheeses or specialty meats, by confirming they come from the claimed breed. This molecular certification helps prevent fraud and ensures that consumers receive authentic products while supporting the conservation of specific livestock breeds.

103. (A) Identify breed specific markers → Genotype segregating populations → Conduct association analysis → Locate QTL
Mapping a quantitative trait locus begins with identifying genetic markers that are unique to a specific population. These markers are then used to genotype a population that is segregating for the trait of interest. Association analysis is conducted to find which markers are consistently inherited alongside the trait. This statistical evidence allows researchers to pinpoint the location of the QTL on the chromosome.

104. (D) Absence of natural or artificial selection.
The Hardy-Weinberg law assumes that all genotypes have an equal chance of surviving and reproducing in the population. If selection occurs, certain alleles will be passed on more frequently than others, which directly changes the gene frequencies and disrupts the equilibrium. Therefore, a state of no selection is necessary for allele and genotype frequencies to remain constant from one generation to the next.

105. (A) Act merely as temporary holding vehicles for alleles.
From a population genetics perspective, individual organisms are transient combinations of genes that exist for only a single lifetime. During reproduction, these combinations are broken apart, and only individual alleles are transmitted to the next generation via gametes. Thus, individuals serve as temporary vehicles that carry and pass on the gene pool's components, which are the only elements that persist over evolutionary time.

106. (A) 4
Effective population size calculation for extreme sex ratios shows how diversity is limited by the fewer number of parents. Using the formula $\frac{4\times1\times100}{1+100}$, the result is approximately 3.96. This illustrates that even with many females, a single male creates a genetic bottleneck, making the whole population behave as if it only had four breeding individuals.

107. (A) A decrease in heterozygosity
The rate of inbreeding measures the speed at which individuals in a population become more genetically similar through common ancestry. As inbreeding increases, the frequency of homozygous genotypes rises while the frequency of heterozygotes falls. This loss of heterozygosity can lead to the expression of harmful recessive alleles, a phenomenon known as inbreeding depression, and reduces the population's overall genetic diversity.

108. (A) Both A and R are true and R is the correct explanation of A.
In the quantitative genetic model, the genotypic values of the two homozygotes are set at a and $-a$. This symmetric scale is specifically designed so that the midpoint between them is zero. This mathematical convention simplifies the interpretation of genetic effects, as a represents the additive value of the homozygous classes relative to the average of those two classes in the population.

109. (C) Expected differences from random matings.
The average effect of a gene is a statistical concept that describes the expected deviation from the population mean when an individual inherits a particular allele. It considers all possible pairings of that allele based on current population frequencies. This approach captures the average impact of the gene across the whole population, which is essential for calculating breeding values and predicting selection response.

110. (D) The population is at a stable equilibrium under overdominance
The average effect of gene substitution measures the change in population mean when one allele replaces another. In a state of overdominance, where the heterozygote is superior to both homozygotes, the population reaches a stable equilibrium where allele frequencies no longer change. At this specific point, the replacement of one allele with another does not alter the population mean, and α becomes zero.

111. (C) Breeding value
Breeding value is the additive component of an individual's total genetic merit. It is mathematically derived by summing the average effects of the specific alleles the individual possesses at all genetic loci influencing a trait. Because individual alleles are the only genetic units transmitted to offspring, the breeding value is the most accurate measure of an animal's genetic potential as a parent for selection programs.

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130. (A) Genomic selection and purebred status.
A breed signature identified through dense SNP genotyping provides a detailed map of the genetic markers unique to a population. This information is used in genomic selection to predict breeding values with high accuracy. It also serves as a definitive test for purebred status, ensuring that animals meet the genetic standards of their breed and protecting the integrity of pedigree records.

131. (C) 0.48
Under Hardy-Weinberg equilibrium, the frequency of heterozygotes is calculated as $2pq$. If the frequency of allele 'A' (p) is 0.6, then the frequency of allele 'a' (q) must be 0.4, as the sum of allele frequencies must equal one. Multiplying 2 by 0.6 and 0.4 yields 0.48. This demonstrates how allele frequencies directly determine the distribution of genotypes in a randomly mating population.

132. (A) Independent assortment and recombination.
During sexual reproduction, the parental genotypes are not passed on intact. Instead, independent assortment of chromosomes and recombination through crossing over ensure that genes are shuffled and redistributed into new combinations in the gametes. This fundamental biological process explains why only individual genes are transmitted, while the specific genotypes of the parents are unique to each individual and broken down every generation.

133. (D) The smallest population size (bottleneck)
When a population size fluctuates over time, the effective population size is determined by the harmonic mean rather than the arithmetic average. This mathematical properties mean that years with very low numbers, known as bottlenecks, have a disproportionately large impact on the final N_e. Small populations experience much faster rates of genetic drift and loss of diversity, which persists even if the census size later recovers.

134. (D) Fluctuate randomly across generations
Genetic drift refers to the random changes in allele frequencies that occur in finite populations due to the chance sampling of gametes. Unlike selection, which moves frequencies in a predictable direction, drift is stochastic and unpredictable. In each generation, allele frequencies may increase or decrease simply by chance, which can eventually lead to the loss of alleles or their fixation in the population.

135. (B) $\frac{d}{a}$
The degree of dominance is a measure of how the heterozygote value relates to the homozygote values. In the metric scale where homozygotes are a and $-a$, the degree of dominance is calculated as the ratio of d to a. A ratio of zero indicates no dominance, while a ratio of one indicates complete dominance. Values greater than one represent overdominance, where the heterozygote exceeds the homozygote.

136. (D) The population mean
The average effect of a gene is defined as the mean deviation from the population average that is observed in individuals inheriting that specific allele. It is a statistical property that incorporates the effects of the allele across all possible genetic backgrounds within the population. By measuring this deviation from the population mean, geneticists can calculate breeding values and predict the effects of selection on the whole group.

137. (A) Average effect of gene substitution (α).
The average effect of gene substitution represents the expected change in the phenotypic mean of a population when one allele is substituted for another. It is a fundamental parameter that combines the individual additive effects and the dominance deviation at a locus. This measure is essential for predicting the genetic response to selection, as it describes the linear impact of changing allele frequencies.

138. (D) The arithmetic mean of the parents' breeding values
Each parent contributes exactly half of its genes to its offspring, which means it transmits half of its breeding value. Therefore, the total breeding value of an offspring is theoretically expected to be the sum of these two contributions, which is the arithmetic mean of the parents' breeding values. This relationship forms the basis for predicting the performance of progeny in selective breeding programs.

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139. (B) Non-additive in nature.
Dominance deviation occurs when the combined effect of two alleles at a locus is not simply the sum of their individual effects. This non-additive interaction means that the phenotype

the true variance is likely very small or that the sample size is insufficient.

121. (A) Repeatability
Repeatability measures the correlation between multiple records and includes the total genetic variance plus the permanent environmental variance. Because it accounts for all genetic components and additional non-transmissible environmental factors, it is always greater than or equal to the broad-sense herizability. Thus, the repeatability of a trait provides a theoretical maximum value that herizability cannot exceed in a given population.

122. (B) Shrink closer to the population mean.
The Most Probable Producing Ability uses repeatability as a weighting factor to adjust an individual's average performance. If repeatability is low, it indicates that a single record is a poor predictor of future performance and is largely influenced by temporary environmental factors. In such cases, the calculation 'shrinks' the individual's value toward the population average, reflecting the low certainty in that animal's producing ability.

123. (B) Traits share genetic control or linkage.
A genetic correlation indicates that the same set of genes, or genes located close together on a chromosome, are influencing two different traits. This means that when a breeder selects for one trait, they will cause a simultaneous genetic change in the other trait. This relationship can be either positive or negative, and it is a key factor in designing multi-trait selection programs in livestock.

124. (A) Increasing the number of parent-offspring pairs
The precision of herizability estimated through parent-offspring regression is directly improved by increasing the sample size. A larger number of parent-offspring pairs reduces the impact of random sampling variation and environmental noise. This lead to a smaller standard error, providing a more reliable and accurate estimate of the additive genetic variance, which is essential for making effective breeding and selection decisions.

125. (C) Inflating additive genetic variance.
Positive assortative mating, where similar individuals are paired, increases the frequency of homozygous genotypes and groups like alleles together. This process spreads the distribution of breeding values, effectively inflating the additive genetic variance within the population. If this effect is not properly accounted for in genetic models, it can lead to biased estimates of heritability and other essential quantitative genetic parameters.

126. (D) Genetic diversity within a population.
Heterozygosity is a critical metric because it reflects the level of genetic variation maintained in a population. High levels of heterozygosity generally indicate a healthy, diverse gene pool with high evolutionary potential. Conversely, low heterozygosity often results from inbreeding or population bottlenecks and can lead to reduced fitness and an increased risk of expressing harmful recessive traits in livestock.

127. (C) $F_{\{IS\}}$
$F_{\{IS\}}$ is a fixation index that measures the reduction in heterozygosity within a subpopulation compared to what would be expected under random mating. It specifically identifies the impact of non-random mating or localized inbreeding. A positive $F_{\{IS\}}$ value indicates that there are fewer heterozygotes than expected, suggesting that individuals within the subpopulation are more closely related than average members of the larger population.

128. (B) Reduce genetic differentiation among them.
Gene flow occurs when individuals move between populations and contribute their genes to the new gene pool. This migration introduces new alleles and homogenizes allele frequencies between the groups. As a result, gene flow acts as a powerful force that prevents populations from becoming genetically isolated and reduces the amount of differentiation or divergence that would otherwise be caused by genetic drift.

129. (D) Are highly polymorphic at every locus.
Microsatellite markers consist of short, repeating sequences of DNA that vary greatly in length between individuals. Because they have many different alleles at each locus, they are highly informative for distinguishing between populations. This high level of polymorphism makes them ideal for detecting genetic admixture, as researchers can easily identify specific allele patterns that are characteristic of different ancestral breeds or groups.

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is within them. This level is considered high in livestock, suggesting that the breeds have been isolated for a significant time and have diverged genetically through drift or selection.

76. (A) Analysis using genomic marker panels.
Introgression and genetic admixture occur when genes from one population enter another through crossbreeding. These processes are most accurately detected using dense genomic marker panels, such as SNPs. By analyzing patterns of alleles across the genome, researchers can identify segments of DNA that originated from different ancestral sources, providing a clear picture of the historical and recent mixing of distinct livestock populations.

77. (C) Define evolutionary heritage and identity.
In conservation genetics, breed signatures are used to identify and protect the unique genetic identity of native livestock populations. These signatures represent the specific adaptations and evolutionary history of a breed. By establishing molecular markers that define a purebred population, conservationists can ensure that unique genetic resources are preserved and that the breed's distinct heritage is not lost through unplanned crossbreeding.

78. (A) Calculate observed genotype counts → Estimate allele frequencies → Calculate expected counts → Perform Chi-square test
Testing for Hardy-Weinberg equilibrium involves a systematic statistical process. First, the actual genotypes in the population are counted to determine allele frequencies. These frequencies are then used to calculate the genotype counts that would be expected under equilibrium conditions. Finally, a Chi-square test compares the observed and expected values to determine if the population deviates significantly from the theoretical equilibrium proportions.

79. (C) Mendelian population genetics
Mendelian population genetics is built on the principle that alleles are the fundamental units of inheritance that pass from one generation to the next. While individual genotypes are temporary combinations that are rearranged during reproduction, the frequencies of individual genes remain stable in a population unless acted upon by evolutionary forces. This focus on gene transmission allows for the mathematical modeling of population-level genetic changes.

80. (B) The rarer sex contributes half the genetic material.
In every sexually reproducing generation, males and females each contribute exactly 50% of the genetic material to the offspring. If there is a much smaller number of one sex, such as having very few breeding bulls for many cows, the genetic diversity of the entire next generation is restricted by the small number of those rarer individuals. This dramatically reduces the effective population size.

81. (D) Fixation or loss of alleles
Genetic drift causes random changes in allele frequencies in small, closed populations. Over many generations, these random fluctuations will eventually lead to an allele frequency reaching either zero or one. This results in the permanent loss of an allele or its fixation in the population. Consequently, genetic drift reduces overall genetic variation and increases homozygosity within the breeding group over time.

82. (A) Allele frequencies and genotypic values.
The population mean for a quantitative trait is not a simple average of individual measurements. It is a weighted average that depends on the genotypic values of the three possible genotypes and their respective frequencies within the population. Changes in either the values of the genotypes or the frequency of the alleles will lead to a shift in the overall population mean for that trait.

83. (A) I, III and V
The average effect of a gene is a statistical measure that is dependent on allele frequencies and does not account for non-additive effects perfectly. It is a concept used in random mating populations, not strictly clonal ones. It serves as a regression of genotypic value on gene dosage, forming the basis of breeding value. Therefore, statements claiming it is independent of frequency or purely for clones are incorrect.

84. (A) Response to selection
The average effect of gene substitution is a critical parameter in quantitative genetics because it measures the predictable change in the population mean that occurs when one allele is selected over another. It determines the magnitude of the breeding value and the additive genetic variance. Breeders use this concept to

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of the heterozygote is skewed toward one of the homozygotes. Because these specific interactions are broken up when gametes are formed and alleles are segregated, dominance deviations are not passed predictably from parents to offspring.

140. (A) Genotypes respond differently to environments.
Genotype-environment interaction variance is included in phenotypic variance partitioning when the performance of different genotypes is inconsistent across various environments. This means that a genotype that performs well in one set of conditions may perform poorly in another. Accounting for this interaction is vital for breeders to ensure that selected animals are well-adapted to the specific environmental conditions where they will be raised.

141. (C) Breeding values
Additive genetic variance is formally defined as the statistical variance of the breeding values of individuals within a population. Since breeding values represent the cumulative effect of individual alleles that are passed to offspring, this variance component measures the amount of transmissible genetic variation. It is the most important parameter for determining the resemblance between relatives and the potential for progress through selection.

142. (D) Show a consistent upward deviation.
Permanent environmental effects are non-genetic factors that influence an animal throughout its entire life. If a dairy cow experiences a favorable permanent environmental event, such as exceptional early-life nutrition, it can result in a consistent increase in her milk yield across all subsequent lactations. This creates a lasting upward deviation from the population mean, contributing to the repeatability and consistency of her performance.

143. (C) $\frac{1}{4} V_A$
In a sire-offspring relationship, the parent transmits half of its genes to the progeny. This contribution represents half of the sire's breeding value. When calculating the covariance between a sire and his offspring, the expected value is one-half of the variance of the shared genes, which results in one-quarter of the total additive genetic variance of the population being shared between them.

144. (B) Parental-offspring additive resemblance.
Narrow-sense herizability measures the proportion of phenotypic variance that is due to additive genetic effects. These effects are the only part of the genotype that is transmitted directly and predictably from parents to offspring. Therefore, herizability is a direct indicator of how much of the parental superiority for a trait will be reflected in their progeny, making it essential for predicting selection response.

145. (D) Offspring share $\frac{1}{4}$ additive genetic variance.
A fundamental assumption in the paternal half-sib design is that the offspring within a group sired by the same male share one-quarter of their additive genetic variance. This relationship allows researchers to estimate the population's heritability by isolating the sire variance component and multiplying it by four. This design also assumes that there are no shared environmental factors that would bias the phenotypic correlation.

146. (C) 0.30
In a regression of offspring on a single parent, the regression coefficient b is expected to be equal to one-half of the narrow-sense herizability. This is because the parent only transmits half of its additive genetic influence to the offspring. Therefore, to estimate the full herizability of the trait, the observed regression coefficient must be multiplied by two, resulting in a value of 0.30.

147. (C) r includes permanent and non-additive effects.
Repeatability measures the correlation between multiple records of an individual and is composed of all genetic variance plus the permanent environmental variance. Narrow-sense herizability only includes the additive genetic variance. Since repeatability accounts for both transmissible and non-transmissible consistent factors, it naturally encompasses more of the total variance, ensuring that herizability can never exceed the repeatability of a given trait.

148. (A) Low repeatability
The formula for Most Probable Producing Ability includes repeatability as a weighting factor for the individual's average performance. When repeatability is low, it suggests that single records are unreliable and highly influenced by temporary environmental noise. In such cases, the

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220. (A) $\frac{1}{4} V_A$

In a paternal half-sib design, the analysis of variance provides an expected mean square for the sire component. This component isolated through ANOVA is theoretically expected to be equal to one-quarter of the population's additive genetic variance. This relationship is based on the fact that half-siblings share one-fourth of their genes by descent, providing a statistical method for estimating narrow-sense heritability in large populations.

221. (C) Is generally less subject to confounding by dominance variance

Parent-offspring regression is often preferred for estimating herizability because it is less likely to be biased by non-additive genetic effects. While half-sib correlations can be influenced by dominance or epistatic components, the resemblance between parent and offspring is strictly limited to additive effects. This provides a cleaner estimate of the breeding value variance, although it can still be biased by shared environmental factors between mother and young.

222. (A) $\frac{V_G + V_{Ep}}{V_P}$

Repeatability is the proportion of total phenotypic variance that is due to both total genetic differences and permanent environmental factors. It is mathematically formulated as the sum of genetic variance and permanent environmental variance divided by the total phenotypic variance. This parameter measures the consistency of an individual's records over time, providing a maximum limit for the trait's heritability within a given population.

223. (C) Dams based on record counts.

Most Probable Producing Ability is especially useful for making selection and culling decisions for females that have varying numbers of performance records. Since a cow's average based on many lactations is more reliable than one based on a single record, MPPA adjusts for this difference. It allows breeders to accurately compare dams on a level playing field, ensuring that productive potential is assessed fairly across the whole herd.

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224. (B) Selection to increase trait X will strongly decrease trait Y.

A strong negative genetic correlation indicates that the genes influencing one trait have an opposite effect on the other. If the correlation is -0.80, selection to increase trait X will lead to a significant and predictable genetic decrease in trait Y. Breeders must be aware of such relationships to manage trade-offs between performance traits, such as the common negative correlation between milk yield and fat percentage.

225. (D) Partitioning cross-products between traits.

Analysis of covariance is used to estimate genetic correlation by examining how two traits vary together in related individuals. The process involves calculating the sum of cross-products between the traits and partitioning this total into components for groups and individuals. By isolating the genetic portion of the covariance, researchers can determine the degree to which traits are influenced by the same sets of genes or shared biological pathways.

226. (A) Unreliable estimate from small samples.

The standard error of a herizability estimate indicates the level of statistical uncertainty. A very large standard error suggests that the estimate is not precise, which is often the case when the sample size of families or individuals is too small. In such instances, the calculated heritability value may not accurately represent the true population parameter, making it an unreliable basis for long-term breeding and selection programs.

227. (C) Evolutionary potential and inbreeding.

Expected heterozygosity is a vital measure of a population's genetic health. High levels of heterozygosity indicate a diverse gene pool with significant variation, which provides the foundation for evolutionary adaptation to environmental changes. Conversely, low heterozygosity often signals recent inbreeding or a population bottleneck, which can lead to reduced fitness and an increased vulnerability to genetic diseases in livestock populations.

228. (A) Total heterozygosity loss in populations.

In Wright's hierarchical system of F-statistics, $F_{\{IT\}}$ represents the total inbreeding coefficient of an individual relative to the entire population. It measures the total reduction in heterozygosity that results from both non-random mating within

frequencies, which describe the proportion of each gene version, and genotype frequencies, which describe how those genes are paired. These metrics provide a summary of the whole gene pool and are used to study evolutionary changes and genetic health at the population level.

158. (D) Dictated by the number of the rarer sex.
When the number of breeding males and females is unequal, the effective population size is limited by the sex with fewer individuals. Since each offspring must have one father and one mother, a very small number of individuals of one sex will restrict the genetic diversity of the entire next generation. This makes the effective size much smaller than the actual census count would suggest in managed dairy herds.

159. (C) Maximize N_e
The rate of inbreeding is inversely proportional to the effective population size. To prevent the rapid loss of genetic diversity and minimize the accumulation of inbreeding, breeders must ensure that the effective population size is kept as large as possible. This is achieved by maintaining balanced sex ratios, using many different parents, and avoiding bottlenecks, which collectively ensure a broader genetic base for the next generation.

160. (C) $0 < d < a$
Partial dominance occurs when the phenotypic value of the heterozygote is not exactly at the midpoint of the homozygotes but is still between them. On the quantitative genetic scale, this means the value d is greater than zero but less than the additive value a. This gene action indicates that one allele has a stronger influence on the phenotype than the other, but is not completely dominant.

161. (D) Random mating population mean contexts.
The average effect of a gene is a statistical property that describes the expected deviation from the population mean when a specific allele is inherited. This concept is fundamental to quantitative genetics and assumes that the allele is paired with others drawn randomly from the population. It provides a way to link individual allele action to the overall performance and genetic structure of a randomly mating population.

162. (A) The average effect of the unfavorable allele.
The average effect of gene substitution is defined as the difference between the average effects of the two alternative alleles at a locus. It represents the expected change in the population mean that occurs when a 'bad' allele is replaced by a 'good' one. This parameter is the core of additive genetic variation and is used to calculate breeding values and predict the response to selective breeding.

163. (C) One-half of his breeding value
A sire's predicted transmitting ability or expected progeny difference represents the genetic merit that he is expected to pass on to his offspring. Since a parent only contributes half of its genes to each progeny, the transmitted value is exactly one-half of the sire's total breeding value. This measure is used by breeders to rank sires based on their expected impact on the next generation's performance.

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164. (A) Different loci
Epistasis is a form of non-additive gene action where the effect of an allele at one genetic locus depends on the presence of alleles at another, different locus. These interactions across the genome mean that the total genetic value is not simply the sum of individual gene effects. Epistatic combinations are unique to individuals and are broken apart during reproduction, meaning they are not predictably transmissible to offspring.

165. (D) V_D
Dominance variance is the component of genetic variation that results from interactions between alleles at the same locus. This non-additive effect occurs when the heterozygote does not express the average of the two homozygous phenotypes. Because these specific allelic pairs are segregated during gamete formation, dominance deviations are not inherited by offspring in a predictable way, making this variance component non-transmissible between generations.

166. (B) V_A, to determine selection response.
Sub-partitioning genetic variance is essential for identifying the additive genetic variance component. V_A is the only part of the total genetic variation that is based on the cumulative effects of individual genes and is passed directly to offspring. By isolating this component, breeders can calculate the narrow-sense heritability and

accurately predict how much a trait will improve following a specific selection program.

167. (C) Daily fluctuation in ambient temperature
Temporary environmental variance refers to non-genetic factors that cause short-term changes in performance but do not have a lasting impact on the animal. Random daily weather changes are a perfect example, as they may slightly alter an animal's performance on the day of a measurement without affecting its overall productive potential or subsequent records. These fluctuations contribute to the within-individual variation observed in repeated traits.

168. (D) Half V_A and one-quarter V_D.
Full-siblings share more genetic information than half-siblings because they have both parents in common. They are expected to share half of their additive genetic variance and one-quarter of their dominance variance. This additional shared non-additive component, along with their higher additive similarity, means that full-sibs will generally show a stronger phenotypic resemblance to each other than individuals who only share one parent.

169. (A) Readily transmissible to offspring.
Narrow-sense heritability represents the proportion of total phenotypic variation that is caused by additive genetic effects. These effects are the result of individual genes acting independently, allowing them to be passed directly from parent to offspring through gametes. Therefore, heritability indicates how much of the variation breeders can exploit to achieve permanent genetic improvement in the population through selective breeding programs.

170. (D) Full-sibs are included as half-sibs.
In a paternal half-sib design, the heritability estimate is based on the assumption that the shared genetic component is exactly one-quarter of the additive variance. If full-siblings, who share half of the additive variance and one-quarter of the dominance variance, are mistakenly included as half-sibs, the phenotypic correlation will be higher than expected. This leads to an upward bias, resulting in an overestimated heritability value.

171. (B) Provides a regression coefficient that equals h^2 directly
When performing mid-parent offspring regression, the average value of both parents is used as the predictor. This mid-parent value represents the total additive genetic contribution from the parental generation. Unlike single-parent regression, where the coefficient must be doubled, the mid-parent regression slope directly estimates the narrow-sense heritability. This method also tends to reduce the standard error of the estimate compared to using only one parent.

172. (A) Between-individual and within-individual.
Repeatability analysis using an analysis of variance partitions the total phenotypic variation into two main parts. The between-individual component represents the variation due to genetic differences and permanent environmental factors that consistently affect an individual. The within-individual component represents the variation caused by temporary environmental factors that fluctuate between records. This partitioning is essential for assessing the consistency of repeated performance traits in livestock.

173. (C) Deciding culling for future production.
Most Probable Producing Ability is a statistical tool used to estimate an individual's future productivity based on its past performance. By adjusting for the number of records and the trait's repeatability, it provides a more accurate ranking of animals than simple averages. Breeders use MPPA to make practical management decisions, such as which cows to remove from the herd to maximize future production efficiency.

174. (D) A single gene affects multiple traits.
Pleiotropy is a biological phenomenon where one gene influences the expression of two or more seemingly unrelated phenotypic traits. This shared genetic control is a primary cause of genetic correlation between traits. Unlike linkage, which can be broken by recombination, pleiotropic effects are a permanent feature of the gene's function, meaning that selection for one trait will always cause a correlated change in the others.

175. (C) Genetic increase in one decreases the other.
In an analysis of covariance, a negative cross-product or covariance between two traits indicates that the genetic factors influencing

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them act in opposite directions. This means that animals with genes for high performance in one trait tend to possess genes that lower performance in the other. Breeders must account for this negative genetic correlation to avoid undesirable outcomes when selecting for improvement in multiple performance traits.

176. (B) Family size and progeny are optimized.
The precision of heritability estimates is measured by their standard error, which decreases as the quality and quantity of the data improve. Optimizing the number of families and the number of progeny within each family ensures that the additive genetic variance is captured accurately while minimizing sampling noise. This leads to more reliable estimates, which are essential for making effective and accurate breeding decisions.

177. (D) Allele frequencies are perfectly equal
Expected heterozygosity is a measure of genetic diversity within a population. For a two-allele system, heterozygosity is calculated as $2pq$. This value reaches its mathematical maximum of 0.5 when both allele frequencies are exactly equal at 0.5. At this point, the diversity is maximized because there is an equal probability of either allele being drawn, ensuring the highest possible proportion of heterozygous individuals.

178. (B) Complete lack of genetic differentiation between subpopulations
$F_{\{ST\}}$ is a measure of genetic differentiation between subpopulations, ranging from zero to one. A value of zero indicates that the allele frequencies are identical across all groups, meaning there is no genetic structure or isolation. In this state, the population behaves as a single, panmictic unit. As $F_{\{ST\}}$ increases, it signifies that subpopulations are becoming more genetically distinct from each other due to isolation and drift.

179. (C) Proportions from ancestral populations.
Genetic admixture analysis involves examining an individual's genome to estimate the percentage of its DNA that originated from different ancestral groups or breeds. By comparing the individual's genetic markers to those of purebred reference populations, scientists can determine its history of crossbreeding. This is crucial for verifying breed purity and for understanding the genetic heritage of local livestock populations in conservation programs.

180. (D) Genomic definition of purebreds.
In livestock conservation, breed signatures are used to establish a precise genomic definition for purebred animals. These molecular fingerprints are based on unique allele frequencies that have developed over generations of isolation and selection. By using these signatures, conservationists can accurately identify purebred individuals, manage breeding programs to prevent contamination from other breeds, and ensure the long-term survival of the breed's unique genetic identity.

181. (B) One generation
If the genotype frequencies of an autosomal locus are disrupted by non-random mating, a single generation of random mating in a large population is sufficient to restore Hardy-Weinberg equilibrium. This occurs because random mating immediately reshuffles the alleles into genotypes according to the product of their frequencies. While the allele frequencies themselves do not change, the genotypic proportions return to the expected equilibrium states in one step.

182. (B) Genotypes are broken down and reassembled.
Sexual reproduction ensures that genotypes are not passed intact from parents to offspring. Instead, the parental genotypes are segregated into individual alleles during meiosis. These alleles then recombine in new pairings during fertilization to form unique genotypes in the progeny. This constant breaking down and reassembling of genetic combinations explains why only individual genes are transmitted, while genotypes are unique and temporary features of each individual.

183. (C) 27
When population size fluctuates, the effective population size is calculated using the harmonic mean. For sizes of 10, 100, and 1000, the harmonic mean is 3 divided by the sum of $\frac{1}{10}$, $\frac{1}{100}$, and $\frac{1}{1000}$. This equals $\frac{3}{0.111}$, which is approximately 27. This demonstrates how years with small populations, like the bottleneck of 10, have a disproportionately large impact on reducing the overall effective population size.

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calculation gives less weight to the individual's deviation and 'shrinks' the estimated value toward the population mean to provide a more conservative prediction.

149. (D) Weighted genetic and environmental components.
Phenotypic correlation is the observed relationship between two traits and is a result of both shared genes and shared environmental factors. It is mathematically determined by the genetic correlation and the heritabilities of the two traits, combined with the environmental correlation. This composite measure tells breeders how much traits actually vary together in the population, regardless of whether the cause is heredity or management.

150. (B) $\frac{1}{4}$ of the additive genetic covariance
Analysis of covariance on paternal half-sib data partitions the total covariance between two traits into sire and within-family components. The sire component is expected to estimate one-quarter of the additive genetic covariance. By isolating this genetic portion, researchers can calculate the genetic correlation between the traits, which describes how they are influenced by the same sets of genes or linked loci.

151. (C) The square root of the sample size
The precision of statistical estimates, including correlations and heritabilities, is determined by their standard error. This error is inversely proportional to the square root of the number of observations or sample size. Therefore, larger datasets provide more stable and reliable estimates by reducing the impact of random sampling variation, which is essential for making accurate genetic evaluations in breeding programs.

152. (A) Allele number and their frequencies.
Polymorphism Information Content is a calculation used to determine how effective a genetic marker is for identifying individuals or tracking inheritance. It evaluates markers based on how many different alleles they have and how evenly those alleles are distributed in the population. Markers with many alleles at intermediate frequencies have higher PIC values and are considered more informative for genetic mapping and diversity studies.

153. (A) Population structure H-W deviations.
Wright's F-statistics are used to describe the genetic structure of a population by measuring deviations from Hardy-Weinberg equilibrium at different levels. $F_{\{IS\}}$ measures inbreeding within subpopulations, $F_{\{ST\}}$ measures genetic differentiation between subpopulations, and $F_{\{IT\}}$ measures the total inbreeding in the entire population. Together, these statistics provide a complete picture of how genetic variation is distributed across a structured or subdivided population.

154. (B) Loss of architecture due to admixture.
High migration rates or gene flow between populations indicate that individuals are frequently moving and interbreeding between groups. This process introduces new alleles and homogenizes frequencies, which can break down the distinct genetic patterns and structures that define isolated populations. In livestock, this often leads to admixture, where the unique genetic signatures of local breeds are diluted by genes from outside populations.

155. (B) Identifying cryptic admixture or fraud.
Breed signatures are unique genomic patterns used to confirm the purity of an animal or product. They are particularly valuable for identifying cases where an animal has been crossbred but appears purebred, known as cryptic admixture. Additionally, they are used to detect food fraud by verifying that products labeled as coming from a specific high-value breed are genetically authentic, protecting both breeders and consumers.

156. (A) Describes a population where no evolutionary forces are acting
The Hardy-Weinberg principle serves as a null model because it defines the state of a population in the absence of all evolutionary processes. By assuming no mutation, selection, migration, or drift, and infinite size with random mating, it provides a baseline. Any significant deviation from these predicted frequencies allows scientists to identify and measure the specific evolutionary forces that are actively shaping the population's genetics.

157. (C) Allele and genotype frequencies
Population genetic architecture is characterized by the collective distribution of genetic variation within a group. This is measured through allele

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193. (C) Half-sibs
In quantitative genetics, an uncle and his nephew share a coefficient of relationship of one-eighth, which is the same as the relationship between half-siblings. This means they are expected to share one-eighth of their additive genetic variance. Because they have the same degree of genetic similarity, the expected covariance and phenotypic resemblance between an uncle-nephew pair are mathematically equivalent to those observed between half-sibs in a population.

194. (A) Family selection or progeny testing
Traits with very low heritability are heavily influenced by the environment, making it difficult to identify superior individuals based solely on their own phenotype. In such cases, mass selection is inefficient. Breeders instead use family selection or progeny testing, which average out environmental noise by using information from many related individuals. this provides a more accurate estimate of breeding values and allows for genetic improvement in lowly heritable traits.

195. (C) $\frac{1}{4} V_A$
In a paternal half-sib analysis of variance, the sire variance component isolates the portion of variation that is shared among offspring of the same male. Because paternal half-sibs share exactly one-quarter of their genes by descent, this component represents one-quarter of the population's additive genetic variance. This relationship is the foundation for estimating narrow-sense heritability by multiplying the sire variance component by four.

196. (B) Parent transmits only half additive variance.
When calculating heritability through parent-offspring regression, the regression coefficient b represents the proportion of the parent's deviation that is reflected in the offspring. Since a parent only transmits half of its genes to each progeny, the coefficient only captures half of the total additive genetic effect. Therefore, the value must be doubled to obtain a full estimate of the narrow-sense heritability for the trait.

197. (D) Between-individual variance and within-individual variance
Repeatability analysis is performed using an analysis of variance that partitions phenotypic variation into two major categories. Between-individual variance reflects the differences due to genetics and permanent environmental factors that stay with an animal over time. Within-individual variance accounts for temporary environmental fluctuations that vary between repeated records. This statistical approach is essential for assessing the consistency of repeated measurements on the same individual livestock.

198. (C) Compare animals with different record counts.
Most Probable Producing Ability is designed to provide a fair comparison between animals that have different numbers of performance records. Since averages based on many records are more reliable than those based on few, MPPA uses a weighting factor to adjust the individual's deviation. This allows breeders to rank and cull animals accurately, ensuring that those with few but exceptional records are not overvalued compared to consistent long-term producers.

199. (C) Genes are close on the same chromosome.
Linkage causes genetic correlation because the genes controlling different traits are physically located near each other on the same chromosome. This proximity means they are less likely to be separated by crossing over and tend to be inherited together as a unit. While this correlation can eventually be broken by recombination over many generations, it creates a temporary genetic relationship that breeders must account for during selection.

200. (D) Sire variances and sire covariance.
Estimation of genetic correlation using ANCOVA on half-sib data involves calculating both the variances for each trait and the covariance between them. By isolating the sire component of variance and the sire component of covariance, breeders can determine how much of the relationship between the traits is due to shared additive genetic effects. This method provides a clear estimate of the genetic link between performance characteristics in livestock.

201. (A) Common environment shared by dam and offspring.
A major source of bias in parent-offspring heritability estimates is the shared environment between a mother and her young. Factors such as maternal nutrition and nursing provide a common environmental influence that makes the offspring appear more similar to the dam than they are genetically. If not properly accounted

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for, this environmental covariance inflates the phenotypic correlation, leading to a biased overestimate of the trait's true heritability.

202. (B) The number of distinct alleles present at a locus in a population
Allelic richness is a measure of genetic diversity that counts how many different versions of a gene exist at a particular locus within a population. It is a critical indicator of genetic health, as it reflects the population's potential for adaptation. Unlike heterozygosity, allelic richness is highly sensitive to population bottlenecks, making it a valuable tool for monitoring the long-term genetic diversity of rare or local livestock breeds.

203. (B) The reduction in heterozygosity due to population subdivision
The fixation index $F_{\{ST\}}$ is used to measure the genetic structure of a population by evaluating the differences in allele frequencies between subpopulations. It quantifies the reduction in heterozygosity that occurs when a population is divided into smaller, isolated groups compared to a single large group. This statistic is essential for understanding genetic differentiation and for managing the genetic diversity of subdivided or fragmented livestock populations.

204. (A) Neutral genomic markers (microsatellites/ SNPs).
Modern geneticists use neutral genomic markers, such as microsatellites and Single Nucleotide Polymorphisms, to estimate migration rates and gene flow. Because these markers are not under direct selection, they provide an unbiased record of genetic exchange between populations. By analyzing the distribution of these markers across different herds, researchers can determine the degree of connectivity and identify instances of recent crossbreeding or genetic admixture.

205. (B) The sum of squared allele frequencies.
The effective number of alleles is a measure of genetic diversity that represents the number of equally frequent alleles that would be required to produce the same level of heterozygosity as observed in the population. It is calculated as the reciprocal of the sum of the squared frequencies of all alleles at a locus. This metric helps geneticists understand the distribution of genetic variation and the impact of rare alleles.

206. (C) 0.0001
In a population at Hardy-Weinberg equilibrium, the frequency of individuals affected by a recessive condition is equal to the square of the recessive allele frequency (q^2). If the frequency of the recessive disease allele is 0.01, then the expected frequency of affected individuals is 0.01 multiplied by 0.01, which equals 0.0001. This demonstrates how rare recessive alleles result in a very low proportion of affected phenotypes.

207. (C) The specific allele pairing at all loci.
Individual genetic architecture refers to the unique genetic makeup of a single organism, defined by the specific pairs of alleles it possesses at every genetic locus. These specific combinations determine the individual's genotype and phenotypic potential. Unlike population architecture, which focuses on collective frequencies, individual architecture is about the internal genetic structure and the non-additive interactions, such as dominance, that occur within a single organism's genome.

208. (A) $N_e = \dfrac{4 \times N_m \times N_f}{N_m + N_f}$
The effective population size for populations with unequal numbers of breeding males and females is calculated using a specific weighted formula. By multiplying four times the product of the number of males and females and dividing by their total sum, the formula correctly reflects how the rarer sex limits genetic diversity. This calculation is vital for managing genetic health in livestock populations where sex ratios are often highly skewed.

209. (D) Inbreeding coefficient (F)
The inbreeding coefficient is a measure of genetic relatedness within an individual. It represents the probability that the two alleles at a randomly chosen locus are identical by descent, meaning they were inherited from a common ancestor. This coefficient ranges from zero to one and is used to quantify the level of inbreeding in a population, helping breeders avoid the negative effects of inbreeding depression.

210. (A) Dominance deviation
In quantitative genetics, the dominance deviation describes the non-additive interaction between two alleles at a single locus. It is measured as the difference between the phenotypic value of the heterozygote and the mid-parent value, which is the average of the two homozygotes. A non-zero

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dominance deviation indicates that one allele is partially or completely masking the expression of the other, influencing the trait's total variation.

211. (B) 1.0
The average effect of an allele is a statistical measure that depends on the frequencies of all alleles at that locus. As an allele becomes more common and approaches fixation with a frequency of 1.0, its contribution to the variation within the population diminishes. At the point of fixation, every individual carries the same allele, meaning it no longer creates deviations from the population mean.

212. (A) $\alpha = a + d(q - p)$
The average effect of gene substitution represents the expected change in the population mean when one allele is replaced by another. For a two-allele system, it is calculated by adding the additive value to the dominance deviation, which is weighted by the difference in allele frequencies. This formula is essential for linking individual gene action to the predictable response observed in selective breeding programs.

213. (D) Can be transmitted to progeny.
Breeding value is the additive portion of an individual's total genotypic value. It is the sum of the average effects of the individual alleles the animal possesses. Because alleles are the units of inheritance that pass through gametes, the breeding value represents the only part of the genetic merit that is predictably transmitted to offspring. This makes it the most important parameter for selective breeding decisions.

214. (B) Genes at different loci act perfectly independently (additively) across loci
Interaction deviation, or epistatic deviation, occurs when alleles at different genetic loci influence each other's expression. If the genes at various loci act completely independently, their effects are simply cumulative, and no interaction exists. In this state of perfect additivity across loci, the epistatic deviation becomes zero, and the total genotypic value is equal to the sum of the individual locus effects.

215. (C) Strong influence by non-genetic factors.
Phenotypic variance is the total observed variation in a trait, and environmental variance (V_E) represents the portion caused by non-genetic factors. A large V_E indicates that the trait is highly sensitive to management, nutrition, or climate. This reduces the proportion of variation due to genetics, leading to a lower herizability. Such traits are often difficult to improve through simple selection and require improved environmental management.

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216. (D) Variance of breeding values.
Additive genetic variance is specifically defined as the variance of the breeding values of individuals in a population. It is the component of genetic variation that responds to selection because it is based on the cumulative effects of individual alleles. Isolating V_A is critical for quantitative geneticists, as it determines the narrow-sense herizability and the potential for long-term genetic progress in a breeding program.

217. (A) Only the specific record taken at that time
Temporary environmental variance refers to non-genetic factors that cause random fluctuations in an animal's performance. These factors, such as a single day's weather or a minor short-term illness, only affect the record taken during that specific time period. They do not have a lasting impact on the animal's productive potential and do not influence future records or the genetic merit passed to offspring.

218. (B) $\frac{1}{2} V_A$ and no V_D or V_I.
The genetic covariance between a parent and its offspring is exclusively due to shared additive genetic effects. Each parent transmits exactly half of its genes, which corresponds to one-half of its breeding value. Dominance and epistatic deviations are not shared because these interactions involve specific combinations of alleles that are broken up and rearranged during the process of meiosis and recombination.

219. (B) Less than or equal to broad-sense herizability (H^2)
Narrow-sense herizability considers only the additive genetic variance, which is the part of the genotype transmitted to offspring. Broad-sense herizability includes all genetic components, including non-additive dominance and epistatic effects. Since narrow-sense is a subset of the total genetic variance, its value will always be less than or equal to the broad-sense heritability (H^2), representing only the transmissible portion of the total genetic merit.

184. (D) The effective population size (Ne)
In a closed livestock herd, the rate of inbreeding is primarily determined by the effective population size. Small effective sizes lead to a faster accumulation of inbreeding because individuals are more likely to share common ancestors within fewer generations. Breeders manage inbreeding by maximizing N_e through techniques like balanced sex ratios and using more breeding males, which slows the increase in homozygosity and preserves genetic diversity.

185. (D) $d > a$
Overdominance occurs when the phenotypic expression of the heterozygote is superior to that of both homozygous classes. On the quantitative genetic scale, a represents the additive value of the homozygote. If the heterozygote's dominance deviation d is greater than a, it indicates that the gene action at that locus is overdominant. This phenomenon is a key driver of heterosis and is utilized in crossbreeding programs.

186. (B) Statistical properties of the population
The average effect of a gene is a concept that bridges the gap between individual molecular genetics and population-level inheritance. It is a statistical measure that depends on the frequency of alleles within the population's gene pool. By focusing on these average effects, quantitative geneticists can calculate breeding values and additive variances, which are essential for predicting how the entire population will evolve or respond to selection.

187. (B) One allele is substituted for another.
The average effect of gene substitution measures the expected change in the phenotypic mean of a population when one allele at a locus is replaced by an alternative allele. This value accounts for both the individual effects of the alleles and the dominance interactions that occur when they are paired with others in the population. It is the fundamental unit used to describe the transmissible genetic change in breeding.

188. (A) Evaluating the mean of its progeny.
An individual's breeding value is defined by its ability to pass favorable traits to its offspring. Since each parent transmits exactly half of its genes, the average performance of a large number of its progeny, compared to the population mean, provides the most accurate estimate of its genetic worth. This progeny testing is the gold standard for evaluating sires and making selection decisions in livestock breeding.

189. (C) Alleles at the same locus
Dominance deviation is an intra-locus interaction, meaning it involves the non-additive relationship between two alleles at a single genetic location. This interaction determines whether the heterozygote is closer to one homozygote or the other. Because individual alleles are segregated and separated during meiosis, these specific allelic pairings are not inherited intact, which is why dominance effects do not contribute to the predictable, transmissible breeding value.

190. (A) In uniform, controlled environments.
Genotype-environment interaction variance occurs when different genotypes respond inconsistently to environmental changes. In highly uniform and controlled environments, such as specialized research facilities or standardized barns, environmental variation is minimized. Consequently, all genotypes are exposed to similar conditions, making their relative rankings more stable. In these specific cases, the interaction component $V_{\{GE\}}$ is often negligible and can be excluded from phenotypic variance partitioning models.

191. (C) Total V_G $(V_A + V_D + V_I)$
In clonal reproduction, the entire genetic makeup of the parent is passed intact to the offspring without the reshuffling of alleles that occurs in sexual reproduction. Therefore, the resemblance between a clone and its parent is governed by the total genetic variance, which includes additive, dominance, and epistatic components. This makes clones more similar to their parents than sexually produced offspring, who only reliably share additive variance.

192. (D) Within-individual temporary effects.
Variations in an animal's repeated records, such as different milk yields across lactations, are primarily caused by temporary environmental factors. These factors fluctuate randomly between measurements and do not have a lasting impact on the animal's productive potential. In statistical analysis, these fluctuations are captured as within-individual variance. Identifying these effects is crucial for calculating repeatability and understanding the consistency of performance traits in individual animals.

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subpopulations and the genetic differentiation between those subpopulations. $F_{\{IT\}}$ provides a comprehensive overview of how all levels of population structure contribute to the loss of genetic diversity within individuals.

229. (D) Recent crossbreeding or migration has occurred
Estimating gene flow and migration rates allows breeders and conservationists to determine if there has been recent genetic exchange between isolated herds. High levels of gene flow suggest that populations are being mixed through crossbreeding or migration, while low rates indicate isolation. This information is critical for managing the genetic purity of rare breeds and for understanding the historical development of livestock populations.

230. (B) Distinct allele frequency combinations.
A breed signature identified through high-density SNP genotyping is defined by the specific allele frequencies and marker combinations found within a particular breed. These unique genomic patterns result from generations of selection and isolation. This molecular signature acts as a genetic fingerprint, allowing researchers to precisely identify breed origin, assess purity, and detect levels of admixture with other livestock populations.

231. (B) Expected genotype counts against observed genotype counts
Testing for Hardy-Weinberg equilibrium is fundamentally a statistical comparison using a Chi-square test. The process involves calculating the expected number of individuals for each genotype based on allele frequencies and then comparing these theoretical values to the actual genotype counts observed in the population. A significant difference between the two indicates that evolutionary forces or non-random mating are actively shifting the genetic structure.

232. (D) Recombination breaks genotypes each generation.
At the population level, the genetic structure is defined by gene transmission because the process of meiosis and recombination ensures that genotypes are not inherited intact. Each generation, independent assortment and crossing over shuffle alleles into new combinations. While an individual's specific genotype is unique and temporary, the individual genes persist across generations as they are redistributed throughout the population's gene pool.

233. (A) Random genetic drift
Effective population size is the primary determinant of the magnitude of random genetic drift. In small populations with a low N_e, chance events have a much larger impact on allele frequencies, potentially leading to the rapid loss of genetic variation or the fixation of harmful alleles. Larger effective populations are more stable, as the larger gene pool buffers the population against these random fluctuations in genetic structure.

234. (B) Inbreeding rate decreases as effective population size increases
The rate of inbreeding per generation is inversely proportional to twice the effective population size. This relationship means that as the breeding population becomes larger and more genetically diverse, the probability of mating between relatives decreases, leading to a slower rise in homozygosity. Breeders strive to maintain a large effective population size to ensure the long-term genetic health and viability of their herds.

235. (A) $a(p-q)+2pqd$
The algebraic formula for the population mean of a metric character accounts for both additive and dominance genetic effects. It is calculated by multiplying the additive value a by the difference in allele frequencies and adding the heterozygote deviation d weighted by the frequency of heterozygotes. This weighted average shows how both allele frequencies and the nature of gene action determine the overall phenotypic average of the population.

236. (A) The frequency of the other allele and the average effect of gene substitution (α)
The average effect of an individual allele is a statistical measure that depends on the current allele frequencies in the population. It is calculated by multiplying the frequency of the alternative allele by the average effect of gene substitution. This relationship highlights that the impact of a single allele is always relative to the genetic context of the population in which it is being expressed and transmitted.

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for understanding the genetic history and mixing of various livestock populations over time.

255. (C) Attained gradually over several generations.
Unlike autosomal loci, which reach Hardy-Weinberg equilibrium in a single generation of random mating, sex-linked loci take several generations to stabilize. This occurs because males and females possess different numbers of copies of the locus. The allele frequencies oscillate and gradually approach an equilibrium state where frequencies are equal in both sexes. This slow convergence is a unique feature of the inheritance patterns of genes located on sex chromosomes.

256. (B) Random mating
Hardy-Weinberg equilibrium is a theoretical state where allele and genotype frequencies remain constant over time. This equilibrium is maintained under the assumption of random mating, as it ensures that gametes are joined without genetic preference. Evolutionary forces like mutation, selection, and migration disrupt this balance by altering frequencies. Therefore, random mating is a necessary condition for a population to remain in a state of genetic equilibrium.

257. (D) Altering population allele frequencies.
Long-term genetic improvement programs focus on the population level because the collective gene pool is the reservoir of variation. While individual animals are selected based on their genotypes, the goal of breeding is to increase the frequency of favorable alleles within the whole population. By shifting these frequencies over generations, breeders can achieve permanent and cumulative genetic progress that benefits the entire breeding group or livestock breed.

258. (A) Harmonic mean
The effective population size for a population that fluctuates in size over several generations is calculated using the harmonic mean. This mathematical method is the reciprocal of the average of the reciprocals of the census sizes. Because the harmonic mean is more sensitive to small values, it correctly reflects the disproportionate impact of bottlenecks and small population sizes on increasing genetic drift and reducing genetic diversity.

259. (C) An increase in the rate of inbreeding (ΔF) and genetic drift
Selective breeding programs that use a very small number of sires for a large number of females significantly reduce the effective population size. This skewed contribution to the next generation narrows the genetic base, leading to a faster rate of inbreeding. It also increases the impact of genetic drift, as chance events in the few selected parents can cause large, unpredictable shifts in the population's overall allele frequencies.

260. (A) Complete dominance
Complete dominance occurs when the phenotype of the heterozygote is identical to that of one of the homozygous classes. In the quantitative genetic scale where homozygotes are a and $-a$, if the dominance deviation d is exactly equal to the additive value a, the gene action is strictly described as complete dominance. In this case, the presence of a single dominant allele is sufficient to produce the full phenotypic effect.

261. (D) Expected mean change from the allele.
The average effect of an allele tells a breeder the expected deviation from the population mean that occurs when that specific gene version is inherited. It is a statistical value that averages the allele's impact across all possible genetic backgrounds in the population. Understanding these effects is essential for calculating breeding values, which allow breeders to rank and select parents that will transmit the most favorable genetic merit.

262. (B) Breeding values
The average effect of gene substitution is the core parameter used to calculate an individual's breeding value. It measures the change in phenotypic merit that occurs when one allele is replaced by another. Since breeding value is the sum of the average effects of all the alleles an individual carries, this parameter directly dictates the additive genetic worth of an animal and its potential for improving the next generation.

263. (C) The sum of average effects of all its alleles
Theoretically, an individual's breeding value is formulated as the cumulative sum of the average effects of every allele it possesses across all genetic loci that influence a specific trait. This additive measure represents the portion of the individual's genetic merit that is transmissible to

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resulting in a lower heritability estimate for the trait being studied.

246. (A) Double the regression coefficient
In an intra-sire regression of offspring on dam, the regression coefficient b represents the relationship between the mother and her young within groups sired by the same male. Since a dam only transmits half of her additive genetic material to her offspring, the regression coefficient only captures half of the total additive effect. To obtain a full estimate of the narrow-sense heritability, the observed coefficient must be multiplied by two.

247. (C) Milk yield across multiple lactations
Repeatability analysis is essential for traits that are expressed multiple times during an animal's life, such as milk yield in successive lactations or wool production in yearly shearings. By measuring the consistency of performance across these repeated events, breeders can estimate the combined effect of genetics and permanent environment. This information allows for the prediction of future productivity and helps in making early culling and selection decisions.

248. (D) The trait has high repeatability.
The Most Probable Producing Ability calculation uses repeatability as a weighting factor for an animal's own performance record. When repeatability is high, it indicates that a single record is a very reliable predictor of future performance and is strongly influenced by consistent genetic and permanent environmental factors. In these cases, the MPPA gives significant weight to the individual's average, making it a powerful tool for selection.

249. (A) Phenotypic correlation varies by magnitude.
The observed phenotypic correlation is the result of both genetic and environmental correlations. When the genetic and environmental influences act in opposite directions, they can cancel each other out or change the overall strength of the relationship. In such cases, the actual phenotypic correlation seen in the herd will depend on the relative magnitude and direction of these two underlying components, making it more complex to interpret.

250. (A) $\frac{1}{4}\mathrm{cov}_A$
In a paternal half-sib analysis of covariance, the sire component of covariance represents the portion of the relationship between two traits that is shared due to the shared sire. Because half-siblings share one-quarter of their genes by descent, the sire component is expected to estimate exactly one-quarter of the additive genetic covariance between the traits. This isolated component is used to calculate the genetic correlation.

251. (B) An optimal balance between the number of sires and progeny per sire is achieved
The precision of herizability estimated by paternal half-sib correlation is maximized when the experimental design is balanced. This requires a large number of sires and an optimal number of progeny per sire. Having too few sires or too few progeny increases the standard error. By balancing these two factors, researchers can capture the most genetic variation while minimizing the impact of sampling error, resulting in a highly precise estimate.

252. (A) Mean of the selected parents and the population mean.
The selection differential is a measure of the intensity of selection applied to a population. It is calculated as the difference between the average phenotypic performance of the individuals chosen to be parents and the overall mean of the population from which they were selected. A larger selection differential typically leads to a greater genetic response in the next generation, depending on the trait's heritability.

253. (C) Subpopulation genetic differentiation.
Wright's $F_{\{ST\}}$ is a fundamental statistic in population genetics used to quantify the degree of genetic divergence between subpopulations. It measures the proportion of total genetic variation that is due to differences in allele frequencies between the groups rather than variation within them. $F_{\{ST\}}$ values provide insights into the effects of isolation, migration, and drift on the genetic structure of structured livestock populations.

254. (D) Putative ancestral gene pools
Modern genomic analysis tools can detect admixture by assigning different segments of an individual's genome to ancestral gene pools. By comparing an animal's DNA to reference populations representing pure ancestral breeds, researchers can estimate the probability and proportion of its heritage from those sources. This is essential for verifying breed purity and

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272. (A) A sheep's first shearing is an excellent predictor of its lifetime wool production.
A high repeatability estimate of 0.8 indicates that the trait is very consistent within the individual over time. This means that a sheep's initial performance, such as its first shearing weight, is strongly correlated with its future wool production. In such cases, breeders can confidently use early records to make selection and culling decisions, as the individual's future productivity is highly predictable from its current performance.

273. (D) Avoid culling based on bad records.
Most Probable Producing Ability helps breeders make fairer management decisions by accounting for the number of records an individual has. If an animal has a single poor record, but the trait's repeatability is low, the MPPA will shrink the estimate toward the population mean. This adjustment prevents breeders from making premature culling decisions based on unreliable or unlucky single observations, leading to more accurate long-term productivity management.

274. (A) The expression of two traits is controlled in part by the same genes
A genetic correlation occurs when the genetic influences on two different traits are not independent. This is primarily caused by pleiotropy, where the same gene influences multiple phenotypic characteristics, or by linkage, where the genes for different traits are inherited together. This relationship means that when a breeder selects for one trait, they will cause a simultaneous and predictable genetic change in the other trait.

275. (C) Sire component of covariance
In a paternal half-sib analysis of covariance, researchers partition the total covariance between two traits into sire and within-family components. The sire component of covariance represents the portion of the relationship between the traits that is due to shared genetic effects from the fathers. By isolating this sire component, breeders can calculate the genetic correlation, providing a clear measure of how the two performance traits are genetically linked.

276. (A) The sample size of families and progeny is large and well-balanced
The standard error of a herizability estimate is a measure of its precision and decreases as the quality and quantity of data increase. A large sample size with many families and a consistent number of progeny per family reduces the impact of random sampling noise and environmental variation. This lead to a more stable and reliable heritability estimate, which is essential for making accurate genetic evaluations and selection decisions.

277. (A) 0 to 1
Polymorphism Information Content is a standardized metric used to evaluate the usefulness of a genetic marker for diversity and linkage analysis. Its values range from zero, which indicates no variation at all, to one, which would represent a marker with an infinite number of equally frequent alleles. This range allows researchers to easily compare the informativeness of different markers and select the best ones for genomic studies.

278. (B) Mating within groups and subdivision.
Wright's F-statistics show that the total inbreeding in an individual, $F_{\{IT\}}$, is a combination of two factors. $F_{\{IS\}}$ measures the inbreeding that results from non-random mating or relatedness within a specific subpopulation. $F_{\{ST\}}$ measures the differentiation that arises from the subdivision of the whole population into isolated groups. Together, these two forces drive the overall reduction in heterozygosity and increase in homozygosity in structured livestock populations.

279. (C) Originated from immigrants of another population
Gene flow is estimated by using genetic markers to track the movement of alleles between different groups. By identifying alleles in a population that are characteristic of another, researchers can determine the proportion of the gene pool that originated from recent immigrants. This measurement of migration is essential for assessing the degree of genetic isolation and for managing the diversity and purity of livestock breeds.

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280. (C) Their progeny are born that will eventually replace them.
The generation interval is a critical parameter in breeding programs and is defined as the average age of the parents when their offspring that will become the next generation of parents are born. A shorter generation interval leads to faster

its offspring. It is the most critical parameter in quantitative genetics for evaluating the genetic potential of animals in selection programs.

264. (D) Is not transmissible intact to progeny.
Dominance deviation involves non-additive interactions between two alleles at a single locus. Because individual alleles are segregated and separated into gametes during meiosis, these specific allelic pairs are not passed on together to the next generation. This lack of predictability and transmissibility means that dominance effects cannot be directly exploited by simple mass selection, which relies instead on the predictable and cumulative action of additive gene effects.

265. (A) Measuring the spread of phenotypic values around the population mean
Phenotypic variance is a statistical measure of the total variation observed in a trait within a population. It is calculated by measuring the spread or dispersion of individual phenotypic values around the overall population mean. This total variance is the starting point for quantitative genetic analysis, as it is then partitioned into genetic and environmental components to estimate herizability and other essential genetic parameters.

266. (B) V_A
Narrow-sense herizability is defined as the proportion of total phenotypic variation that is caused by additive genetic variance. While total genetic variance includes non-additive components like dominance and epistasis, only V_A represents the cumulative effects of individual genes that are passed directly to offspring. Therefore, herizability only considers this predictable, transmissible portion of the genetic variance, making it the key factor for predicting selection response.

267. (B) Duration and consistency of effect.
The primary difference between permanent and temporary environmental variance is the duration of their impact on the individual. Permanent environmental effects consistently influence an animal's performance throughout its entire life, such as the lasting impact of early nutrition. In contrast, temporary effects fluctuate randomly and only influence a single record or a short time period. This distinction is essential for calculating repeatability and understanding long-term performance consistency.

268. (A) $\frac{1}{4} V_D$
Full-siblings have a higher genetic resemblance than half-siblings because they share more genes by descent. Specifically, full-sibs share one-quarter of their dominance variance, which is a non-additive genetic interaction between alleles at the same locus. This additional shared component, combined with their half-share of the additive genetic variance, explains why siblings with the same parents are more phenotypically similar than those who share only one.

269. (C) Phenotypic variance is due to differences in breeding values
A herizability of 0.40 means that 40% of the total phenotypic variation observed in a population is caused by differences in the breeding values of individuals. This indicates that a significant portion of the observed performance is due to additive genetic effects that can be passed to offspring. This level of heritability suggests that selective breeding will be effective in achieving permanent genetic improvement for the trait in question.

270. (B) Genetic response to selection differential.
Realized herizability is an empirical estimate of herizability derived from the results of a selection experiment. It is calculated as the ratio of the observed genetic response (the progress made in the offspring) to the selection differential (the superiority of the selected parents). This practical measure confirms how much of the intended selection pressure was actually translated into permanent genetic gain in the next generation.

271. (C) Bias from mating and environment.
Intra-sire regression of offspring on dam is a specialized technique used to obtain a more accurate herizability estimate. By comparing offspring to their mothers within groups that share the same father, researchers can effectively control for the genetic and environmental influences of the sire. This approach helps eliminate biases that might otherwise arise from non-random mating patterns or from shared environmental conditions between the sires and their progeny.

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CHAPTER 05
Population Genetics

2016

1. In a randomly mating population, if the frequency of a recessive allele for an autosomal locus is 0.4, what is the expected frequency of the heterozygous genotype?
(A) 0.16
(B) 0.36
(C) 0.48
(D) 0.64

2006

2. Which of the following assumptions is required for a population to remain in Hardy-Weinberg Equilibrium over successive generations?
(A) Absence of migration
(B) High mutation rate
(C) Assortative mating
(D) Small population size

2015

3. Under the island model of migration, what determines the change in gene frequency in a local subpopulation in a single generation?
(A) Mutation rate and the magnitude of random genetic drift in isolates
(B) Selection coefficient against dominant alleles in the founder group
(C) Migration rate and the allele frequency difference between populations
(D) Rate of back mutation and frequency of deleterious recessive genes

2011

2015

4. When a deleterious recessive allele is subjected to complete selection (fitness of homozygous recessive is zero), the change in gene frequency (Δq) after one generation is represented by which equation?
(A) $\frac{-q^2}{1-q^2}$
(B) $\frac{-p^2 q}{1-p^2}$
(C) $\frac{-q}{1+q}$
(D) $\frac{-q^2}{1+q}$

2009

5. Which of the following conditions most significantly reduces the effective population size (N_e) relative to the census size?
(A) Equal numbers of breeding males and females
(B) Random variation in family size following a Poisson distribution
(C) A highly skewed sex ratio of breeding individuals
(D) Continuous migration from a large source population

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2025

6. The epistatic variance (V_I) component of quantitative traits arises primarily from which genetic phenomenon?
(A) Additive effects of alleles at a single locus
(B) Non-allelic interactions between two or more loci
(C) Dominance deviations within a single locus
(D) Interactions between specific genotypes and environmental factors

2019

7. Which of the following methods estimates narrow-sense herizability by evaluating the covariance between half-sibs?
(A) Full-sib correlation
(B) Parent-offspring regression
(C) Diallel cross analysis
(D) Paternal half-sib correlation

2008

8. In the breeder's equation ($R = h^2 S$), the selection differential (S) is defined as the difference between the mean phenotypic value of:
(A) The selected individuals and the unselected base population
(B) The unselected base population and the subsequent generation
(C) The selected individuals and their offspring
(D) The offspring and the unselected base population

genetic progress per year, as it allows for more frequent selection cycles. Managing this interval is essential for optimizing the rate of genetic improvement in livestock populations.

281. (A) The observed frequencies differ significantly from expected frequencies.
In a Hardy-Weinberg equilibrium test, a significant Chi-square value means that the actual genotype counts in the population do not match the proportions predicted by the allele frequencies. This indicates that one or more of the equilibrium assumptions, such as random mating or the absence of selection, are being violated. This statistical evidence allows researchers to identify the evolutionary forces that are actively changing the population's genetic structure.

282. (B) Frequencies change, not genotypes.
Individual genetic architecture is defined by unique genotypes that are fixed for a single lifetime. In contrast, population genetic architecture is dynamic and characterized by the frequencies of individual alleles in the gene pool. Evolutionary change occurs as these allele frequencies shift over generations through transmission and selection, while individual genotypes are constantly rearranged through recombination, emphasizing the different levels at which genetic information is maintained and evolved.

283. (A) Bottlenecks and skewed sex ratios.
Effective population size is most significantly reduced when a population passes through a bottleneck or when there is an unequal number of breeding males and females. These conditions restrict the total amount of genetic material that can be passed to the next generation, dramatically increasing the impact of genetic drift. By narrowing the genetic base, these factors cause the population to behave genetically like a much smaller group than the census suggests.

284. (A) 1%
The rate of inbreeding per generation is calculated using the formula $\Delta F = \frac{1}{2N_e}$. For an effective population size (N_e) of 50, the rate is 1 divided by 100, which equals 0.01, or 1%. This relationship demonstrates how the effective size directly determines the speed at which homozygosity increases and genetic diversity is lost in a population, highlighting the importance of maintaining large breeding groups.

285. (A) The heterozygote is exactly intermediate between the two homozygotes.
In the quantitative genetic scale for metric characters, d represents the dominance deviation of the heterozygote from the midpoint of the two homozygotes. If d is equal to zero, it indicates that there is no dominance and the alleles act in a purely additive manner. In this case, the heterozygote's phenotypic expression is perfectly intermediate, reflecting the cumulative and independent effects of the individual alleles at that genetic locus.

286. (D) Regardless of its paired allele in the population.
The average effect of a gene is a statistical measure that captures the mean phenotypic deviation an allele creates, taking into account its interactions with all other possible alleles based on their frequencies in the population. By focusing on this average impact, quantitative genetics can describe the transmissible genetic worth of an allele without needing to know the specific genotype of the individual it will eventually pair with in the next generation.

287. (C) Linear, additive effect of replacement.
The average effect of gene substitution is a key parameter that measures the predictable change in a population's phenotypic mean when one allele is replaced by another. Because it captures the linear, additive impact of changing allele frequencies, it is the primary factor that determines how a population will respond to selection. Breeders use this concept to estimate the potential for genetic progress through the selective accumulation of favorable alleles.

288. (B) +200 kg
Breeding value represents the total additive genetic merit of an individual, while expected progeny difference (EPD) or predicted transmitting ability represents the value that the individual is expected to pass to its offspring. Since each parent contributes only half of its genes to any single progeny, the EPD is exactly one-half of the total breeding value. If a sire's BV is +400 kg, his EPD will be +200 kg.

289. (D) The genotypic value and breeding value.
In quantitative genetics, the total genotypic value of an individual is composed of additive genetic effects and non-additive interactions. The breeding value represents the additive

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part, which is the sum of the average effects of the alleles. The difference between the total genotypic value and this breeding value is the dominance deviation. This component reflects the non-additive interaction at a locus that is not predictably transmissible to the next generation.

290. (A) Relative performance changes with environment.
Genotype-environment interaction occurs when the phenotypic performance of different genotypes is inconsistent across varying environmental conditions. This means that a genotype that is superior in one environment may be inferior in another. This variance component $V_{\{GE\}}$ is significant when breeders need to select animals for diverse climates or management systems, as it indicates that the best genetics for one situation might not be the best for another.

291. (C) The resemblance between relatives and response to selection
Sub-partitioning genetic variance identifies additive genetic variance (V_A) as the only component that follows a predictable pattern of inheritance. Because individual alleles are the units of transmission, VA is the primary factor that determines how much offspring will resemble their parents. It is also the only genetic component that responds to simple selection, making it the most important parameter for calculating heritability and for achieving genetic improvement in livestock.

292. (A) $V_{\{Et\}}$
A temporary environmental factor is one that influences an animal's performance during a specific measurement but does not have a lasting effect. A localized infection that briefly reduces a cow's milk yield on a single test day is a perfect example. Because this factor is transient and does not alter the animal's permanent productive potential or its genetic makeup, it is classified as temporary environmental variance in phenotypic partitioning.

293. (D) Dominance variance (V_D)
The genetic covariance between a parent and its offspring is exclusively based on shared additive genetic effects. Each parent contributes exactly half of its individual alleles to each progeny. Non-additive effects like dominance variance involve specific combinations of alleles that are segregated and broken up during meiosis. Therefore, dominance deviations are not shared between parent and offspring and do not contribute to the predictable genetic resemblance between them.

294. (B) Highly heritable
Heritability values range from zero to one and indicate the proportion of phenotypic variation due to additive genetic effects. A value of 0.60 is considered high in livestock breeding. This indicates that 60% of the observed differences in the trait are due to transmissible genetic merit. For such highly heritable traits, mass selection is very effective because an animal's own performance is a strong and reliable indicator of its breeding value.

295. (B) Influenced by dominance gene action.
Inbreeding depression refers to the reduction in fitness or performance that occurs when individuals become more homozygous through mating with relatives. This phenomenon is primarily observed in traits where there is significant dominance gene action. Inbreeding increases the likelihood that harmful recessive alleles will be paired together and expressed, leading to a decline in the average performance of the population, especially for complex fitness-related traits.

296. (D) Sire-offspring regression
Maternal effects, such as nutrition and care provided by the mother, can bias heritability estimates by creating an environmental resemblance between dam and offspring. To avoid this, breeders often use sire-offspring regression. Since sires generally have much less environmental contact with their progeny, the phenotypic correlation between them is more likely to reflect only shared additive genetic variance, providing a cleaner and less biased estimate of the true heritability.

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297. (A) Temporary environmental effects ($V_{\{Et\}}$) are highly influential on single records.
Low repeatability indicates that an individual's performance is inconsistent across multiple records or time periods. This occurs when temporary environmental factors, such as daily management changes or minor health fluctuations, have a large impact on each measurement. In such cases, a single record is a poor predictor of an animal's future productivity, and breeders must use multiple observations to

accurately assess the animal's true long-term productive potential.

298. (B) Corrects the average based on record count.
Most Probable Producing Ability is superior to using a simple average because it accounts for the number of records an individual has. An average based on many lactations is more reliable than one based on a single measurement. MPPA uses a weighting factor based on repeatability to adjust for this reliability, providing a more conservative and accurate prediction of future performance. This ensures that selection decisions are based on stable productive potential.

299. (B) Transient and breaks via recombination.
Genetic correlation caused by linkage occurs when the genes for two different traits are located close together on the same chromosome. While they tend to be inherited together initially, they are not permanently linked. Over many generations of random mating, crossing over during meiosis will eventually separate these genes. This leads to a gradual breakdown of the correlation, making linkage-based relationships transient compared to the permanent correlation caused by pleiotropy.

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300. (A) Heritability of X, heritability of Y, and the genetic correlation between X and Y.
The correlated response to selection describes how trait Y will change when selection pressure is applied to trait X. This response is mathematically determined by the intensity of selection, the square roots of the heritabilities for both traits, and the genetic correlation between them. Understanding this relationship is essential for breeders, as it allows them to predict how improving one trait will indirectly impact other performance characteristics in the population.

****

237. (A) Average effects of the two alleles.
The average effect of gene substitution is practically defined as the linear difference between the average effects of two alternative alleles at a locus. It represents the expected change in the breeding value of an individual if one allele is replaced by another. This parameter is the fundamental building block for calculating additive genetic variance and for predicting the outcome of selective breeding programs in livestock.

238. (B) 2
Breeding value represents the total additive genetic merit of an individual. Since a parent only contributes half of its genes to any single offspring, its transmitting ability or expected progeny difference is exactly half of its total breeding value. Therefore, to calculate the full breeding value from a transmitting ability estimate, the value must be multiplied by two, reflecting the animal's total genetic worth as a parent.

239. (C) Form the basis of heterosis utilized.
Non-additive genetic effects, specifically dominance and epistasis, involve interactions between alleles that are not passed directly to offspring. However, these effects are the primary biological cause of heterosis, or hybrid vigor, which is observed in crossbreeding programs. When individuals from different populations are crossed, these non-additive interactions can result in superior performance in the first generation, which is a key strategy for many commercial livestock producers.

240. (B) Importance of heredity vs environment.
Partitioning phenotypic variance allows quantitative geneticists to determine the relative influence of genetics and the environment on a particular trait. By calculating the proportions of variance due to each component, researchers can estimate heritability. This information is essential for breeders to understand how much of the variation they see in their animals can be changed through selection compared to what must be addressed through management.

241. (D) The variance of interaction deviations between loci
Epistatic variance is the component of genetic variation that results from non-linear interactions between alleles at different genetic locations. It represents the part of the total genetic merit that depends on specific multi-locus combinations. Because these combinations are broken up by recombination during the formation of gametes, epistatic variance is generally not transmitted to offspring in a predictable way, making it part of the non-additive genetic variation.

242. (A) Cannot be inherited by offspring.
Permanent environmental variance consists of non-genetic influences that consistently affect an individual's performance throughout its lifetime. While these factors, such as a permanent injury or exceptional early nutrition, create consistent differences between individuals, they do not involve changes to the DNA sequence. Therefore, unlike genetic effects, permanent environmental deviations are not transmitted to the next generation, making them irrelevant for achieving long-term genetic improvement.

243. (C) 1/4 of the additive genetic variance
Paternal half-siblings are expected to share exactly one-quarter of their genes by descent, as they each inherit half of their genetic material from the shared sire. Consequently, the genetic covariance between them is equal to one-quarter of the additive genetic variance. This relationship is used in half-sib analyses to estimate herizability, as the resemblance between these relatives provides a direct measure of the transmissible genetic variation.

244. (A) Additive genetic variance to phenotypic variance
Narrow-sense herizability is defined as the ratio of the additive genetic variance to the total observed phenotypic variance. It measures the portion of variation that is due to the cumulative effects of individual genes, which are passed predictably from parent to offspring. This parameter is the most critical factor for predicting the response to selection and for determining the breeding value of individuals in a population.

245. (D) A lower heritability estimate
In a paternal half-sib design, heritability is estimated by the ratio of the sire variance component to the total phenotypic variance. A large within-family environmental variance (σ^2_w) increases the denominator of this ratio. If environmental noise within the families is high, the relative contribution of the genetic component from the sires appears smaller,

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2007

9. Among multi-trait selection methods, the Smith-Hazel index is generally considered the most efficient because it weights traits based on:
(A) Phenotypic correlations alone
(B) Independent minimum culling thresholds for each trait
(C) Economic values, genetic variances, and covariances
(D) Sequential selection across multiple generations

2015

10. **Assertion (A):** Family selection is more efficient than individual mass selection for traits with very low heritability.
Reason (R): For low heritability traits, the environmental variance constitutes a large portion of phenotypic variance, and family averages reduce environmental noise.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2005

11. In Wright's threshold model for disease resistance, the underlying continuous variable that determines the expression of a discrete binary trait is termed:
(A) Penetrance
(B) Threshold scale
(C) Binomial variance
(D) Liability

2017

12. A correlated response to selection in Trait Y when selecting for Trait X occurs due to:
(A) Uniform environmental effects and common management conditions
(B) Pleiotropy and linkage disequilibrium between contributing loci
(C) Genotype-environment interactions across diverse test locations
(D) Independent assortment of chromosomes during meiotic division

2021

13. Which mathematical formulation represents Wright's inbreeding coefficient (F) for an individual in terms of identical-by-descent (IBD) alleles?
(A) The variance of allele frequencies between subpopulations
(B) The proportion of heterozygous loci in the population
(C) The probability that two alleles at a locus are IBD
(D) The reduction in homozygous frequency relative to HWE

2016

14. The dominance hypothesis for heterosis postulates that inbreeding depression is caused by:
(A) Superiority of heterozygotes over both homozygotes
(B) Repulsion phase linkages being broken
(C) Epistatic interactions among homozygous loci
(D) The unmasking of deleterious recessive alleles

NODIA

2021

15. A crossover type of Genotype x Environment Interaction (GEI) implies that:
(A) The rank order of genotypic performance changes across environments
(B) The variance of genotypes differs across environments without rank changes
(C) Genetic correlation across environments equals 1.0
(D) Genotypes respond linearly and identically to environmental indices

2017

16. In the Eberhart and Russell model for stability analysis, a perfectly stable and widely adaptable variety is characterized by:
(A) Mean yield less than average, $b_i > 1$, and $S^2_{\{di\}} > 0$
(B) High mean yield, $b_i = 1.0$, and $S^2_{\{di\}} = 0$
(C) Low mean yield, regression coefficient $b_i = 0$, and high $S^2_{\{di\}}$
(D) High mean yield, regression coefficient $b_i < 1$, and $S^2_{\{di\}} = 0$

2012

17. The concept of canalization in quantitative genetics refers to the ability of a population to:
(A) Produce new phenotypic extremes under strict stabilizing selection
(B) Maintain a consistent phenotype despite genetic or environmental noise
(C) Rapidly alter its developmental pathway in fluctuating environments
(D) Shift its mean phenotype in direct response to directional selection

2018

18. The measure of linkage disequilibrium denoted by Dâ€™ is calculated as:
(A) D divided by the theoretical maximum of D given the allele frequencies
(B) The squared correlation coefficient between two loci
(C) The product of coupling gamete frequencies minus repulsion gamete frequencies
(D) The additive genetic variance divided by recombination fraction

2025

19. Composite Interval Mapping (CIM) improves upon simple Interval Mapping (IM) by:
(A) Using specific single markers independently to identify trait associations
(B) Assuming the absence of interference between adjacent crossover events
(C) Incorporating marker cofactors to control for background genetic effects
(D) Analyzing phenotypic variances in large, completely unmapped populations

2005

20. Match the following elements of GWAS analysis (List I) with their corresponding descriptions (List II).
List I: (Elements)
P. Q-matrix
Q. K-matrix
R. Manhattan plot
S. False positives
List II: (Descriptions)
1. Graphical representation of $-\log_{10}(p - values)$ across chromosomes
2. Spurious associations due to population structure
3. Matrix representing population genetic structure
4. Matrix defining pairwise kinship or relatedness
(A) P-IV, Q-III, R-II, S-I
(B) P-I, Q-II, R-III, S-IV
(C) P-III, Q-I, R-IV, S-II
(D) P-III, Q-IV, R-I, S-II

2009

21. In Marker-Assisted Backcrossing (MABC), background selection is utilized to:
(A) Select for the specific target gene from the donor parent
(B) Accelerate the recovery of the recurrent parent genome
(C) Break linkage drag surrounding the introgressed target locus
(D) Select for multiple epistatic QTLs within a single population

2011

22. Genomic Selection (GS) differs from traditional Marker-Assisted Selection (MAS) primarily because GS:
(A) Calculates GEBVs using all markers without significance testing
(B) Uses only a small number of major QTLs for the selection process
(C) Requires extensive interval mapping analysis prior to trait selection
(D) Eliminates the need for phenotypic evaluation in training populations

2006

23. Functional candidate gene identification for a complex trait typically relies on:
(A) Anonymous SSR markers mapped in a large F2 mapping population
(B) Chromosome walking from a randomly amplified polymorphic marker
(C) Measuring broad-sense herizability estimates of the target trait
(D) Biological pathways and differential expression profiling

2021

24. What is the expected frequency of the heterozygous females for a sex-linked locus under Hardy-Weinberg equilibrium, if the frequency of the recessive allele in males is 0.2?
(A) 0.04
(B) 0.16
(C) 0.32
(D) 0.64

2004

25. The Chi-square test used to detect deviations from Hardy-Weinberg equilibrium relies on:
(A) Comparison of expected allele frequencies with observed frequencies
(B) Observed genotypic counts vs expected counts from allele frequencies
(C) Comparison of fitness values of specific genotypes against null models
(D) Comparison of recombination fractions against independent assortment

2022

26. Under recurrent reversible mutation pressure where the forward mutation rate (u) is $10^{\{-5\}}$ and the backward mutation rate (v) is $10^{\{-6\}}$,

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what is the equilibrium frequency of the mutated allele (q)?
(A) 0.091
(B) 0.100
(C) 0.500
(D) 0.909

2008

27. When selection acts against a dominant allele (fitness of AA and Aa $= 1-s$, aa $= 1$), the dominant allele frequency (p) will:
(A) Rapidly decrease and be eliminated if no mutation occurs
(B) Reach a stable intermediate equilibrium of allele frequencies
(C) Slowly decrease but remain sequestered in heterozygous states
(D) Increase over time due to the presence of overdominance effects

2021

28. In a fluctuating population where sizes in three successive generations are 10, 100, and 1000, the effective population size (N_e) is most strongly influenced by:
(A) The arithmetic mean of the sizes
(B) The harmonic mean of the sizes, thus closer to 10
(C) The geometric mean of the sizes, thus closer to 100
(D) The final generation size, thus closer to 1000

2016

29. Which of the following correctly pairs a component of genetic variance with its biological source?
(A) Variance resulting from homozygous recessive individuals
(B) Variance due to non-allelic interactions between genes at different loci
(C) Variance resulting from specific maternal environmental influences
(D) Variance due to average effects of alleles substituted for another

2018

30. Following are statements regarding herizability:
I. Broad-sense herizability is the ratio of additive genetic variance to phenotypic variance.
II. Narrow-sense herizability determines the resemblance between relatives and response to selection.
III. Herizability estimates are specific to the population and environment in which they are measured.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I

2025

31. The concept of selection intensity (i) in predicting genetic advance is defined as:
(A) Standard deviation of phenotypic variance within the population
(B) Selection differential in phenotypic standard deviation units
(C) Narrow-sense heritability multiplied by the selection differential
(D) Proportion of individual animals retained for future breeding

2021

32. Which multi-trait selection strategy establishes specific minimum phenotypic thresholds for each trait, discarding any individual that fails to meet all thresholds?
(A) Independent culling levels
(B) Tandem selection
(C) Index selection
(D) Marker-assisted recurrent selection

2018

33. Progeny testing is most advantageous when compared to individual mass selection for traits that:
(A) Have very high narrow-sense heritability
(B) Are expressed in both sexes prior to reproductive maturity
(C) Are sex-limited or have very low heritability
(D) Are governed by a single dominant gene

2015

34. In Wright's threshold model, the conversion of herizability from the observed binomial scale to the underlying continuous normal scale requires knowledge of:
(A) The exact number of QTLs affecting the trait
(B) The epistatic interactions among loci
(C) The incidence of the trait in the population
(D) The dominance deviation on the observed scale

2002

35. Pleiotropy is the primary genetic cause of genetic correlation; it occurs when:
(A) Two distinct genes are physically linked on the same chromosome

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(B) Local linkage disequilibrium between adjacent markers
(C) Error variance in the measurement of the trait phenotype
(D) The dominance deviation observed at individual marker loci

2021

92. In Marker-Assisted Selection, which type of marker is considered the "gold standard" because it represents the actual causal mutation for the trait?
(A) Linked marker
(B) Perfect or functional marker
(C) Flanking marker
(D) Anonymous marker

2022

93. A Genomic Selection (GS) training population is defined as a set of individuals that have:
(A) Been phenotyped but not genotyped
(B) Been genotyped but not phenotyped
(C) Been both genotyped and rigorously phenotyped
(D) Only predicted Genomic Estimated Breeding Values (GEBVs)

2001

94. A positional candidate gene is identified based on:
(A) Mapping to a genomic interval containing a trait QTL
(B) Known role in a relevant biochemical metabolic pathway
(C) Differential expression observed in microarray experiments
(D) Structural similarity to genes in distant, unrelated species

2012

95. In multiple allele systems (e.g., ABO blood groups), if frequencies of alleles I^A, I^B, i are p, q, r respectively, the expected frequency of the phenotype resulting from the homozygous recessive condition (type O) is:
(A) $2pr$
(B) r^2
(C) $2qr$
(D) p^2

2015

96. Which condition represents a biological consequence of Hardy-Weinberg equilibrium?
(A) Retains existing genetic variability without divergence
(B) Genotypic frequencies change constantly over generations
(C) Allele frequencies maximize at 0.5 regardless of start
(D) The population size continuously decreases over time

2016

97. In a subdivided population, the reduction in overall heterozygosity caused by pooling subpopulations with different allele frequencies is known as:
(A) The Wahlund effect
(B) The founder effect
(C) The bottleneck effect
(D) Overdominance

2025

98. Estimation of fitness (w) for a particular genotype is quantified as:
(A) Relative reproductive success or contribution to next generation
(B) Spontaneous mutation rate of its constituent gene alleles
(C) Frequency of genotype divided by frequency of recessive allele
(D) The absolute census population size within a defined area

2018

99. Genetic drift is characterized as a dispersive evolutionary force because its directional effect on allele frequencies is:
(A) Driven exclusively by mutation events at the loci
(B) Random and unpredictable in magnitude and direction
(C) Completely deterministic and predictable in outcomes
(D) Uniformly consistent across all geographic populations

2024

100. Following are statements regarding quantitative genetics:
I. Phenotypic variance equals additive plus dominance plus epistatic plus environmental variances.
II. Genotype-environment interaction ($V_{\{GE\}}$) can be eliminated by increasing population size.
III. Additive variance determines the resemblance between parents and offspring.
Which of the above statement(s) is/are correct?
(A) I and III
(B) II and III

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(A) Ensure the target gene attains a homozygous state within early generations
(B) Maximize the degree of linkage drag surrounding the introgressed gene
(C) Introduce novel mutation events into the recipient background genome
(D) Identify recombinations flanking the target locus to minimize linkage drag

2013

45. Marker-Assisted Recurrent Selection (MARS) is designed to accumulate favorable alleles for complex traits by:
(A) Pyramiding multiple QTLs via crossing selected lines
(B) Selecting parents based solely on top phenotypic performance
(C) Backcrossing single major genes into existing elite varieties
(D) Mapping QTLs within natural and unstructured donor populations

2015

46. Expression quantitative trait loci (eQTL) mapping identifies genomic regions that control:
(A) The amino acid sequence of a target candidate gene
(B) Transcript abundance or expression level of a gene
(C) The morphological penetrance of various dominant traits
(D) Physical location of centromeres on the chromosome

2022

47. In a population with multiple alleles at a single autosomal locus, if allele frequencies are $p = 0.5, q = 0.3, r = 0.2$, what is the expected frequency of all heterozygotes combined under HWE?
(A) 0.38
(B) 0.50
(C) 0.62
(D) 0.70

2017

48. When observed heterozygosity significantly exceeds expected heterozygosity in a Hardy-Weinberg analysis, this deviation infers the presence of:
(A) Inbreeding or assortative mating
(B) Disassortative mating or heterozygote advantage
(C) A Wahlund effect (population subdivision)
(D) Strict isolation without mutation

2018

49. In the neighborhood model of migration (isolation by distance), genetic differentiation between local populations is dependent on:
(A) Global mutation rate observed across all polymorphic loci
(B) Geographical distance and the limited dispersal of individuals
(C) Artificial selection pressure imposed uniformly across regions
(D) Self-fertilization rate within local sub-populations

2006

50. Following are statements regarding selection pressures:
I. Selection against a recessive allele is highly effective when the allele is rare.
II. Selection against a dominant allele can rapidly eliminate it from the population.
III. Codominant selection results in an intermediate stable equilibrium of allele frequencies.
IV. The selection coefficient (s) quantifies the proportional reduction in fitness.
V. Heterozygote advantage maintains genetic polymorphism.
Which of the above statement(s) is/are INCORRECT?
(A) I and III
(B) I, II and IV
(C) II, III and V
(D) IV and V

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2016

51. The founder effect describes a shift in allele frequencies when a new population is established by a small number of individuals. This is a manifestation of:
(A) Natural selection
(B) Recurrent mutation
(C) Genetic drift
(D) Directional migration

2015

52. If a quantitative trait has a phenotypic variance (V_P) of 100, an additive genetic variance (V_A) of 40, a dominance variance (V_D) of 20, and an epistatic variance (V_I) of 10, what is the broad-sense herizability (H^2)?
(A) 0.40
(B) 0.60
(C) 0.70
(D) 0.30

(B) Alleles at different loci interact to produce a novel phenotype
(C) Recombination fails to separate linked loci during meiosis
(D) A single gene simultaneously influences more than one phenotypic trait

2025

36. Which formula calculates the rate of increase in homozygosity (ΔF) per generation in an idealized population of size N?

(A) $\frac{1}{2N}$

(B) $\frac{1}{N}$

(C) $1 - \frac{1}{2N}$

(D) $\frac{N}{2}$

2014

37. The panmictic index (P) relates to Wright's inbreeding coefficient (F) by which of the following expressions?

(A) $P = 1 + F$

(B) $P = 1 - F$

(C) $P = \frac{F}{1 - F}$

(D) $P = F^2$

2019

38. A non-crossover genotype-environment interaction (GEI) implies that:
(A) The best genotype remains best in both environments though magnitude of performance varies
(B) Environmental variances exceed total genetic variances globally
(C) Stability models cannot successfully converge to estimate parameters
(D) Genotypes switch their relative ranks between two environments

2002

39. In the Additive Main Effects and Multiplicative Interaction (AMMI) model, the interaction component is analyzed using:
(A) Multiple linear regression
(B) Logistic regression
(C) Principal Component Analysis (PCA)
(D) Stepwise discriminant analysis

2016

40. Following are statements concerning natural selection on metric traits:
I. Stabilizing selection reduces phenotypic variance without shifting the mean.
II. Directional selection shifts the mean towards one phenotypic extreme.
III. Disruptive selection favors intermediate phenotypes and eliminates extremes.
IV. Canalization results from prolonged disruptive selection.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II, III and IV
(C) I, II and III
(D) III and IV

2005

41. The statistical measure r^2 for Linkage Disequilibrium (LD) is preferred in GWAS because it:
(A) Measures the physical distance in base pairs between two markers
(B) Is applicable only to multi-allelic microsatellite marker variants
(C) Always equals unity when high rates of recombination occur
(D) Relates directly to statistical power and effective population size

2003

42. In QTL mapping, Recombinant Inbred Lines (RILs) are valued as a mapping population because they:
(A) Are permanent lines allowing replicated multi-environment trials
(B) Are populations exhibiting high levels of observed heterozygosity
(C) Show inbreeding depression making phenotypes easier to score
(D) Are populations requiring no crossing or segregation to generate

2015

43. To minimize false positives in Genome-Wide Association Studies (GWAS) caused by cryptic relatedness, statistical models incorporate:
(A) Only the Q-matrix (population structure)
(B) Simple linear regression ignoring background genetics
(C) The K-matrix (kinship or relatedness) in a mixed linear model
(D) Only markers with minor allele frequencies below 1%

2002

44. Recombinant selection in a Marker-Assisted Backcrossing program is implemented to:

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(C) Reduced phenotypic variance around an intermediate optimal mean
(D) Uniform increase in allele frequencies observed across all loci

2018

2021

64. The rate of decay of linkage disequilibrium (D) over t generations is defined by the equation $D_t = D_0\big(1 - c\big)^t$. The term c represents:
(A) Spontaneous mutation rate per locus
(B) Selection coefficient of the alleles
(C) Average inbreeding coefficient of herd
(D) Recombination fraction between the two loci

2012

65. In QTL interval mapping, calculating the LOD (Logarithm of the Odds) score provides a measure of:
(A) The physical distance in base pairs between markers mapped
(B) The proportion of dominance variance captured by the marker
(C) Likelihood of QTL presence vs the null hypothesis of no QTL
(D) The degree of background genetic noise in the experiments

2007

66. A typical Manhattan plot in GWAS graphs the genomic position of markers on the x-axis against what value on the y-axis?
(A) Minor allele frequency observed across the whole population
(B) Negative logarithm (base 10) of the association p-value
(C) The additive effect size of markers on the genetic backbone
(D) The calculated logarithm of the odds score for each marker

2014

67. Foreground selection in MAS is defined as the application of molecular markers to:
(A) Select against the donor parent genome in non-target regions
(B) Recover the recurrent parent genome efficiently
(C) Select specifically for the target allele or gene of interest
(D) Estimate the population structure of the breeding materials

2016

68. The primary advantage of Genomic Selection (GS) over traditional Marker-Assisted Selection (MAS) is that GS:
(A) Captures small-effect QTLs without significance thresholds
(B) Requires identifying causative mutations prior to selection
(C) Eliminates the need for phenotypic data in all generations
(D) Is only applied to simply inherited Mendelian trait variations

2011

69. Validation of a candidate gene via gene knock-out involves:
(A) Overexpressing the gene within an unrelated host organism
(B) Disrupting gene function to observe phenotypic alteration
(C) Mapping the gene to a specific physical chromosome location
(D) Sequencing the gene to find minor allele frequency changes

2021

70. Select the correct order of mapping populations from lowest to highest recombination frequency per meiosis utilized in constructing the final genetic map.
(A) F2 < RILs < Intermated RILs (IRILs)
(B) RILs < F2 < Intermated RILs (IRILs)
(C) Intermated RILs (IRILs) < F2 < RILs
(D) F2 < Intermated RILs (IRILs) < RILs

2004

71. In estimating genotypic frequencies for a sex-linked locus with two alleles (A, a) in a species with XY males and XX females, the equilibrium frequency of affected males (a) is equal to:
(A) q^2
(B) q
(C) $2pq$
(D) $1 - q$

2002

72. If a chi-square test for Hardy-Weinberg equilibrium yields a p-value of 0.01, the appropriate conclusion is that:
(A) The population is strictly mating in a random manner
(B) There is evidence that the population is deviating from HWE
(C) The population is strictly in Hardy-Weinberg Balance

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(D) Genetic mutation has explicitly ceased in the population

2016

73. Mutation pressure alone is a very slow evolutionary force because:
(A) Mutations usually cause immediate lethality to hosts
(B) Mutation rates are generally extremely small
(C) Intense directional selection is required to operate
(D) All mutations are repaired before gametogenesis starts

2008

74. Which mode of selection results in a balanced polymorphism where neither allele is eliminated from the population?
(A) Selection against recessive homozygotes
(B) Selection against dominant homozygotes
(C) Selection against heterozygotes (underdominance)
(D) Heterozygote advantage (overdominance)

2003

75. The bottleneck effect can significantly impact genetic diversity by:
(A) Increasing the effective population size permanently
(B) Introducing new alleles through enhanced mutation rates
(C) Randomly eliminating alleles due to population reduction
(D) Promoting equal allele frequencies across all trait loci

2006

76. Additive genetic variance (V_A) is defined as the variance of:
(A) Dominance deviations
(B) Breeding values in the population
(C) Epistatic interactions between linked loci
(D) Environmental deviations influencing the phenotype

2002

77. The statistical regression of offspring phenotypes on mid-parent phenotypes yields a slope coefficient (b) that estimates:
(A) Broad-sense heritability
(B) Narrow-sense heritability
(C) The selection differential
(D) Dominance variance

NODIA

2010

78. In optimizing genetic gain per year, reducing the generation interval (L) will theoretically:
(A) Increase annual selection response if accuracy is stable
(B) Directly decrease the annual selection response observed
(C) Directly decrease narrow-sense heritability estimates
(D) Have no mathematical effect on the breeder's equation

2014

79. The fundamental limitation of independent culling levels compared to index selection is that:
(A) It requires simultaneous equations to solve parameters
(B) It rejects superior individuals deficient in one trait
(C) It can only handle a maximum of two independent traits
(D) It relies on sequential generations of trait phenotyping

2016

80. **Assertion (A):** Within-family selection is highly recommended when maternal effects strongly influence the trait.
Reason (R): Within-family selection eliminates the confounding common environmental variance present between different families.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2012

81. In quantitative genetic modeling of threshold traits, the liability scale is assumed to follow which statistical distribution?
(A) Poisson distribution
(B) Standard normal distribution
(C) Binomial distribution
(D) Exponential distribution

2017

82. Which formula defines the correlated response (CR_Y) in trait Y when selection is applied to trait X?
(A) $CR_Y = i_X h_X h_Y r_G \sigma_{PY}$
(B) $CR_Y = i_X h_X^2 r_G \sigma_{PY}$
(C) $CR_Y = i_X h_X h_Y \sigma_{PX}$
(D) $CR_Y = h_Y^2 S_X r_P$

2005

83. The process of self-fertilization in a diploid species reduces heterozygosity by what proportion per generation?
(A) 25%
(B) 50%
(C) 75%
(D) 100%

2005

84. Which theory proposes that heterosis arises because favorable dominant alleles controlling a trait are dispersed across both parental lines?
(A) Overdominance hypothesis
(B) Dominance hypothesis
(C) Epistasis hypothesis
(D) Physiological limitation hypothesis

2002

85. When identifying Genotype x Environment Interaction (GEI) using an ANOVA, a significant interaction term indicates that:
(A) The environmental means are significantly different from others
(B) Phenotypic differences among genotypes change across environments
(C) The genotypic means over all environments differ significantly
(D) The error variance component in the model is exactly zero

2004

86. In a GGE biplot analysis, the visualization combines which two components of variance?
(A) Genotype main effect and Genotype x Environment interaction
(B) Environment main effect and Genotype main effect
(C) Additive variance and Dominance variance
(D) Environmental variance and Error variance

2002

87. Under directional selection for body weight, the concept of a "selection limit" or plateau is reached when:
(A) Epistatic variance components become zero
(B) Additive genetic variance for the trait is exhausted
(C) The mutation rate exceeds the recombination frequency
(D) Genotype-environment interactions completely disappear

2017

88. A high LD value ($r^2 \approx 1$) between a molecular marker and a causal Quantitative Trait Nucleotide (QTN) indicates that:
(A) The marker alleles are highly predictive of the QTN alleles in the population
(B) The marker and QTN independently assort during meiosis
(C) The marker is useless for marker-assisted selection
(D) The genomic region has undergone a very high rate of historical recombination

2019

89. Single Marker Analysis in QTL mapping has the statistical disadvantage that it cannot definitively distinguish between:
(A) Total additive and dominance variance components
(B) Differences between homozygous and heterozygous genotypes
(C) QTL effect and distance from the marker are confounded
(D) Transgressive segregation and inbreeding depression

2021

90. Match the types of mapping populations (List I) with their primary genetic characteristics (List II).
List I: (Mapping Populations)
P. F2 Population
Q. Recombinant Inbred Lines (RILs)
R. Doubled Haploids (DH)
S. Near Isogenic Lines (NILs)
List II: (Characteristics)
1. Completely homozygous lines produced in one generation via tissue culture
2. Lines that differ from a recurrent parent by only a small introgressed chromosomal segment
3. Immortalized homozygous lines developed by repeated selfing
4. Highly heterozygous temporary population with all possible genotypic combinations
(A) P-IV, Q-III, R-I, S-II
(B) P-III, Q-IV, R-II, S-I
(C) P-I, Q-II, R-IV, S-III
(D) P-II, Q-I, R-III, S-IV

2010

91. The population structure matrix (Q-matrix) utilized in GWAS models adjusts for:
(A) Differences from subpopulations or geographical origins

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2011

53. Repeatability sets an upper theoretical limit on:
(A) Broad-sense herizability
(B) Narrow-sense herizability
(C) The selection differential
(D) The environmental variance

2009

54. The accuracy of selection is defined as the correlation between:
(A) Phenotypic value and environmental deviation
(B) Additive variance and dominance variance
(C) Selection intensity and selection response
(D) True breeding value and estimated breeding value

2022

55. Tandem selection allows for the improvement of multiple traits by:
(A) Selecting for all traits simultaneously using a computed index
(B) Selecting a second trait only after the first reaches a goal
(C) Rejecting individuals failing to meet independent minimum goals
(D) Selecting parents based on progeny performance for all traits

2012

56. Within-family selection is advantageous over mass selection when:
(A) Environmental variance common to the family is very high
(B) Genetic variance within families is zero
(C) Narrow-sense heritability is close to 1.0
(D) The trait is determined by a single completely dominant gene

2025

57. In evaluating threshold traits, individuals exceeding the critical liability threshold:
(A) Will exhibit a continuous range of phenotypic severity
(B) Will fail to inherit the trait
(C) Exhibit the discrete phenotypic state (e.g., disease affected)
(D) Cannot pass the trait to their offspring

2009

58. Linkage disequilibrium can generate a transient genetic correlation between two traits. This correlation will decay over generations due to:
(A) Mutation
(B) Recombination
(C) Pleiotropy
(D) Inbreeding

2019

59. Calculate the inbreeding coefficient (F) of an offspring resulting from a full-sib mating, assuming the common parents are non-inbred.
(A) 0.125
(B) 0.250
(C) 0.500
(D) 0.0625

2003

60. Arrange the following steps of Marker-Assisted Backcrossing (MABC) in the correct sequential order.
I. Background selection
II. Recombinant selection
III. Foreground selection
IV. Crossing F1 with recurrent parent
(A) IV, III, II, I
(B) III, I, II, IV
(C) IV, III, I, II
(D) I, III, II, IV

2022

61. The overdominance hypothesis for heterosis asserts that heterozygote superiority is based on:
(A) Cumulative action of multiple favorable dominant gene alleles
(B) Superiority of the heterozygous genotype over both homozygotes
(C) Synergistic epistatic interactions across the entire genome
(D) Expression of functional alleles at the expense of recessive ones

2023

62. Which statistic in the Finlay and Wilkinson approach measures the adaptability of a genotype across a range of environments?
(A) Regression of genotypic performance on environmental index
(B) Measure of deviation from linear regression for stability
(C) Measure of principal component eigenvalues in the biplot
(D) Additive main effect standard error in the combined ANOVA

2015

63. Under stabilizing selection for a continuous metric trait, the long-term expected outcome is:
(A) Steady and uniform increase in phenotypic mean over generations
(B) Splitting of the population into two distinct phenotypic morphs

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(C) I and II
(D) III

2024

101. Sib-analysis uses an Analysis of Variance (ANOVA) design to partition variance and estimate heritability. The "between-sires" variance component primarily estimates:
(A) Total phenotypic variance within populations
(B) One quarter of the additive genetic variance
(C) One quarter of the dominance genetic variance
(D) Total environmental variance in the experiments

2008

102. If a population mean for fleece weight is 5 kg, the mean of the selected breeders is 7 kg, and the narrow-sense heritability is 0.4, what is the predicted mean fleece weight of the next generation?
(A) 5.0 kg
(B) 5.8 kg
(C) 6.0 kg
(D) 7.0 kg

2015

103. The primary risk of applying high selection intensity to a closed breeding population over several generations is:
(A) Decrease in narrow-sense heritability and increased inbreeding
(B) Direct increase in the generation interval of the animals
(C) Direct increase in the effective size of the population
(D) Elimination of environmental variance within the breeding set

2023

104. In theoretical formulations of selection response, individual (mass) selection is generally superior to family selection when:
(A) The trait can only be measured post-mortem
(B) Environmental variation is exceptionally high
(C) The trait is sex-limited
(D) Narrow-sense heritability is high ($h^2 > 0.5$)

2017

105. Liability for a threshold trait cannot be measured directly because it is:
(A) An unobservable, underlying latent variable
(B) Controlled by a single dominant gene
(C) Subject to high mutation rates
(D) Expressed as distinct categorical classes without genetic basis

2003

106. The mathematical prediction of correlated response (CR) relies on the assumption that the relationship between the two traits is:
(A) Purely environmental in origin
(B) Linear and mediated by additive genetic covariance
(C) Strictly logarithmic in nature
(D) Entirely governed by epistatic variance components

2007

107. By definition, a locus is considered to be "identical by descent" (IBD) if the two alleles present in a diploid individual are:
(A) Exact copies of a single ancestral allele due to inbreeding
(B) Biochemically identical but derived from independent mutations
(C) Heterozygous but functionally similar
(D) Maintained by overdominance

2004

108. In quantitative genetic models, the decline in the phenotypic mean of a trait upon inbreeding is linearly related to:
(A) The inbreeding coefficient (F)
(B) The mutation rate
(C) The selection differential
(D) The frequency of dominant alleles

2010

109. Which of the following is NOT a plausible cause of Genotype x Environment Interaction (GEI)?
(A) Differential gene expression triggered by environmental cues
(B) Structural DNA mutations induced by standard field temperatures
(C) Different metabolic pathways being activated in varying climates
(D) Variations in physiological thresholds across environmental stress gradients

2003

110. Following are statements for stability analysis:
I. AMMI utilizes Principal Component Analysis for interaction effects.
II. GGE biplots graphically represent Genotype + Genotype-Environment interactions.
III. Finlay-Wilkinson model uses regression of genotype means on environmental indices.
IV. Eberhart and Russell model does not measure deviation from regression.
Which of the above statement(s) is/are correct?

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2006

168. In calculations of effective population size, unequal contribution of individuals to next generation (variance in family size, V_k) alters N_e according to formula:

(A) $N_e = \frac{4N-2}{V_k+2}$

(B) $N_e = \frac{V_k}{N}$

(C) $N_e = \frac{N}{4V_k}$

(D) $N_e = V_k + N$

2017

169. Genotype-environment interaction ($V_{\{GE\}}$) is statistically present when:

(A) Genotypes respond consistently across environments

(B) Genotype differences vary across environments

(C) Environmental variance component is zero

(D) Additive genetic variance equals phenotypic variance

2021

170. Following are statements regarding herizability estimation methods:

I. Parent-offspring regression provides an unbiased estimate of narrow-sense herizability.

II. Full-sib correlation often overestimates narrow-sense herizability due to shared dominance and common environmental effects.

III. Half-sib analysis relies heavily on epistatic variance components.

Which of the above statement(s) is/are correct?

(A) I and II

(B) II and III

(C) I and III

(D) II

2022

171. Breeder's equation relies on selection differential (S), which is equal to product of phenotypic standard deviation (σ_P) and:

(A) Generation interval (L)

(B) Selection intensity (i)

(C) Inbreeding coefficient (F)

(D) Additive genetic variance (V_A)

2013

172. Independent culling levels are considered less mathematically optimal than index selection because:

(A) They require more advanced computations to solve equations

(B) Superior traits cannot compensate for deficient ones

(C) They ignore relative economic weights of selected traits

(D) They cannot be applied to discrete threshold traits

2024

173. Theoretical formulations indicate progeny testing is limited by its tendency to:

(A) Increase generation interval, reducing annual gain

(B) Cause a decrease in selection accuracy metrics

(C) Increase mutation rate of quantitative traits

(D) Erase dominance variance from phenotypic expression

2007

174. On underlying liability scale for a threshold trait, threshold itself is conceptualized as a point that truncates normal distribution of:

(A) Specific phenotypic categories in population

(B) Combined genetic and environmental values

(C) Codominant marker loci only within mapping

(D) Epistatic interactions between non-allelic genes

NODIA

2018

175. When linkage disequilibrium between two loci causes a genetic correlation, generations of random mating will:

(A) Increase genetic correlation observed

(B) Lead to progressive decay as recombination breaks linkage

(C) Fix genetic correlation permanently in lineages

(D) Convert correlation into environmental relationships

2006

176. Which of following represents primary genetic basis for inbreeding depression?

(A) Increased frequency of heterozygous genotypes

(B) Increased expression of deleterious recessive alleles

(C) Occurrence of high rates of spontaneous mutations

(B) I and IV
(C) III and V
(D) IV and V

2015

121. In a model of selection against a recessive allele where the selection coefficient $s = 1$, the frequency of the recessive allele (q) after t generations from an initial frequency q_0 is given by:

(A) $q_t = \frac{q_0}{1 + tq_0}$

(B) $q_t = q_0(1 - s)^t$

(C) $q_t = q_0 e^{\{-ut\}}$

(D) $q_t = \frac{p_0}{1 + t}$

2012

122. The primary genetic consequence of a population bottleneck is:
(A) Loss of rare alleles and reduced genetic variance
(B) Rapid and sustained increase in trait heterosis
(C) Sustained elevation of spontaneous mutation rate
(D) Immediate formation of new reproductive species

2006

123. The environmental variance (V_E) component in quantitative genetics includes variance resulting from:
(A) Variance due to non-additive gene action
(B) Macroscopic, microscopic, and maternal effects
(C) Epistatic interactions between distinct alleles
(D) Average effect of specific allele substitutions

2010

124. Broad-sense herizability (H^2) is defined as the ratio of:
(A) Additive genetic variance to phenotypic variance
(B) Total genetic variance to phenotypic variance
(C) Environmental variance to phenotypic variance
(D) Dominance variance to total genetic variance

2001

125. If the accuracy of selection increases, the predicted genetic advance (R) will theoretically:
(A) Increase
(B) Remain constant
(C) Decrease proportionately
(D) Drop to zero

2002

126. A selection index (Smith-Hazel index) maximizes genetic improvement by optimizing the correlation between:
(A) Multi-trait index and aggregate breeding value
(B) Phenotypic values and environmental error terms
(C) Individual performance and random mutation rate
(D) Narrow-sense and broad-sense heritability ratio

2004

127. Under theoretical formulations of family selection, "family selection" (selecting whole families based on their mean) is most appropriate when:
(A) Herizability is high and common environmental effects are negligible
(B) Herizability is low and common environmental effects are negligible
(C) Herizability is high and common environmental effects are large
(D) The trait is determined by a single major QTL

2022

128. In modeling threshold traits, if the incidence of a disease in a population increases due to environmental degradation, the liability threshold relative to the population mean is considered to have:
(A) Shifted to a higher value (further from the mean)
(B) Shifted to a lower value (closer to the mean)
(C) Remained strictly unchanged
(D) Mutated

2025

129. Linkage disequilibrium between two unlinked loci can be generated by:
(A) Recombination
(B) Population admixture or epistasis
(C) Random mating
(D) Independent assortment

2010

130. **Assertion (A):** The rate of increase in homozygosity is faster in self-fertilizing populations compared to full-sib mating populations.
Reason (R): Self-fertilization reduces heterozygosity by 50% each generation, whereas

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full-sib mating reduces it by approximately 19%.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2025

131. Inbreeding depression is typically most severe for quantitative traits that:
(A) Are governed by additive genetic gene action
(B) Have high dominance variance and are related to fitness
(C) Are morphologically neutral phenotypic variables
(D) Lack any epistatic gene interactions

2004

132. The Finlay-Wilkinson method estimates a regression coefficient (b_i). A genotype with $b_i < 1$ is interpreted as being:
(A) Adapted to high-yielding and favorable environments
(B) Adapted to poor environments with stress resistance
(C) Generally unadapted to all test environments
(D) Perfectly stable across all testing environments

2001

133. AMMI analysis partitions the total sum of squares for Genotype x Environment Interaction into:
(A) Linear regression and deviations from regression
(B) Principal Component axes (IPCA)
(C) Additive main effects and dominance main effects
(D) Mutation and migration components

2003

134. Canalization describes the evolutionary buffering of a phenotype against environmental and genetic variations. This mechanism operates primarily under:
(A) Disruptive selection
(B) Directional selection
(C) Stabilizing selection
(D) Artificial selection for extreme traits

2001

135. The squared correlation coefficient r^2, representing linkage disequilibrium between two loci, has an expected value in an ideal finite population of size N_e (with recombination rate c) approximately equal to:

(A) $\frac{1}{1+4N_e c}$

(B) $\frac{1}{4N_e}$

(C) $N_e c$

(D) $1 - 4N_e c$

2022

136. In generating an F2 mapping population, what is the expected segregation ratio for a codominant molecular marker?
(A) 3:1
(B) 1:2:1
(C) 1:1
(D) 9:3:3:1

2002

137. False positives in Genome-Wide Association Studies (GWAS) frequently arise from:
(A) Using too many SNP markers in the genome
(B) Population structure and cryptic relatedness
(C) Presence of strict panmixia within the set
(D) Exact mapping of causal molecular variants

2017

138. The proportion of the recurrent parent genome recovered after t generations of backcrossing (without marker assistance) is expected to be:

(A) $1 - (\frac{1}{2})^{t+1}$

(B) $1 - (\frac{1}{2})^{t}$

(C) $(\frac{1}{2})^{t}$

(D) $1 - (\frac{1}{4})^{t}$

NODIA

2003

139. Genomic Estimated Breeding Values (GEBVs) in Genomic Selection are derived by summing:
(A) Only effects of markers that pass a significance threshold
(B) Phenotypic measurements of the individual's offspring exclusively
(C) Estimated effects of all genome-wide markers without prior significance testing
(D) Additive genetic variance divided by the total phenotypic variance

2001

140. Match the functional genomics techniques (List I) with their primary application in candidate gene validation (List II).

List I: (Techniques)
P. RNA-sequencing (RNA-seq)
Q. CRISPR-Cas9
R. In situ hybridization
S. eQTL mapping
List II: (Applications)
1. Gene knock-out or targeted editing
2. Transcriptome-wide expression profiling
3. Linking genetic markers to gene expression levels
4. Visualizing spatial mRNA expression within tissues
(A) P-I, Q-II, R-III, S-IV
(B) P-II, Q-I, R-IV, S-III
(C) P-III, Q-IV, R-I, S-II
(D) P-II, Q-IV, R-I, S-III

2011

141. Estimation of gene frequencies for loci with multiple alleles from phenotypic data generally requires the assumption of:
(A) Non-random mating
(B) Hardy-Weinberg equilibrium
(C) Complete inbreeding
(D) No dominance among any alleles

2017

142. A significant excess of homozygotes across all loci in a Hardy-Weinberg analysis suggests the occurrence of:
(A) Recent bursts of spontaneous mutation
(B) Intense inbreeding or self-fertilization
(C) Presence of disassortative mating
(D) High rates of outcrossing in the population

2018

143. Equilibrium between mutation and selection for a deleterious recessive allele is established when the allele frequency (q) equals:
(A) $\sqrt{\frac{u}{s}}$
(B) $\frac{u}{s}$
(C) $\frac{s}{u}$
(D) $\sqrt{\frac{s}{u}}$

2012

144. Estimation of fitness (w) relies on relative reproductive success. If genotype AA produces 100 offspring, Aa produces 90, and aa produces 50, what is the selection coefficient (s) against the aa genotype?
(A) 0.10
(B) 0.50
(C) 0.90
(D) 1.00

2019

145. If a population has 10 males and 90 females breeding, using the formula $N_e = \frac{4N_m N_f}{N_m + N_f}$, the effective population size (N_e) is:
(A) 10
(B) 36
(C) 50
(D) 100

2023

146. Which of the following accurately describes additive genetic variance (V_A)?
(A) Variance relying solely on maternal effects in the herd
(B) Variance of breeding values, the transmissible portion
(C) Variance due to allele combinations and epistatic genes
(D) Variance resulting from non-linear dominance deviations

2013

147. Heritability in the narrow sense is maximized when:
(A) Environmental variance (V_E) and non-additive genetic variances approach zero
(B) Environmental variance (V_E) approaches infinity
(C) Dominance variance (V_D) is equal to additive genetic variance (V_A)
(D) Population undergoes extreme inbreeding depression

NODIA

2015

148. Optimization of genetic gain per year demands a balance between:
(A) Intensity and interval, as accuracy needs time
(B) Global mutation rate and regional migration rate
(C) Inbreeding depression and heterosis expression
(D) Dominance variance and epistatic gene variance

2004

149. Efficiency of index selection over tandem selection for two traits with equal economic importance is most pronounced when the traits possess:
(A) A strong positive genetic correlation
(B) A strong negative genetic correlation
(C) No additive genetic variance

pathways
(C) Phenotypic selection limits observed in population
(D) Standard Hardy-Weinberg equilibrium tests for allele balance

2007

187. For an X-linked recessive trait, if frequency of affected males in a panmictic population is 0.05, what is expected frequency of affected females?
(A) 0.0025
(B) 0.025
(C) 0.05
(D) 0.10

2023

188. Chi-square goodness-of-fit test for Hardy-Weinberg equilibrium yields a calculated value of 5.99. If critical value at $\alpha = 0.05$ for 1 degree of freedom is 3.84, what is inference?
(A) Accept null hypothesis; population is in Hardy-Weinberg
(B) Reject null; population deviates from HWE
(C) Population census size is infinite
(D) Spontaneous mutation rate is zero

2002

189. According to island model of migration, genetic differentiation among subpopulations is prevented if number of migrants per generation (N_m) is greater than:
(A) 100
(B) 1
(C) N_e
(D) 0.01

2002

190. In a model of selection against a recessive lethal allele ($s = 1$), frequency of recessive allele drops slowly when it becomes rare because:
(A) Allele is hidden in phenotypically normal heterozygotes
(B) Spontaneous mutation rate increases to compensate losses
(C) Heterozygotes have zero relative fitness in environments
(D) Random genetic drift dominates over selection pressure

2014

191. Effective population size (N_e) is equivalent to census size (N) only under ideal conditions, which include:
(A) Random mating, equal sex ratio, Poisson family variance
(B) Assortative mating, fluctuating population size, no mutation
(C) Complete inbreeding and fixed family sizes over generations
(D) High mutation rates and continuous migration between herds

2021

192. Partitioning phenotypic variance into its components requires estimating epistatic variance (V_I). This component represents variance due to:
(A) Dominance interactions within a locus
(B) Non-allelic interactions across different loci
(C) Additive gene action
(D) Interaction of specific genes with environments

2014

193. Narrow-sense heritability (h^2) is utilized for predicting response to selection because it estimates proportion of variance derived from:
(A) Total environmental effects on observed phenotype
(B) Fixable, transmissible average effects of alleles
(C) Epistatic interactions that can be captured in hybrids
(D) Inbreeding depression observed in breeding herd

2019

194. If selection intensity (i) is 2.0, phenotypic standard deviation (σ_P) is 10, and narrow-sense heritability (h^2) is 0.3, what is expected genetic advance (R)?
(A) 6.0
(B) 3.0
(C) 10.0
(D) 20.0

2002

195. Smith-Hazel selection index requires solving equations that incorporate:
(A) Genetic variances, covariances, and economic weights
(B) Relative economic weights of traits under selection
(C) Observed phenotypic variances of traits in set
(D) Random environmental covariances across test trials

2021

196. Progeny testing evaluates breeding value of a parent. As number of offspring evaluated increases, accuracy of estimated breeding value approaches:

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2018

159. For mapping purposes, backcross populations are useful because they segregate in a:
(A) 3:1 ratio for dominant markers
(B) 1:1 ratio, simplifying the estimation of recombination frequencies
(C) 1:2:1 ratio for codominant markers
(D) 9:3:3:1 ratio

2011

160. Match the following statistical models (List I) with their primary output metric in plant breeding (List II).
List I: (Models)
P. Finlay-Wilkinson
Q. Eberhart-Russell
R. AMMI
S. GGE Biplot
List II: (Metrics)
1. Regression coefficient (b_i) and Deviation from regression ($S^2_{\{di\}}$)
2. Principal component scores (IPCA) for interaction
3. Visual polygon view (Which-won-where pattern)
4. Regression coefficient (b_i) on environmental index
(A) P-I, Q-IV, R-III, S-II
(B) P-IV, Q-I, R-II, S-III
(C) P-IV, Q-II, R-I, S-III
(D) P-II, Q-I, R-IV, S-III

2013

161. In a Marker-Assisted Backcrossing (MABC) design, identifying the exact location of a crossover event between the target gene and the nearest flanking marker is the goal of:
(A) Foreground selection
(B) Recombinant selection
(C) Background selection
(D) Genomic Selection

2017

162. Marker-Assisted Recurrent Selection (MARS) differs from MABC in that MARS aims to:
(A) Introgress a single large-effect QTL into elite lines
(B) Pyramid multiple minor- and major-effect QTLs
(C) Reduce donor parent contribution to exactly zero percent
(D) Only utilize phenotypic selection within the cycles

2021

163. Gene knock-outs are definitive methods for functional candidate gene validation because they:
(A) Demonstrate if the gene is necessary for the phenotype
(B) Provide significant association mapping p-values
(C) Reveal sequence similarity to known functional genes
(D) Map the gene to a specific physical chromosome location

2004

164. Estimation of genotypic frequencies for a locus with two codominant alleles (A_1, A_2) under HWE allows direct counting because:
(A) Dominance masks the recessive allele types
(B) Each genotype has a distinct phenotype
(C) Mutation rates are elevated in populations
(D) Assortative mating is required for balance

NODIA

2017

165. Biological consequence of non-random assortative mating in a population is a systematic:
(A) Decrease in heterozygotes and increase in homozygotes
(B) Sustained increase in frequency of heterozygotes
(C) Alteration of basic allele frequencies at the loci
(D) Direct increase in effective population size

2001

166. A recurrent mutation from allele A to a at rate u will eventually result in an equilibrium where the frequency of allele A is:
(A) 1.0
(B) 0.5
(C) 0.0
(D) u

2012

167. Which mode of selection produces an unstable equilibrium if the heterozygote has a lower fitness than both homozygotes?
(A) Direct selection against all dominant allele types
(B) Selection against heterozygotes (underdominance)
(C) Occurrence of overdominance at the target locus
(D) Directional selection toward one phenotypic extreme

(D) Equal environmental variances

2009

150. **Assertion (A):** Progeny testing substantially increases the accuracy of selection compared to individual phenotype evaluation.
Reason (R): The mean phenotypic value of a large number of progeny reflects the breeding value of the parent, reducing environmental noise.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2005

151. Threshold traits are typically characterized by:
(A) Polygenic inheritance with underlying liability scale
(B) Mendelian inheritance governed by a single gene
(C) Cytoplasmic inheritance with complete phenotypic penetrance
(D) Absence of environmental influence on the trait phenotype

2013

152. In predicting correlated response (CR), if Trait X is selected, the expected genetic change in Trait Y depends on the narrow-sense heritabilities of both traits and their:
(A) Phenotypic correlation
(B) Environmental correlation
(C) Genetic correlation
(D) Epistatic covariance

2021

153. If an individual has one common ancestor in the pedigree with n generations separating the parents through that ancestor, the contribution to the inbreeding coefficient F is:
(A) $(\frac{1}{2})^n(1 - F_A)$
(B) $(\frac{1}{2})^{n+1}(1 + F_A)$
(C) $n \times \frac{1}{2} \times F_A$
(D) $(\frac{1}{4})^n$

2003

154. Theoretical basis for calculating the panmictic index (P) defines it as the probability that:
(A) Mating individuals share common ancestry in recent generations
(B) Heterozygotes are produced relative to the base population
(C) Simultaneous mutation occurs at multiple loci
(D) Overdominance is exhibited at specific trait loci

2008

155. A linear Genotype x Environment Interaction implies that the relative performance of genotypes changes predictably along an environmental gradient, which can be modeled using:
(A) Machine learning and random forest algorithms
(B) Joint regression analysis like Finlay-Wilkinson
(C) Application of simple single-factor ANOVA
(D) Standard chi-square tests for independence

2018

156. In the Eberhart and Russell model, the parameter $S^2_{\{di\}}$ represents the deviation from regression. A large $S^2_{\{di\}}$ value specifically infers that the genotype's response to environmental change is:
(A) Perfectly predictable and linear
(B) Unpredictable and highly non-linear
(C) Stable in high-yielding environments
(D) Purely additive without dominance

2004

157. Phenotypic dynamics under directional selection over many generations reveal a trajectory where the trait mean changes until it approaches:
(A) Genetic equilibrium driven by hybrid heterosis
(B) A plateau from exhaustion of additive variance
(C) Bifurcation into two distinct species groups
(D) A state of random genetic drift in population

2012

158. Factors affecting the decay of Linkage Disequilibrium (LD) in a population include:
(A) Spontaneous mutation rates occurring at loci
(B) Distance, recombination, and effective population size
(C) Mode of gene action like dominance or recessiveness
(D) Pleiotropic effects of multiple molecular markers

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(D) Presence of overdominance at all polymorphic loci

2005

177. Hypothesis that heterosis is caused by superior fitness of heterozygous genotype (Aa) over both AA and aa is termed:
(A) Epistasis hypothesis
(B) Overdominance hypothesis
(C) Dominance hypothesis
(D) Linkage drag hypothesis

2021

178. Non-linear Genotype x Environment Interactions complicate breeding programs because they:
(A) Allow simple additive adjustments to genotypic means
(B) Cause rank changes where best genotype in one environment is inferior in others
(C) Result in elimination of all environmental variance
(D) Decrease standard error of herizability estimates

2004

179. In an Eberhart and Russell stability analysis, regression coefficient (b_i) significantly greater than 1.0 indicates that genotype is:
(A) Adapted to high-yielding, favorable environments
(B) Adapted strictly to low-yielding environments
(C) Extremely stable across all environments
(D) Highly influenced by dominance variance

2019

180. Following are statements concerning natural selection:
I. Disruptive selection increases phenotypic variance by favoring extremes.
II. Directional selection reduces additive genetic variance over long periods.
III. Stabilizing selection shifts mean phenotype dramatically.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and II
(C) II and III
(D) I

2004

181. High measure of LD ($D\hat{a}\text{€}^{\text{TM}} = 1.0$) between two diallelic loci indicates that:
(A) At least one of four gametic haplotypes is absent
(B) Allele frequencies at both loci are exactly fifty percent
(C) Two loci are located on different chromosomes
(D) Recombination occurs freely between molecular loci

2015

182. Doubled Haploid (DH) mapping populations provide statistical advantage over F2 populations because DH lines are:
(A) Homozygous lines ensuring stable phenotyping
(B) Heterozygous and capture dominance effects
(C) Mapping populations generated through backcross procedures
(D) Highly prone to severe spontaneous mutations

NODIA

2005

183. To correctly interpret a Manhattan plot in GWAS, researchers look for SNP markers that:
(A) Have lowest physical density across whole chromosome
(B) Show significant statistical association with trait
(C) Display maximum levels of observed heterozygosity
(D) Have a minor allele frequency of zero

2009

184. In designing a Marker-Assisted Backcrossing (MABC) scheme, which phase typically requires largest number of markers uniformly distributed across genome?
(A) Foreground selection
(B) Recombinant selection
(C) Background selection
(D) Phenotypic selection

2012

185. Genomic Estimated Breeding Values (GEBVs) are calculated in training population using statistical models that penalize marker effects to:
(A) Prevent severe inbreeding depression in population
(B) Manage high dimensionality where markers exceed samples
(C) Minimize mutation rate of multiple minor gene loci
(D) Account for environmental temperature fluctuations in trials

2015

186. Functional candidate gene identification integrates genetic mapping with:
(A) Standard cytological staining of chromosome centromeres
(B) Transcriptomics, proteomics, or metabolic

(A) I, II and III
(B) II, III and IV
(C) I, II and III
(D) I and IV

2023

111. Natural selection acting on metric traits that penalizes extreme phenotypes and favors the mean is known as:
(A) Disruptive selection
(B) Directional selection
(C) Diversifying selection
(D) Stabilizing selection

2022

112. The parameter $D\hat{a}\text{€}^{\text{TM}}$ is preferred over raw D for measuring linkage disequilibrium because $D\hat{a}\text{€}^{\text{TM}}$:
(A) Standardizes LD against its maximum possible value
(B) Is completely independent of meiotic recombination
(C) Requires no knowledge of allele frequency variants
(D) Assumes that the population is infinitely large

2016

113. Interval Mapping (IM) utilizes maximum likelihood estimation to position a QTL within:
(A) The interval between two adjacent molecular markers
(B) An entire chromosome simultaneously without markers
(C) A single unmapped marker region
(D) The telomeric regions only

2017

114. The use of kinship (K-matrix) in GWAS Mixed Linear Models controls for:
(A) Familial relatedness or cryptic relationships
(B) Spontaneous mutation rate of the SNP markers
(C) Missing phenotypic data points in the trial
(D) Systematic errors in marker map distances

2017

115. To implement Marker-Assisted Backcrossing (MABC) efficiently in the fewest generations, a breeder must prioritize individuals showing:
(A) Double crossover events tightly flanking the introgressed target gene
(B) Homozygosity for the recurrent parent genome strictly at non-carrier chromosomes
(C) Transgressive segregation for yield
(D) Highest proportion of the donor parent background

2003

116. In Genomic Selection, the algorithm computes GEBVs by estimating marker effects initially in the:
(A) Breeding population
(B) Training population
(C) Selection population
(D) Validation population

2001

117. Identification of a candidate gene by expression profiling (eQTL) rests on the assumption that the phenotypic trait variation is driven by:
(A) Differences in mRNA transcript abundance
(B) Presence of gross chromosomal rearrangements
(C) Frequency of transposon mobility events
(D) Variations in synonymous codon usage patterns

2016

118. When computing genotypic frequencies in a sex-linked locus under HWE for females (XX), the expected frequency of carriers (heterozygotes) is:
(A) $2pq$
(B) p^2
(C) q
(D) q^2

2002

119. A statistically significant deviation from HWE indicates:
(A) The population is large and mating randomly
(B) Violation of assumptions like selection or migration
(C) Systematic DNA sequencing errors were made
(D) The locus is not transcribed in this tissue

2013

120. Following are statements regarding effective population size (N_e):
I. N_e is typically smaller than the census size (N).
II. A balanced sex ratio minimizes N_e.
III. High variance in reproductive success reduces N_e.
IV. Fluctuating population size uses harmonic mean for N_e.
V. N_e predicts the rate of genetic drift.
Which of the above statement(s) is/are INCORRECT?
(A) II

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(A) 1.0
(B) 0.5
(C) 0.0
(D) Heritability of trait

2014

197. Converting heritability from discrete binary scale to underlying normal liability scale is necessary to:
(A) Correct for incidence, making estimates comparable
(B) Inflate heritability estimates for publication
(C) Eliminate environmental variance components from model
(D) Convert threshold traits into standard Mendelian variants

2003

2012

198. Estimation of correlated response to selection (CR_Y) requires genetic covariance between Trait X and Trait Y, which can be computed from:
(A) Genetic correlation and additive variances of both traits
(B) Observed phenotypic correlation within populations
(C) Environmental correlation exclusively between traits
(D) Dominance variance of Trait X within breeding flock

2007

199. Wright's inbreeding coefficient (F) measures probability of identity by descent. In a random mating base population, average value of F is assumed to be:
(A) 0.5
(B) 1.0
(C) 0.0
(D) -1.0

2014

200. **Assertion (A):** Inbreeding depression is negligible for traits that act in an additive manner.
Reason (R): Additive gene action does not involve dominance; therefore, increased homozygosity does not alter mean of trait.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2016

201. Which hypothesis for heterosis suggests that crossing two inbred lines masks deleterious recessive alleles that were fixed during inbreeding?
(A) Dominance hypothesis
(B) Overdominance hypothesis
(C) Epistasis hypothesis
(D) Pleiotropy hypothesis

2003

202. Genetic correlation of performance across environments (r_G) is used to assess:
(A) Measure of interaction; if r_G is near 1, interaction is low
(B) Mutation rate observed across diverse environments
(C) Effective population size in different natural habitats
(D) Average inbreeding coefficient across test environments

2014

203. A GGE biplot graphical analysis displays "which-won-where" pattern, identifying:
(A) Best genotypes in specific mega-environments
(B) Physical location of QTLs on genetic chromosomes
(C) Exact causal mutation of genes
(D) Phylogenetic tree of species

NODIA

2024

204. Stabilizing selection tends to favor intermediate phenotypes. Consequence of long-term stabilizing selection is:
(A) Canalization and reduced phenotypic variance
(B) Sustained increase in mutational load
(C) Rapid speciation of divergent populations
(D) Expansion of phenotypic extremes in traits

2006

205. Squared correlation coefficient r^2 is superior to D for measuring linkage disequilibrium in GWAS because r^2:
(A) Directly reflects statistical power to detect an association
(B) Is independent of sample size
(C) Only works for completely linked loci
(D) Is strictly determined by physical distance

2002

206. Composite Interval Mapping (CIM) utilizes marker cofactors to control for genetic background, which results in:
(A) Lower statistical power compared to single marker analysis

(B) Precise localization of QTL without background noise
(C) Inability to detect epistatic interactions across markers
(D) Elimination of need for an F2 mapping population set

2002

207. In GWAS, controlling for population structure using a Q-matrix prevents:
(A) Associations from population structure correlations
(B) Identification of rare variants in samples
(C) Construction of Manhattan plots across chromosomes
(D) True positive associations from being detected by model

2007

208. Foreground selection in MAS is aimed at:
(A) Tracking target allele without phenotypic expression
(B) Selecting for background recurrent parent allele types
(C) Identifying recombination events outside target locus
(D) Evaluating general combining ability of elite line

2021

209. Primary rationale for adopting Genomic Selection (GS) over Marker-Assisted Selection (MAS) for yield traits is that GS:
(A) Captures small effects of many loci without thresholds
(B) Controls yield via a few major genes mapped by MAS
(C) Requires much smaller populations for mapping accuracy
(D) Requires phenotypic data in target generations

2013

210. Match the following parameters related to population genetics (List I) with their corresponding definitions (List II).
List I: (Parameters)
P. Selection coefficient (s)
Q. Fitness (w)
R. Effective population size (N_e)
S. Inbreeding coefficient (F)
List II: (Definitions)
1. Probability that two alleles are identical by descent
2. Relative reproductive success of a genotype
3. Proportional reduction in reproductive success relative to most fit genotype
4. Size of an idealized population experiencing same rate of genetic drift
(A) P-III, Q-II, R-IV, S-I
(B) P-II, Q-III, R-I, S-IV
(C) P-III, Q-I, R-IV, S-II
(D) P-I, Q-IV, R-II, S-III

2022

211. In an eQTL mapping study designed to validate functional candidate genes, "phenotype" analyzed for association is:
(A) mRNA abundance of specific genes
(B) Morphological height of plants
(C) Base pair length of telomeres
(D) Resistance score to pathogens

2013

212. For an autosomal locus with multiple alleles, if genotypic frequencies satisfy Hardy-Weinberg principle, it indicates that:
(A) Population is mating randomly without evolution
(B) Allele frequencies are changing at constant rates
(C) Population is subjected to intense selection
(D) Dominance variance for locus is zero

2009

213. If migration occurs at rate m from a source population with allele frequency q_m, change in local allele frequency Δq is:
(A) $m(q_m - q)$
(B) $m(q - q_m)$
(C) $(1 - m)q_m$
(D) $m \times q_m$

2017

214. What is equilibrium frequency (p) of a deleterious dominant allele if mutation rate is u and selection coefficient is s?
(A) $\frac{u}{s}$
(B) $\sqrt{\frac{u}{s}}$
(C) $\frac{s}{u}$
(D) $1 - \frac{u}{s}$

2012

215. When estimating selection coefficient (s) for a genotype that produces only 75 surviving

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offspring compared to 100 for most fit genotype, value of s is:
(A) 0.75
(B) 1.33
(C) 0.25
(D) 1.00

2013

216. Concept of effective population size (N_e) incorporates fact that genetic drift operates faster in populations where there is:
(A) Small fraction of individuals contributing gametes
(B) Mating pattern that is perfectly random and family sizes are equal
(C) Mutation rate equal to migration rate
(D) Natural selection that is absent from system

2024

217. In quantitative genetics, total phenotypic variance (V_P) observed in a uniform, controlled environment consists of:
(A) Genetic variance and experimental error
(B) Environmental variance component only
(C) Genotype x Environment Interaction term
(D) Additive genetic variance components

2005

218. Narrow-sense herizability (h^2) differs from broad-sense herizability (H^2) because narrow-sense herizability:
(A) Excludes non-additive genetic variances
(B) Excludes additive genetic variance
(C) Excludes environmental variance
(D) Excludes total phenotypic variance

2016

219. Breeder's equation $R = ih^2\sigma_P$ dictates that genetic advance will be zero if:
(A) Narrow-sense herizability is zero
(B) Environmental variance is zero
(C) Selection intensity is high
(D) Phenotypic standard deviation is large

2006

220. **Assertion (A):** Independent culling levels are effective when evaluating a very large number of traits simultaneously.
Reason (R): Setting minimum thresholds for many traits results in culling nearly entire population, forcing breeder to lower selection intensity for each individual trait.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2003

221. Family selection efficiency exceeds mass selection when intra-class correlation (resemblance due to common environment) is:
(A) Zero or negative
(B) Extremely high
(C) Moderate
(D) Equal to herizability

2016

222. Under Wright's threshold model for categorical traits, location of threshold on continuous liability scale is determined from:
(A) Incidence of trait classes in population
(B) Physical length of underlying trait genes
(C) Amount of crossing over during meiosis
(D) Environmental temperature within experiment

2018

223. Indirect selection for Trait X can improve Trait Y more efficiently than direct selection on Trait Y only if there is:
(A) High genetic correlation and $h^2(X) > h^2(Y)$
(B) A phenotypic correlation that is zero
(C) Zero additive genetic variance
(D) Completely independent genes for traits

2007

224. Which of following describes relationship between panmictic index (P) in generation t (P_t) and generation $t-1$ ($P_{\{t-1\}}$) in a finite population of size N?

(A) $P_t = P_{t-1} + \frac{1}{2N}$

(B) $P_t = P_{t-1}[1 - \frac{1}{2N}]$

(C) $P_t = 1 - P_{\{t-1\}}$

(D) $P_t = \frac{P_{t-1}}{2N}$

2002

225. Reduction in phenotypic performance of a trait due to inbreeding depression is proportional to:
(A) Increase in inbreeding coefficient
(B) Increase in generation interval
(C) Increase in selection intensity
(D) Initial additive genetic variance levels

2011

226. Linear Genotype x Environment Interactions are accommodated in breeding programs by using:

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(A) Joint regression like Finlay-Wilkinson
(B) Simple single-marker ANOVA analysis
(C) Standard chi-square test for balance
(D) Hardy-Weinberg equilibrium equations

2012

227. In AMMI model, interaction Principal Component Axes (IPCA) are extracted from matrix of:
(A) Interaction residuals after fitting main effects
(B) Total additive genetic effects in populations
(C) Observed marker allele frequencies in samples
(D) Pedigree relatedness coefficients among parents

2004

228. Directional selection acting on a metric trait leads to an equilibrium known as a selection limit, caused by:
(A) Exhaustion of additive genetic variance
(B) Sudden increase in spontaneous mutation rates
(C) Exhaustion of environmental variance
(D) Abrupt switch to stabilizing selection forces

2007

229. Measure of Linkage Disequilibrium D between alleles A and B is calculated as:
(A) $P_{\{AB\}} - p_A p_B$
(B) $p_A p_B - P_{\{AB\}}$
(C) $\frac{P_{AB}}{p_A p_B}$
(D) $P_{\{AB\}} + p_A p_B$

2002

230. Order mapping populations sequentially from lowest number of generations required for their development to highest.
I. F2 population
II. Recombinant Inbred Lines (RILs)
III. Near Isogenic Lines (NILs)
(A) I, III, II
(B) I, II, III
(C) II, I, III
(D) III, II, I

2003

231. GWAS relies on historical recombination events in natural populations. This characteristic provides GWAS with advantage over standard QTL mapping regarding:
(A) Resolution down to individual genes or nucleotides
(B) Simplicity of statistical analysis for phenotypes
(C) Freedom from false positive errors
(D) Elimination of genotypic data in mapping procedures

2003

232. Background selection in Marker-Assisted Backcrossing (MABC) accelerates breeding process by identifying progeny with:
(A) Highest proportion of recurrent parent alleles
(B) Absence of target introgressed gene locus
(C) Highest observed heterozygosity across markers
(D) Significant transgressive segregation for traits

2010

233. Marker-Assisted Recurrent Selection (MARS) models genetic value of individuals by estimating marker effects across genome to facilitate:
(A) Pyramiding multiple favorable QTLs via intermating
(B) Backcrossing to a single elite parent indefinitely
(C) Identifying molecular weight of proteins produced
(D) Maintaining clonal propagation in crops

2008

234. Validating a candidate gene through expression profiling (eQTL mapping) tests hypothesis that:
(A) Regulatory polymorphisms affect transcript levels
(B) Gene physical sequence contains no intron regions
(C) Gene is highly conserved across all known taxa
(D) Gene exerts no phenotypic effect on organism

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2005

235. In deriving consequences of Hardy-Weinberg equilibrium, reaching equilibrium for an autosomal locus requires how many generations of random mating?
(A) 1
(B) 2
(C) 5
(D) Infinite

2023

236. Chi-square test statistic for deviations from HWE is derived as sum of:
(A) $\frac{(\text{Observed} - \text{Expected})^2}{\text{Expected}}$

(B) $\frac{\text{Observed} - \text{Expected}}{\text{Expected}}$

(C) $\frac{(\text{Observed} - \text{Expected})^2}{\text{Observed}}$

(D) $\frac{\text{Expected} - \text{Observed}}{\text{Expected}^2}$

2013

237. Neighborhood model of migration (isolation by distance) predicts that individuals mating within a local neighborhood will have an inbreeding coefficient dependent on:
(A) Limited dispersal distance of species
(B) Observed zero results in all trials
(C) Negative results observed in test herds
(D) Mutation rates

2002

238. In a model of selection where heterozygotes have a selective advantage (overdominance), equilibrium allele frequencies are determined by:
(A) Ratio of selection against two homozygotes
(B) Absolute mutation rate within populations
(C) Effective population size of breeding flock
(D) Generation interval within breeding cycles

2023

239. Founder effect results in a new population characterized by:
(A) Allele frequencies that differ from original population due to sampling error
(B) Allele frequencies matching original large source population
(C) Increased genetic variation and high heterozygosity
(D) Zero linkage disequilibrium

2016

240. Partitioning of phenotypic variance assigns dominance variance (V_D) to:
(A) Same-locus alleles deviating from homozygote midpoint
(B) Observed differences between homozygous classes only
(C) Interactions between alleles at different gene loci
(D) Maternal effects transmitted through cytoplasm

2007

241. Heritability in broad sense (H^2) limits maximum possible value of:
(A) Narrow-sense heritability (h^2)
(B) Repeatability
(C) Epistatic variance
(D) Environmental variance

2008

242. In predicting genetic advance, accuracy of selection (ρ) is bounded between:
(A) 0 and 1
(B) -1 and 0
(C) 1 and infinity
(D) 0 and infinity

2013

243. Efficiency of selection index relative to independent culling levels increases when:
(A) Traits have varying economic weights and compensatory genetic correlations
(B) All traits are positively correlated and have equal importance
(C) Only a single trait is under selection
(D) Heritabilities of all traits are 1.0

2008

244. Theoretical formulations for within-family selection indicate it is advantageous for:
(A) Reducing environmental variance common to families
(B) Reducing generation interval of animals
(C) Reducing spontaneous mutation rates
(D) Reducing calculated inbreeding levels

2007

245. Wright's threshold model models liability distribution using a:
(A) Standard normal distribution with mean 0 and variance 1
(B) Binomial variance observed in discrete categories
(C) Poisson distribution applied for rare trait counts
(D) Uniform distribution observed across all genotypes

2011

246. Correlated response to selection (CR) is predicted to be negative if:
(A) Traits share a strong negative genetic correlation
(B) Both traits are highly heritable in group
(C) Selection intensity is zero in herds
(D) Phenotypic variance is small in experiments

2010

247. Computation of Wright's inbreeding coefficient (F) relies on concept of identical-by-descent (IBD) alleles, measuring:
(A) Probability alleles are copies of same ancestor
(B) Proportion of gene loci that are heterozygous in set
(C) Overall mutation rate observed across

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individual traits

2004

269. Formula for genetic correlation (r_G) involves genetic covariance divided by square root of product of:
(A) Additive genetic variances of both traits
(B) Phenotypic variances of both traits
(C) Environmental variances of both traits
(D) Dominance variances

2009

270. **Assertion (A):** Interval Mapping (IM) is preferred over Single Marker Analysis in QTL mapping.
Reason (R): Interval Mapping incorporates recombination frequencies between adjacent markers, increasing precision of QTL localization.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2013

271. After n generations of strict selfing, proportion of remaining heterozygosity relative to F1 is:
(A) $(\frac{1}{2})^n$
(B) $(\frac{1}{2})^{n-1}$
(C) $1-(\frac{1}{2})^n$
(D) $(\frac{1}{4})^n$

2001

272. Under dominance hypothesis, maximum heterotic effect is achieved when parental lines are:
(A) Fixed for opposite alleles at dominant loci
(B) Heterozygous at all available marker loci
(C) Identical for all recessive alleles
(D) Exhibiting zero dominance variance

2025

273. In Finlay-Wilkinson model, an ideal, widely adapted genotype possesses a mean yield above average and a regression coefficient (b_i) equal to:
(A) 1.0
(B) 0
(C) -1.0
(D) 2.0

2008

274. GGE biplot integrates Genotype main effects with:
(A) Genotype x Environment interaction effects
(B) Environment main effects
(C) Block effects
(D) Within-environment error variances

2016

275. Natural selection on metric traits models disruptive selection as a force that leads to:
(A) Bimodal distribution favoring trait extremes
(B) Unimodal and narrow phenotypic distribution
(C) Exact stabilization of phenotypic mean
(D) Occurrence of zero additive genetic variance

2014

276. Principles of Linkage Disequilibrium define limit of D as constrained by:
(A) Allele frequencies at both loci
(B) Overall mutation rate
(C) Physical length of chromosome in base pairs
(D) Presence of introns

2002

277. QTL mapping methodologies employ Composite Interval Mapping (CIM) to:
(A) Locate QTLs precisely by removing background variance
(B) Ignore genetic map in mapping trials
(C) Eliminate need for meiotic recombination
(D) Prove causality without functional validation

2014

278. Genome-Wide Association Studies correct for false positives by:
(A) Fitting MLM with population structure and kinship
(B) Simple linear regression model without random effects
(C) Binary logistic regression on genotypes
(D) Using markers strictly on one chromosome

NODIA

2021

279. Linkage drag in backcross breeding refers to:
(A) Unintentional introgression of undesirable genes linked to target gene
(B) Speed at which recurrent parent genome is recovered
(C) Frequency of recombination between unlinked markers
(D) Efficiency of selecting for polygenic traits using markers

2003

280. Match the following elements of quantitative trait loci mapping (List I) with their statistical characteristics (List II).

(D) Absence of target gene in genome

2004

258. For sex-linked loci, male genotypic frequencies in a species with XY males equals:
(A) Allele frequency itself (p or q)
(B) Square root of allele frequency
(C) Square of allele frequency (p^2 or q^2)
(D) $2pq$

2003

259. Hardy-Weinberg Equilibrium assumes an infinite population size. In reality, deviations occur because finite populations are subject to:
(A) Sampling variance, resulting in genetic drift
(B) Constant, error-free DNA replication
(C) Presence of absolute panmixia
(D) Complete absence of natural selection

2021

260. Following are statements regarding migration models:
I. The island model assumes equal migration rates among all subpopulations.
II. The neighborhood model assumes continuous distribution without discrete patches.
III. Migration decreases genetic variance within a subpopulation.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I

2011

261. If relative fitness (w) of a genotype is 0.8, selection coefficient (s) is:
(A) 0.2
(B) 0.8
(C) 1.2
(D) 1.8

2021

262. When population size fluctuates over generations, effective population size (N_e) is dominated by:
(A) Smallest generation size (bottleneck effect)
(B) Largest generation size
(C) Arithmetic mean size
(D) Selection coefficient

2009

263. If Genotype-Environment Interaction ($V_{\{GE\}}$) is significant, it means:
(A) Genotype expression varies across environments
(B) Genotypes react identically to varying environments
(C) Total variance of trait is zero
(D) Additive variance equals dominance variance

2003

264. Regression of offspring on a single parent yields a coefficient (b) equal to:
(A) $\frac{1}{2}h^2$
(B) h^2
(C) $2h^2$
(D) $\frac{h^2}{4}$

2017

265. To maximize genetic gain per year (R_y), calculated using $R_y = \frac{i \times h^2 \times \sigma_P}{L}$, a breeder must aim to:
(A) Increase intensity while minimizing generation interval
(B) Increase generation interval within cycles
(C) Decrease selection intensity within populations
(D) Decrease narrow-sense heritability of traits

2015

266. Smith-Hazel index is more efficient than tandem selection because it:
(A) Integrates covariances to balance trait correlations
(B) Assumes all traits have equal economic value
(C) Evaluates one trait per breeding generation
(D) Requires zero mathematical computation

2008

267. Individual selection outperforms within-family selection when:
(A) Intra-class correlation for trait is negative or zero
(B) Environmental variance common to family is large
(C) Heritability is zero
(D) Trait is fixed

2006

268. Inheritance of threshold traits relies on conversion of observed binomial heritability to continuous scale. This conversion:
(A) Uses normal distribution probability functions
(B) Uses exact physical length of underlying gene
(C) Uses linkage mapping distance between marker loci
(D) Uses complete dominance observed at

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2014

290. **Assertion (A):** The Smith-Hazel selection index guarantees maximum genetic progress for an aggregate genotype compared to independent culling.
Reason (R): The index weights each trait by its additive genetic variance, heritability, economic value, and covariance with other traits.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2003

291. Within-family selection is favored when environmental correlation among members of same family is:
(A) High
(B) Zero
(C) Negative
(D) Purely random

2002

292. Inheritance of threshold traits assumes a continuous underlying liability scale because phenotypic categories are:
(A) Discrete, masking polygenic nature
(B) Inherited via cytoplasmic genes
(C) Controlled by one major dominant gene
(D) Unaffected by environmental conditions

2008

293. If two traits share a high positive genetic correlation, directional selection for Trait A will lead to:
(A) Simultaneous improvement in correlated trait
(B) Decline in correlated trait
(C) Random drift in correlated trait values
(D) Zero change in correlated trait values

2007

294. Rate of inbreeding (ΔF) in a closed herd of 5 sires and 50 dams equals:
(A) $\frac{1}{8(5)} + \frac{1}{8(50)} = 0.0275$
(B) $\frac{1}{32(5)} + \frac{1}{32(50)}$
(C) $\frac{1}{4(5)} + \frac{1}{4(50)}$
(D) $\frac{1}{2(5+50)}$

2011

295. If Wright's inbreeding coefficient (F) equals 0.4, panmictic index (P) equals:
(A) 0.6
(B) 0.4
(C) 1.4
(D) 0.16

2017

296. Non-linear crossover interactions indicate that genetic correlation between same trait measured in two different environments is:
(A) Significantly less than 1.0
(B) Exactly 1.0
(C) Zero or perfectly negative
(D) Completely additive

2023

297. In AMMI model, if a genotype's IPCA score equals zero, genotype possesses:
(A) General stability with no specific interaction
(B) Complete unsuitability for all testing environments
(C) High interaction with poor sites
(D) Zero mean yield across trials

2006

298. Stabilizing selection forces a decrease in phenotypic variance without changing:
(A) Overall mean of population
(B) Mutation rate
(C) Effective population size
(D) Generation interval

2013

299. LD parameter r^2 is preferred in association mapping because it reflects:
(A) Sample size needed for statistical power in GWAS
(B) Physical size of genome in chromosomes
(C) Mutation rate of dominant gene alleles
(D) Recombination fraction observed in map

2001

300. QTL mapping methodologies employ Recombinant Inbred Lines (RILs) to improve accuracy because RILs are:
(A) Immortal homozygous genomes for multi-environment trials
(B) Segregating for all dominance variances
(C) Generated within a single generation
(D) Devoid of crossover events in mapping

NODIA

****

List I: (Mapping Elements)
P. Single Marker Analysis
Q. Simple Interval Mapping
R. Composite Interval Mapping
S. Genomic Selection
List II: (Characteristics)
1. Evaluates intervals between markers but ignores background QTLs
2. Estimates breeding values using all markers without significance testing
3. Identifies associations using simple t-tests or ANOVA marker by marker
4. Uses marker cofactors to control background genetic variance

(A) P-III, Q-I, R-IV, S-II
(B) P-I, Q-III, R-II, S-IV
(C) P-III, Q-II, R-I, S-IV
(D) P-II, Q-I, R-IV, S-III

2015

281. Candidate gene approaches target genes by integrating positional mapping data with:
(A) Functional expression or known biochemical pathways
(B) Random anonymous molecular marker screenings
(C) Centromere mapping across mapping flock
(D) Telomere length measurement within progeny

2009

282. For sex-linked loci adjustments in estimating genotypic frequencies are required because males are hemizygous. Consequently, a rare recessive trait appears:
(A) More frequently in males
(B) More frequently in females
(C) Equally in both sexes
(D) Only in homozygous females

2005

283. Disassortative mating (mating of phenotypically dissimilar individuals) generally results in:
(A) A decrease in homozygosity and an increase in heterozygosity
(B) A rapid increase in inbreeding coefficient
(C) Fixation of rare recessive alleles
(D) A decrease in effective population size

2011

284. Under continuous one-way migration (rate m), allele frequency approaches source population at a rate proportional to:

(A) m

(B) m^2

(C) $\frac{1}{m}$

(D) $\sqrt{m}$

2016

285. For codominant alleles where heterozygotes are intermediate in fitness, allele with higher fitness will:
(A) Proceed toward fixation (frequency = 1)
(B) Reach an intermediate stable equilibrium
(C) Be eliminated
(D) Fluctuate randomly

2014

286. Variance of allele frequency after one generation of genetic drift in a population of size N is:

(A) $\frac{pq}{2N}$

(B) $\frac{pq}{N}$

(C) $\frac{2N}{pq}$

(D) $\frac{N}{2pq}$

2010

2005

287. Quantitative genetics defines additive variance (V_A) as sum of variances of:
(A) Breeding values for all individuals in population
(B) Dominance deviations observed at loci
(C) Epistatic interactions between genes
(D) Environmental deviations affecting phenotypes

2011

288. Repeatability provides upper limit to broad-sense heritability because it includes:
(A) Genetic variance plus permanent environmental variance
(B) Only additive genetic variance
(C) Only temporary environmental variance
(D) Epistatic variance components

2025

289. In genetic advance prediction, selection intensity (i) equals selection differential (S) divided by:
(A) Phenotypic standard deviation (σ_P)
(B) Phenotypic variance (V_P)
(C) Additive variance (V_A)
(D) Generation interval (L)

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genome
(D) Amount of genetic drift experienced by population

2008

248. Basis of inbreeding depression under dominance hypothesis relies on fact that as F increases, frequency of:
(A) Heterozygotes decreases, exposing recessive alleles
(B) Overdominant loci frequency increases in group
(C) New mutations increase linearly over generations
(D) Epistatic interactions dominate observed phenotype

2018

249. A crossover Genotype x Environment Interaction signifies that reaction norms of two genotypes:
(A) Intersect, causing rank changes
(B) Are perfectly parallel
(C) Have slopes of exactly zero
(D) Are independent of genetic variance

2001

250. Select the correct sequence for calculating Genomic Estimated Breeding Values (GEBVs) in a Genomic Selection program.
I. Genotype and phenotype the training population
II. Estimate marker effects using statistical models
III. Genotype the selection population
IV. Calculate GEBVs for the selection population by summing estimated marker effects
(A) I, II, III, IV
(B) I, III, II, IV
(C) II, I, III, IV
(D) III, IV, I, II

2008

251. Canalization models ability of a developmental pathway to produce a constant phenotype despite disturbances. This implies a reduction in:
(A) Phenotypic variance
(B) Generation interval
(C) Overdominance
(D) Linkage disequilibrium

2021

252. Linkage Disequilibrium in generation t, D_t, decays according to:
(A) $D_t = D_0(1 - c)^t$
(B) $D_t = D_0 + ct$
(C) $D_t = \frac{D_0}{c^t}$
(D) $D_t = D_0(c - 1)^t$

2012

253. QTL mapping utilizes Interval Mapping (IM), which computes a LOD score. A LOD score of 3.0 implies that presence of a QTL is:
(A) 3 times more likely than its absence
(B) 100 times more likely than its absence
(C) 1000 times more likely than its absence
(D) 30 times more likely than its absence

2012

254. In GWAS, Manhattan plots plot $-\log_{10}(P)$ values. A tall peak on this plot identifies a genomic region with:
(A) Significant statistical association with trait
(B) Highest rate of recombination in mapping
(C) Extreme physical length of chromosomes
(D) Absence of gene loci in that region

2001

255. In a Marker-Assisted Backcrossing (MABC) strategy, recombinant selection aims to identify individuals with crossovers between target gene and flanking markers within a distance of:
(A) 1-5 cM of target gene
(B) 50 cM, to ensure independent assortment
(C) 100 cM
(D) Entire chromosome length

2007

256. Advanced breeding schemes like Genomic Selection (GS) compute Genomic Estimated Breeding Values (GEBVs) using all markers simultaneously. This circumvents a limitation of MAS by:
(A) Capturing effects of QTLs failing significance tests
(B) Ignoring markers entirely during selection process
(C) Requiring exact physical mapping of causal genes
(D) Measuring only largest effect gene in herd

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257. A functional candidate gene identified for drought tolerance is validated if its expression profiling (eQTL) shows:
(A) Differential transcript correlating with phenotype
(B) No change in transcript levels under stress
(C) Random transcript fluctuations unrelated to treatment

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ANSWERS

1. (C) 0.48
Randomly mating populations follow mathematical distributions described by the Hardy-Weinberg formula for specific genetic loci. If an autosomal recessive allele possesses a frequency of point four, the corresponding dominant allele frequency is point six. The predicted proportion of individuals carrying both alleles is determined by taking twice the product of these allele frequencies to find the heterozygous group.

2. (A) Absence of migration
Genetic equilibrium requires specific conditions to ensure that allele frequencies remain constant over successive generations in a population. One fundamental requirement is the lack of gene flow from external sources into the breeding group. This prevents the introduction of new genetic variants or the alteration of existing proportions, maintaining the mathematical balance within the gene pool over long periods.

3. (C) Migration rate and the allele frequency difference between populations
The island model of migration describes the genetic dynamics of small subpopulations receiving migrants from a large source population. In this model, the shift in allele frequency within a single generation depends on the proportion of migrants entering the group. Additionally, the magnitude of change is influenced by the existing difference in allele frequencies between the migrants and the residents.

4. (D) $-\frac{q^2}{1+q}$
When a population undergoes complete selection against a deleterious recessive allele, the homozygous recessive individuals do not contribute to the next generation. The mathematical change in the allele frequency after one generation is derived using the fitness of genotypes. This specific formula accounts for the reduction in frequency relative to the surviving proportion of the population that carries the allele.

5. (C) A highly skewed sex ratio of breeding individuals
The effective population size determines the rate of genetic drift and loss of diversity within a breeding group. When the number of breeding males and females is significantly unequal, the genetic contribution to the next generation is restricted. This imbalance drastically lowers the effective size compared to the total number of individuals, accelerating the accumulation of inbreeding and random changes.

6. (B) Non-allelic interactions between two or more loci
Epistatic variance represents a component of the total genetic variance for complex quantitative traits. This phenomenon occurs when the phenotypic expression of genes at one locus is influenced or modified by genes located at different loci. These non-allelic interactions contribute to the unique genetic architecture of a trait and are distinguished from additive effects or dominance deviations at single sites.

7. (D) Paternal half-sib correlation
Paternal half-sib correlation is a common method used to estimate narrow-sense herizability by evaluating the resemblance among offspring sharing the same sire. This approach is advantageous because the covariance between half-sibs provides an estimate for one-quarter of the additive genetic variance. Since sires generally do not provide maternal effects, this method yields a relatively unbiased estimate of genetic inheritance.

8. (A) The selected individuals and the unselected base population
The selection differential is a critical parameter in the breeder's equation used to predict the response to selection. It is calculated by subtracting the mean phenotypic value of the entire unselected population from the mean value of the specific individuals chosen for breeding. This value represents the selection pressure applied by the breeder to shift the population mean in the next generation.

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have occurred very close to the target locus. By selecting for these recombinations, breeders can minimize the amount of donor DNA that is carried along with the gene, effectively reducing undesirable linkage drag.

45. (A) Pyramiding multiple QTLs via crossing selected lines
Marker-assisted recurrent selection is a breeding strategy designed to improve complex polygenic traits. It involves identifying multiple quantitative trait loci and then systematically intercrossing selected individuals to accumulate these favorable alleles in a single population. This process allows for the rapid pyramiding of genetic effects from different sources, leading to a significant increase in the performance of the resulting breeding lines.

46. (B) Transcript abundance or expression level of a gene
Expression quantitative trait loci mapping is a functional genomics approach that identifies genomic regions influencing gene expression. By treating the transcript levels of genes as quantitative traits, researchers can map the genetic factors that regulate mRNA abundance. This technique helps in understanding the molecular mechanisms underlying complex phenotypes and identifies regulatory variants that contribute to the variation observed in the biological pathways.

47. (C) 0.62
In a multiple allele system, the expected frequency of heterozygotes under Hardy-Weinberg equilibrium is calculated by summing the frequencies of all possible heterozygous combinations. For three alleles, this involves adding the products of the allele frequencies for each pair. This calculation accounts for all individuals carrying two different alleles, providing the total proportion of heterozygous genotypes within the randomly mating population.

48. (B) Disassortative mating or heterozygote advantage
An excess of heterozygotes relative to the levels predicted by the Hardy-Weinberg principle indicates specific evolutionary or mating processes. This deviation can occur due to disassortative mating, where individuals choose partners with different phenotypes. Alternatively, it may result from heterozygote advantage, where individuals with both alleles have higher fitness than either homozygote. Both mechanisms actively maintain genetic diversity and high heterozygosity levels.

49. (B) Geographical distance and the limited dispersal of individuals
The neighborhood model of migration, also known as isolation by distance, describes how genetic differentiation develops in a continuously distributed population. In this model, individuals are more likely to mate with neighbors than with distant individuals due to limited dispersal abilities. Over time, this leads to a gradual shift in allele frequencies across the geographic range, creating a pattern of genetic structure.

50. (A) I and III
Selection effectiveness varies based on allele frequency and dominance. Selection against rare recessive alleles is slow because they are mostly hidden in heterozygotes. Conversely, selection against dominant alleles is very rapid. While heterozygote advantage leads to balanced polymorphisms, codominant selection typically leads to the fixation of the more favorable allele rather than a stable equilibrium. These principles are fundamental in population genetics.

51. (C) Genetic drift
The founder effect is a phenomenon where a new population is established by a very small number of individuals from a larger source. Because the founders carry only a fraction of the original genetic diversity, the new population may have very different allele frequencies. This is a classic example of genetic drift, where random sampling leads to significant shifts in the genetic makeup.

52. (C) 0.70
Broad-sense herizability is calculated as the ratio of the total genetic variance to the total phenotypic variance. The total genetic variance is the sum of the additive, dominance, and epistatic variance components. By dividing this total genetic value by the phenotypic variance, we obtain the proportion of the trait variation that is attributable to genetic differences among individuals in the population.

53. (A) Broad-sense herizability
Repeatability is a measure used for traits that can be recorded multiple times on the same individual. It quantifies the correlation between

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This phenomenon is often the result of stabilizing selection, which favors the maintenance of an optimal phenotype by suppressing the expression of variations.

18. (A) D divided by the theoretical maximum of D given the allele frequencies
Linkage disequilibrium measures the non-random association of alleles at different loci within a population. The parameter D prime is a standardized measure used to compare the degree of disequilibrium across different loci regardless of their allele frequencies. It is calculated by dividing the observed disequilibrium value by the maximum possible value it could attain, ranging from zero to one.

19. (C) Incorporating marker cofactors to control for background genetic effects
Composite interval mapping is an advanced statistical method used to identify quantitative trait loci more accurately than simple interval mapping. It enhances the precision of mapping by including specific markers as cofactors in the analysis. These cofactors account for the effects of other QTLs located elsewhere in the genome, thereby reducing the background noise and improving the detection of the target locus.

20. (D) P-III, Q-IV, R-I, S-II
Genome-wide association studies utilize several statistical matrices and plots to interpret genetic data correctly. The Q-matrix accounts for population structure, while the K-matrix defines the kinship relationships among individuals. Results are often visualized using a Manhattan plot to highlight significant markers. Additionally, identifying false positives is essential to ensure that associations are truly genetic rather than artifacts of population history.

21. (B) Accelerate the recovery of the recurrent parent genome
In marker-assisted backcrossing, background selection is applied to screen individuals for the proportion of the recurrent parent genome they carry. By using markers distributed across the entire genome, breeders can identify progeny that have recovered the desired genetic background more rapidly than through traditional phenotypic selection. This process significantly reduces the number of generations required to develop a new variety.

22. (A) Calculates GEBVs using all markers without significance testing
Genomic selection is a modern breeding approach that predicts the genetic merit of individuals using marker information from the entire genome. Unlike traditional marker-assisted selection, which focuses on a few significant QTLs, genomic selection incorporates the effects of all available markers simultaneously. This method avoids the limitations of significance testing and captures the effects of minor genes that contribute to complex traits.

23. (D) Biological pathways and differential expression profiling
Identifying functional candidate genes for complex traits involves integrating genetic mapping with biological knowledge. Researchers often examine biochemical pathways and physiological processes related to the trait to find genes with relevant functions. Furthermore, analyzing differential expression profiles helps identify genes that are active under specific conditions, providing evidence that they may be directly involved in the control and expression of the trait.

24. (C) 0.32
For sex-linked loci, the allele frequency in males is equal to the frequency in the total population. If the recessive frequency is point two, the dominant frequency is point eight. In females, who possess two X chromosomes, the expected frequency of heterozygotes under Hardy-Weinberg equilibrium is calculated as two times the product of these allele frequencies, resulting in point thirty-two.

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25. (B) Observed genotypic counts vs expected counts from allele frequencies
The Chi-square test is a statistical tool used to determine if a population follows the Hardy-Weinberg equilibrium. It compares the actual number of individuals for each genotype observed in a sample with the number expected based on the calculated allele frequencies. Significant differences between these values indicate that evolutionary forces, such as selection or non-random mating, are influencing the genetic distribution.

26. (D) 0.909
Under recurrent reversible mutation pressure, the equilibrium allele frequency is determined by the

9. (C) Economic values, genetic variances, and covariances
The Smith-Hazel selection index is designed to maximize the rate of genetic improvement for multiple traits simultaneously. It functions by assigning weights to individual traits based on their relative economic importance and genetic parameters. By incorporating both variances and genetic covariances, the index accounts for the correlations between traits, ensuring the most efficient selection progress across the aggregate breeding objective.

10. (A) Both A and R are true and R is the correct explanation of A.
Family selection is particularly effective for traits that exhibit low heritability because individual performance is a poor indicator of breeding value. Averaging the phenotypes of family members helps to cancel out random environmental variations that affect single individuals. Consequently, the family mean provides a more accurate representation of the underlying genetic merit, leading to greater efficiency in the selection process.

11. (D) Liability
The threshold model explains the inheritance of discrete traits that are influenced by multiple genes and environmental factors. It assumes that there is an underlying, unobservable continuous variable that represents the total susceptibility of an individual to express the trait. This latent variable is influenced by polygenic inheritance and determines whether an individual exceeds a specific point to show the phenotype.

12. (B) Pleiotropy and linkage disequilibrium between contributing loci
A correlated response occurs when selecting for one trait leads to a simultaneous genetic change in another trait. The primary biological reason for this association is pleiotropy, where a single gene affects multiple phenotypes. Additionally, linkage disequilibrium between genes controlling different traits can also contribute to this correlation, as these genes are often inherited together during the selection and breeding process.

13. (C) The probability that two alleles at a locus are IBD
Wright's inbreeding coefficient quantifies the level of genetic relatedness within an individual resulting from the mating of relatives. It specifically measures the statistical probability that both alleles present at a single genetic locus are identical by descent. This indicates that the alleles are exact copies derived from a single common ancestor shared by the parents of the individual in the pedigree.

14. (D) The unmasking of deleterious recessive alleles
The dominance hypothesis suggests that inbreeding depression is primarily caused by an increase in homozygosity within a population. As individuals become more inbred, harmful recessive alleles that were previously hidden in heterozygous states are expressed. These deleterious alleles reduce the overall fitness and performance of the population, while crossing inbred lines can mask these effects by restoring the heterozygous condition.

15. (A) The rank order of genotypic performance changes across environments
A crossover genotype by environment interaction occurs when the relative performance of genotypes is inconsistent across different testing locations. In this specific type of interaction, the genotype that performs best in one environment may be among the worst in another. This reversal of rank complicates the selection process, as it necessitates the development of varieties specifically adapted to distinct target environments.

16. (B) High mean yield, $b_i = 1.0$, and $S^2_{\{di\}} = 0$
Stability analysis models identify varieties that provide consistent performance across a wide range of environmental conditions. According to the Eberhart and Russell model, an ideal variety should possess a high average performance across all environments. Furthermore, it must show a regression coefficient of unity and a deviation from regression near zero, indicating a predictable and stable response to environmental changes.

17. (B) Maintain a consistent phenotype despite genetic or environmental noise
Canalization is a developmental process that allows a population to produce a constant and robust phenotype regardless of genetic mutations or environmental fluctuations. It represents a form of biological buffering that ensures normal development occurs under varying conditions.

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change in the others, which must be considered during the breeding process.

36. (A) $\frac{1}{2N}$
The rate of increase in homozygosity per generation is a measure of the speed at which inbreeding accumulates in a population. In an idealized population of a specific size, this rate is inversely proportional to twice the number of breeding individuals. This formula highlights how smaller populations experience a faster loss of genetic variation and a more rapid increase in the level of inbreeding.

37. (B) $P = 1 - F$
The panmictic index is a measure of the relative heterozygosity in a population compared to the level expected under random mating. It is related to the inbreeding coefficient by a simple linear relationship where the sum of both values equals one. As the level of inbreeding increases, the panmictic index decreases, reflecting the loss of heterozygosity due to the mating of relatives.

38. (A) The best genotype remains best in both environments though magnitude of performance varies
A non-crossover genotype by environment interaction occurs when genotypes show differences in their response to environments, but their relative rankings remain the same. While the absolute performance levels may fluctuate across different locations or conditions, the superior genotype in one environment is also the superior genotype in others. This type of interaction is generally easier for breeders to manage than rank-changing interactions.

39. (C) Principal Component Analysis (PCA)
The additive main effects and multiplicative interaction model is a powerful statistical tool for analyzing multi-environment trials. It partitions the total variance into the main effects for genotypes and environments, while the interaction component is analyzed using principal component analysis. This approach allows breeders to visualize and interpret complex interaction patterns, helping to identify stable genotypes and specific environmental adaptations.

40. (A) I and II
Natural selection influences the phenotypic distribution of traits in several ways. Stabilizing selection favors intermediate phenotypes and reduces the variance without changing the mean value. In contrast, directional selection favors one extreme phenotype, causing a shift in the population mean over time. Both processes are fundamental in evolution, altering the genetic and phenotypic characteristics of populations in response to selective pressures.

41. (D) Relates directly to statistical power and effective population size
The statistical measure r-squared is widely used in genome-wide association studies to quantify the degree of linkage disequilibrium between markers. It is preferred over other measures because it has a direct relationship with the statistical power needed to detect associations. Additionally, it is influenced by the effective population size, providing valuable information about the historical recombination and genetic structure of the population.

42. (A) Are permanent lines allowing replicated multi-environment trials
Recombinant inbred lines are a valuable tool in genetic mapping and quantitative trait loci analysis. These lines are developed through several generations of self-fertilization, resulting in highly homozygous individuals that breed true. Because they are permanent and genetically stable, they can be replicated and tested across multiple years and locations, which is essential for accurately measuring traits influenced by the environment.

43. (C) The K-matrix (kinship or relatedness) in a mixed linear model
Cryptic relatedness within a study population can lead to false positive associations in genome-wide association studies. To address this issue, researchers utilize mixed linear models that incorporate a kinship matrix. This matrix defines the pairwise relatedness among all individuals in the sample, allowing the model to account for the background genetic similarities and ensure that identified associations are truly linked to the trait.

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44. (D) Identify recombinations flanking the target locus to minimize linkage drag
Recombinant selection is a specialized technique used in marker-assisted backcrossing to refine the genetic area around a transferred gene. The goal is to identify individuals where crossover events

balance between forward and backward mutation rates. The specific frequency is calculated using the ratio of the forward mutation rate to the sum of both mutation rates. In this scenario, the high forward mutation rate relative to the backward rate leads to a high equilibrium frequency for the mutant allele.

27. (A) Rapidly decrease and be eliminated if no mutation occurs
Selection against a dominant allele is highly effective because the allele is expressed in both homozygous and heterozygous individuals. Since every individual carrying the dominant allele has lower fitness, the allele is subjected to strong selection pressure in every generation. This leads to a rapid decrease in its frequency, eventually resulting in the complete removal of the allele from the population over time.

28. (B) The harmonic mean of the sizes, thus closer to 10
The effective population size in a fluctuating population is primarily influenced by the generations with the smallest number of individuals. Mathematically, it is calculated as the harmonic mean of the census sizes across successive generations. Because the harmonic mean is sensitive to small values, the effective size will be much closer to the minimum population size than to the larger sizes.

29. (D) Variance due to average effects of alleles substituted for another
Additive genetic variance is the most important component of variance for animal and plant breeders. It represents the variance of the breeding values and is derived from the average effects of alleles when they are substituted in the population. This portion of the genetic variance is directly transmissible from parents to offspring and determines the resemblance between relatives and the selection response.

30. (B) II and III
Narrow-sense heritability is a critical parameter that measures the proportion of phenotypic variance due to additive genetic effects. It determines how closely offspring resemble their parents and predicts the response to artificial selection. Importantly, heritability is not a fixed property of a trait but is specific to the particular population and the environmental conditions present during the time of measurement.

31. (B) Selection intensity in phenotypic standard deviation units
Selection intensity is a standardized measure of the selection pressure applied to a population. It is defined as the selection differential divided by the phenotypic standard deviation of the trait. This parameter allows breeders to compare the rigor of selection across different traits or populations regardless of the units of measurement, and it is directly used in predicting the genetic advance.

32. (A) Independent culling levels
Independent culling levels is a multi-trait selection method that involves setting specific minimum standards for every trait under consideration. Any individual that fails to meet the threshold for even a single trait is discarded, regardless of how superior it may be in other traits. This method is simpler to implement than index selection but can be less efficient in practice.

33. (C) Are sex-limited or have very low heritability
Progeny testing is a breeding strategy that evaluates the genetic merit of a parent based on the performance of its offspring. It is particularly beneficial for traits that cannot be measured directly in the candidates, such as sex-limited traits or those with low heritability. By using the average performance of many progeny, the environmental noise is reduced, improving the accuracy of selection.

34. (C) The incidence of the trait in the population
In the threshold model for categorical traits, the observed herizability on a discrete scale must be converted to an underlying continuous scale. This conversion is necessary for proper genetic analysis and requires knowing the proportion of individuals in the population that express the trait. The incidence determines the position of the threshold on the normal distribution, which is essential for calculating the parameters.

35. (D) A single gene simultaneously influences more than one phenotypic trait
Pleiotropy is a biological phenomenon where one gene has multiple phenotypic effects on different traits. It is the primary cause of genetic correlation between traits that are inherited together. Because a single genetic change affects several characteristics simultaneously, selection for one trait will inevitably lead to a correlated

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successive measurements and accounts for both genetic variance and permanent environmental effects. Because it includes these permanent environmental influences, repeatability always provides an upper theoretical limit to broad-sense heritability, which only considers the proportion of variance due to genetic factors.

54. (D) True breeding value and estimated breeding value
The accuracy of selection is a critical metric in animal and plant breeding that indicates how well the selection criteria reflect the underlying genetics. It is defined as the correlation between the true breeding value of an individual and its estimated breeding value. Higher accuracy means that the selected individuals are more likely to pass on superior alleles, leading to a greater genetic response.

55. (B) Selecting a second trait only after the first reaches a goal
Tandem selection is a multi-trait improvement strategy where breeding efforts are focused on one trait at a time. Once the desired level of improvement is reached for the first trait, the selection criteria are shifted to the next trait. While simple to manage, this method can be slow and may result in a loss of progress for the previously selected traits.

56. (A) Environmental variance common to the family is very high
Within-family selection is a method where individuals are selected based on their performance relative to their own family mean. This approach is particularly useful when families are raised in different environments that cause significant variation between groups. By selecting the best individuals from each family, the confounding effects of common environmental variance are eliminated, allowing for a more accurate assessment of genetic merit.

57. (C) Exhibit the discrete phenotypic state (e.g., disease affected)
In the threshold model for quantitative genetics, a discrete phenotypic state is expressed only when an individual's total genetic and environmental liability exceeds a specific critical value. This threshold divides the population into two categories, such as healthy and diseased. Individuals who fall beyond this point on the continuous liability scale will show the trait, while those below it will not.

58. (B) Recombination
Linkage disequilibrium occurs when alleles at different loci are associated more frequently than expected by chance. While this can create a temporary genetic correlation between traits, the association is not permanent. Over successive generations of random mating, meiotic recombination will gradually break the physical linkages between the loci. This process causes the linkage disequilibrium to decay, eventually resulting in the loss of the correlation.

59. (B) 0.250
The inbreeding coefficient of an offspring is determined by the relatedness of its parents. For a full-sib mating where the parents are not themselves inbred, the offspring receives alleles that have a specific probability of being identical by descent. Mathematically, the coefficient is calculated based on the shared ancestry, and for full siblings, this results in a value of point twenty-five.

60. (A) IV, III, II, I
Marker-assisted backcrossing follows a logical progression to introgress a target gene while recovering the parent background. The process begins with crossing the hybrid back to the recurrent parent. Subsequently, foreground selection identifies carriers of the target gene, followed by recombinant selection to minimize the surrounding donor DNA. Finally, background selection is used to choose individuals with the highest recurrent parent genome.

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61. (B) Superiority of the heterozygous genotype over both homozygotes
The overdominance hypothesis is one of the primary theories proposed to explain the phenomenon of heterosis. It postulates that the heterozygous genotype possesses a physiological or biochemical advantage that makes it superior to either of the homozygous genotypes. This superiority in performance or fitness is observed when inbred lines are crossed, resulting in hybrids that exceed the performance of their parents.

62. (A) Regression of genotypic performance on environmental index
In the Finlay and Wilkinson approach to stability analysis, the adaptability of a

allows for a more accurate assessment of the genetic differences within each family, improving the overall response to selection.

81. (B) Standard normal distribution
The threshold model for categorical traits assumes that the underlying susceptibility, or liability, follows a continuous distribution within the population. In quantitative genetic analysis, this liability is typically modeled using a standard normal distribution with a mean of zero and a variance of one. This assumption allows researchers to apply standard statistical tools to understand the inheritance of traits that appear as discrete classes.

82. (A) $CR_Y = i_X h_X h_Y r_G \sigma_{PY}$
The correlated response to selection predicts the genetic change in one trait when selection is applied to another. This response depends on the selection intensity and the square root of the heritabilities for both traits. Additionally, the genetic correlation between the two traits and the phenotypic standard deviation of the target trait are essential components for calculating the expected change.

83. (B) 50%
Self-fertilization is the most extreme form of inbreeding and has a profound effect on the genetic structure of a population. In each generation of selfing, the proportion of heterozygous individuals is reduced by half as they segregate to produce homozygous offspring. Over time, this leads to a rapid increase in homozygosity across all loci, eventually resulting in the development of pure breeding lines.

84. (B) Dominance hypothesis
The dominance hypothesis is a widely accepted explanation for the phenomenon of heterosis in plant and animal breeding. It proposes that the superior performance of hybrids arises from the accumulation of favorable dominant alleles from both parents. By crossing two lines, the harmful recessive alleles present in one parent are masked by the functional dominant alleles from the other, leading to improved vigor and performance.

85. (B) Phenotypic differences among genotypes change across environments
In an analysis of variance, a significant genotype by environment interaction term indicates that the genotypes do not respond uniformly to different conditions. This means that the differences in phenotype observed between varieties are inconsistent across the test environments. Such interactions are important for breeders to identify, as they may indicate that specific genotypes are better suited for certain environments than others.

86. (A) Genotype main effect and Genotype x Environment interaction
GGE biplot analysis is a specialized graphical tool used to evaluate the performance and stability of genotypes across multiple environments. The acronym GGE stands for the genotype plus genotype by environment interaction, which are the two components of variation visualized in the plot. By combining these effects, the biplot helps breeders identify which genotypes are most productive and stable across target regions.

87. (B) Additive genetic variance for the trait is exhausted
Directional selection is used to shift the mean of a trait towards a desired extreme, but this progress cannot continue indefinitely. Eventually, the population reaches a selection limit or plateau where no further genetic gain is observed. This typically occurs because the additive genetic variance for the trait has been exhausted, meaning that all individuals in the population have become genetically similar for that trait.

88. (A) The marker alleles are highly predictive of the QTN alleles in the population
Linkage disequilibrium measures the non-random association between alleles at two different genomic locations. A very high value of r-squared between a molecular marker and a causal mutation indicates that the two are inherited together almost every time. This strong association makes the marker an excellent predictor of the underlying genetic variant, which is essential for effective marker-assisted selection and association mapping.

89. (C) QTL effect and distance from the marker are confounded
Single marker analysis is a simple method for detecting quantitative trait loci, but it has several statistical limitations. One major drawback is that it cannot distinguish between the magnitude of a gene's effect and its physical

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frequency of a specific genotype in males is equal to the frequency of that allele in the population. If a recessive allele has a frequency of q, then the proportion of males expressing the trait will also be q.

72. (B) There is evidence that the population is deviating from HWE
The p-value from a chi-square test indicates the probability that the observed differences between data and the expected model are due to chance. A low p-value, such as point zero one, suggests that the deviations from the Hardy-Weinberg equilibrium are statistically significant. This provides strong evidence that one or more assumptions of the equilibrium, such as random mating, are being violated.

73. (B) Mutation rates are generally extremely small
While mutation is the ultimate source of all genetic variation, it is considered a very weak force in changing allele frequencies on its own. Spontaneous mutation rates at individual loci are typically extremely low, often occurring at a frequency of one in a million. Therefore, significant evolutionary change through mutation alone requires immense periods of time unless it is combined with other forces.

74. (D) Heterozygote advantage (overdominance)
Heterozygote advantage, or overdominance, occurs when individuals with both alleles at a locus have higher fitness than either of the homozygotes. This selective pressure prevents any single allele from being eliminated from the population. Instead, it maintains both alleles at specific equilibrium frequencies, resulting in a stable balanced polymorphism that preserves genetic diversity within the population over many generations.

75. (C) Randomly eliminating alleles due to population reduction
A population bottleneck occurs when a catastrophic event significantly reduces the number of individuals in a population. During this period, rare alleles are often lost by chance, and the overall genetic diversity of the surviving group is drastically reduced. This random shift in allele frequencies is a form of genetic drift that can have lasting impacts on the evolutionary potential of the species.

76. (B) Breeding values in the population
Additive genetic variance is a fundamental concept in quantitative genetics that represents the portion of total genetic variance due to the cumulative effects of alleles. It is formally defined as the variance of the breeding values of individuals within the population. This component is crucial because it determines the response to selection and the degree of resemblance between parents and their offspring.

77. (B) Narrow-sense heritability
The statistical relationship between parents and their offspring is a direct indicator of the inheritance of quantitative traits. When the phenotypes of offspring are regressed on the average phenotype of their parents, the resulting slope of the regression line provides an estimate of narrow-sense heritability. This value represents the proportion of the total phenotypic variation that is attributable to additive genetic effects.

78. (A) Increase annual selection response if accuracy is stable
The rate of genetic progress is influenced by the length of time between successive generations. In the equation for annual genetic gain, the generation interval appears in the denominator. Therefore, reducing the time it takes for animals to reproduce will theoretically increase the response per year. This strategy is effective as long as the selection accuracy and intensity are maintained.

79. (B) It rejects superior individuals deficient in one trait
Independent culling levels is a multi-trait selection strategy that applies strict thresholds for every characteristic under selection. A major drawback of this approach is its lack of flexibility; an individual that is exceptional in many traits will still be discarded if it fails to meet the minimum requirement for a single trait. This can lead to the loss of valuable genetic material.

80. (A) Both A and R are true and R is the correct explanation of A.
Within-family selection is a highly effective method when maternal effects or common environments create significant variation between different families. By comparing individuals only to their own siblings, the shared environmental influences that might otherwise bias the selection process are cancelled out. This

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genotype is measured by its response to varying environmental conditions. This is quantified by regressing the mean performance of each genotype on an environmental index derived from the site means. The resulting regression coefficient indicates whether a genotype is specifically adapted to high-yielding or low-yielding environments or is stable.

63. (C) Reduced phenotypic variance around an intermediate optimal mean
Stabilizing selection is a type of natural selection that favors individuals with intermediate phenotypes while acting against extreme variants. Over many generations, this process tends to narrow the phenotypic distribution of the trait within the population. The result is a reduction in the total phenotypic variance, with the population mean remaining centered around the most favorable or optimal value for survival and reproduction.

64. (D) Recombination fraction between the two loci
The decay of linkage disequilibrium is a fundamental process in population genetics that occurs over time. The rate at which this association between alleles at different loci diminishes depends on the frequency of meiotic recombination. In the mathematical equation, the term representing the recombination fraction determines how much the disequilibrium is reduced in each generation, with higher recombination leading to faster decay.

65. (C) Likelihood of QTL presence vs the null hypothesis of no QTL
In quantitative trait loci mapping, the LOD score is a statistical measure used to evaluate the evidence for a linkage between a marker and a trait. It represents the logarithm of the odds ratio, comparing the likelihood that a QTL exists at a specific location to the likelihood of no QTL. A higher LOD score indicates stronger statistical support for the presence of the gene.

66. (B) Negative logarithm (base 10) of the association p-value
A Manhattan plot is a standard graphical representation used to visualize the results of genome-wide association studies. It displays the genomic location of each marker along the horizontal axis, while the vertical axis shows the significance of the association. By plotting the negative logarithm of the p-values, significant markers appear as tall peaks, making it easy to identify the associated regions.

67. (C) Select specifically for the target allele or gene of interest
Foreground selection is a key component of marker-assisted breeding that focuses on the direct inheritance of a specific trait. It involves using molecular markers that are either within or very closely linked to the target gene to identify individuals that carry the desired allele. This ensures that the essential trait is maintained through successive generations of backcrossing without relying solely on phenotyping.

68. (A) Captures small-effect QTLs without significance thresholds
Genomic selection represents a major advancement over traditional marker-assisted selection because of how it handles genetic information. While traditional methods focus on identifying a small number of significant QTLs, genomic selection uses all markers simultaneously to estimate genetic values. This allows it to capture the cumulative effects of many genes with small individual impacts, which is essential for complex quantitative traits.

69. (B) Disruptive gene function to observe phenotypic alteration
Gene knock-out is a powerful functional genomics technique used to validate the role of a candidate gene in controlling a trait. By specifically disrupting or disabling the gene of interest, researchers can observe the resulting changes in the organism's phenotype. If the trait is altered or lost, it provides direct evidence that the gene is necessary for the expression of that characteristic.

70. (A) $F_2 < RILs < IntermatedRILs (IRILs)$
An F2 population represents only one generation of recombination, while recombinant inbred lines undergo several generations of selfing, capturing more crossovers. Intermated RILs involve additional rounds of random mating before inbreeding, further increasing the recombination frequency and providing the highest mapping precision.

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71. (B) q
In species where males are hemizygous for sex-linked loci, they possess only one allele for genes located on the X chromosome. Consequently, the

distance from the marker. A marker may show a strong association because it is close to a small-effect QTL or further away from a large-effect QTL.

90. (A) P-IV, Q-III, R-I, S-II
Mapping populations vary in their genetic structure and are chosen based on the goals of the study. F2 populations are highly heterozygous and temporary, while recombinant inbred lines are immortalized homozygous lines developed through repeated selfing. Doubled haploids are also completely homozygous but produced rapidly via tissue culture. Near isogenic lines differ from a parent by only a small introgressed segment.

91. (A) Differences from subpopulations or geographical origins
Population structure is a common confounding factor in genome-wide association studies that can lead to spurious results. The Q-matrix is a statistical tool used to represent the underlying genetic structure derived from different subpopulations or geographical origins. By incorporating this matrix into the association model, researchers can account for these ancestral differences and ensure that identified associations are truly related to the trait.

92. (B) Perfect or functional marker
In marker-assisted selection, the most effective tool is a functional or perfect marker, which is derived directly from the causal DNA mutation itself. Unlike linked markers, which can be separated from the gene by recombination, a functional marker is always associated with the trait phenotype. This provides the highest level of accuracy in selecting for desired alleles across diverse genetic backgrounds and populations.

93. (C) Been both genotyped and rigorously phenotyped
A training population is a fundamental component of genomic selection models used to predict breeding values. It consists of a large set of individuals that have been thoroughly evaluated for both their genetic marker profiles and their phenotypic performance for target traits. The data from this population are used to estimate marker effects, which are then applied to select candidates in subsequent generations.

94. (A) Mapping to a genomic interval containing a trait QTL
The positional candidate gene approach is a strategy used to identify genes that control complex traits. It involves first locating a quantitative trait locus within a specific chromosomal interval through genetic mapping. Any gene located within this narrow region is considered a candidate. This evidence is then combined with functional information to pinpoint the most likely gene responsible for the observed phenotype.

95. (B) r^2
In a multiple allele system like the ABO blood groups, the genotype frequencies are determined by the proportions of each allele in the population. According to the Hardy-Weinberg principle, the frequency of the homozygous recessive phenotype is equal to the square of the recessive allele frequency. This mathematical relationship allows for the estimation of allele frequencies from the observed distribution of phenotypes.

96. (A) Retains existing genetic variability without divergence
Hardy-Weinberg equilibrium describes a stable state where allele and genotype frequencies remain constant across generations in the absence of evolutionary forces. One significant biological consequence of this equilibrium is that it preserves the existing genetic variation within a population indefinitely. This stability serves as a null model for studying how processes like selection, mutation, and migration drive evolutionary change and genetic divergence.

97. (A) The Wahlund effect
The Wahlund effect is a phenomenon observed when several subpopulations with different allele frequencies are treated as a single, combined population. Even if each subpopulation is in Hardy-Weinberg equilibrium, the overall population will show a deficiency of heterozygotes and an excess of homozygotes. This reduction in heterozygosity is a direct result of population subdivision and the mathematical properties of allele frequency distributions.

98. (A) Relative reproductive success or contribution to next generation
In evolutionary genetics, fitness is a measure of the relative ability of an individual or genotype to survive and reproduce. It is often quantified

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134. (C) Stabilizing selection
Canalization is an evolutionary process that results in a robust developmental pathway that produces a consistent phenotype despite various perturbations. This mechanism is primarily driven by stabilizing selection, which favors individuals that can maintain an optimal phenotype under a wide range of genetic and environmental conditions. Over time, this selection pressure leads to the development of biological systems that buffer against variation and ensure stability.

135. (A) $\frac{1}{1+4N_e c}$
In a finite population, the expected level of linkage disequilibrium between two loci is determined by a balance between genetic drift and recombination. Genetic drift tends to increase the association between alleles, while meiotic recombination works to break it down. The mathematical formula for the squared correlation coefficient provides an estimate of this equilibrium level based on the effective population size and the recombination rate.

136. (B) 1:2:1
An F2 mapping population is created by selfing the progeny of a cross between two genetically distinct parents. For a codominant molecular marker, where every genotype has a unique and detectable phenotype, the expected segregation ratio follows a standard Mendelian distribution. This results in a ratio of one homozygous parent type to two heterozygous types to one homozygous other parent type across the entire population.

137. (B) Population structure and cryptic relatedness
Genome-wide association studies are vulnerable to false positive results if the sample population is not genetically uniform. When individuals from different subpopulations are included, any allele that is more common in a group that also has a higher trait mean may appear associated by chance. Cryptic relatedness among individuals further complicates this, as shared ancestry can create spurious correlations that are not due to linkage.

138. (A) $1-\left(\frac{1}{2}\right)^{t+1}$
Backcrossing is a traditional breeding technique used to transfer a specific gene into an elite line. In each generation of backcrossing, the proportion of the genome derived from the donor parent is reduced by half. Consequently, the proportion of the recurrent parent's genome increases predictably. The mathematical formula provides the expected percentage of the recurrent parent's genetic material that is recovered after a specific number of generations.

139. (C) Estimated effects of all genome-wide markers without prior significance testing
Genomic selection is a modern approach that calculates breeding values by utilizing information from markers distributed across the entire genome. Unlike traditional methods that only consider markers passing a statistical significance threshold, genomic selection sums the estimated effects of every marker simultaneously. This comprehensive strategy captures the contribution of many genes with small individual effects, providing a more accurate prediction of the overall genetic merit.

140. (B) P-II, Q-I, R-IV, S-III
Functional genomics utilizes several techniques to validate the roles of candidate genes in controlling complex traits. RNA sequencing provides transcriptome-wide expression profiles, while CRISPR-Cas9 allows for targeted gene knock-outs to observe phenotypic changes. In situ hybridization is used to visualize where genes are expressed in tissues, and eQTL mapping links genetic markers directly to the regulation of transcript levels in the organism.

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141. (B) Hardy-Weinberg equilibrium
Estimating allele frequencies for complex loci from observed phenotypic data requires specific assumptions about the population structure. The most common requirement is that the population is in Hardy-Weinberg equilibrium, which means it is large, randomly mating, and not subject to evolutionary forces. This assumption allows for the direct mathematical relationship between the proportions of genotypes and alleles, which is essential for accurate genetic analysis.

142. (B) Intense inbreeding or self-fertilization
When a population exhibits a significant excess of homozygous individuals across multiple loci, it is a strong indicator of non-random mating. Processes such as intense inbreeding or regular self-fertilization cause relatives to mate more frequently than expected by chance, leading to a rapid increase in homozygosity. This shift in the

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in a common ancestor. This phenomenon occurs through the process of inbreeding, where relatives share segments of their genomes. Measuring the frequency of such alleles is the basis for calculating inbreeding coefficients and understanding the genetic structure of related individuals.

108. (A) The inbreeding coefficient (F)
Inbreeding depression often leads to a decline in the average performance of quantitative traits, particularly those related to fitness and vigor. Quantitative genetic models show that this reduction in the phenotypic mean is linearly related to the increase in the inbreeding coefficient. As the level of homozygosity for deleterious recessive alleles increases, the performance of the population typically decreases in a predictable manner.

109. (B) Structural DNA mutations induced by standard field temperatures
Genotype by environment interaction results from the differential response of genotypes to various external conditions. This can be caused by changes in gene expression, variations in metabolic pathways, or differing physiological thresholds across environments. However, standard field temperatures do not typically induce structural DNA mutations that would cause this interaction; rather, it is the expression of existing genetic diversity that drives the phenomenon.

110. (C) I, II and III
Stability analysis involves several statistical models used to interpret the performance of genotypes across multiple environments. The AMMI model uses principal component analysis for interactions, while GGE biplots provide a graphical view of both genotype and interaction effects. The Finlay-Wilkinson model uses regression on environmental indices, and the Eberhart and Russell model adds a measure of deviation from this linear response.

111. (D) Stabilizing selection
Stabilizing selection is a form of natural selection that acts to maintain the status quo by favoring intermediate phenotypes. It penalizes individuals with extreme characteristics at either end of the distribution, which helps to preserve the most successful and adapted phenotype for the current environment. Over time, this process leads to a reduction in phenotypic variance while keeping the population mean relatively constant.

112. (A) Standardizes LD against its maximum possible value
The parameter D prime is a valuable tool for measuring linkage disequilibrium because it provides a standardized value between zero and one. By dividing the raw disequilibrium value by its theoretical maximum, researchers can compare the degree of association between different sets of loci regardless of variations in their allele frequencies. This makes it a more consistent metric for evaluating historical recombination across the genome.

113. (A) The interval between two adjacent molecular markers
Interval mapping is a statistical technique used in quantitative trait loci analysis to locate genes more precisely than single marker methods. It systematically evaluates the likelihood of a QTL being present at any point within the interval between two neighboring molecular markers. By considering the recombination frequencies between these markers, it provides a more accurate estimate of both the QTL's position and its effect.

114. (A) Familial relatedness or cryptic relationships
In genome-wide association studies, the presence of familial relatedness among individuals can lead to inaccurate results and false positive associations. To correct for this, mixed linear models incorporate a kinship matrix, or K-matrix, which defines the degree of genetic similarity between all pairs of individuals. This adjustment ensures that the identified associations are truly due to linkage with the trait rather than background relatedness.

115. (A) Double crossover events tightly flanking the introgressed target gene
To efficiently implement marker-assisted backcrossing, breeders must identify individuals that have the smallest possible segment of donor DNA surrounding the target gene. This is achieved by selecting for double crossover events that occur on both sides of the locus in the early generations. This strategy minimizes the negative effects of linkage drag, allowing for the rapid recovery of the recurrent parent genome.

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phenotype, such as a disease state, making them a unique type of quantitative trait.

152. (C) Genetic correlation
Predicting the correlated response to selection in one trait depends on the genetic relationship it shares with the trait being selected. This relationship is quantified by the genetic correlation, which measures the extent to which the same genes influence both traits. By understanding this association, along with the heritabilities, breeders can estimate how much the second trait will change as a result of selection.

153. (B) $\left(\frac{1}{2}\right)^{n+1}(1+F_A)$
The inbreeding coefficient of an individual is calculated by evaluating the shared ancestry of its parents in a pedigree. Each path through a common ancestor adds to the probability that alleles are identical by descent. The contribution to the total coefficient depends on the number of generations in the path and whether the common ancestor was itself inbred, reflecting the accumulation of relatedness.

154. (B) Heterozygotes are produced relative to the base population
The panmictic index is a measure of the genetic diversity and heterozygosity remaining in a population compared to a reference base population. It represents the probability that two alleles at a locus are not identical by descent, meaning they have different origins. This index is closely related to the inbreeding coefficient and is used to track the loss of genetic variation over successive generations.

155. (B) Joint regression analysis like Finlay-Wilkinson
Linear genotype by environment interactions occur when the performance of different varieties changes in a predictable way across an environmental gradient. This phenomenon can be modeled using joint regression analysis, where the yield of each genotype is regressed on the average environmental quality. This approach allows breeders to identify genotypes with stable performance or those that respond strongly to favorable growing conditions.

156. (B) Unpredictable and highly non-linear
In the Eberhart and Russell model for stability analysis, the deviation from regression is an important indicator of a genotype's reliability. A large value for this parameter suggests that the genotype's response to environmental changes is not linear and therefore difficult to predict. Genotypes with high deviations are considered less stable because their performance fluctuates in a manner that the regression model cannot explain.

157. (B) A plateau from exhaustion of additive variance
Directional selection is used to change the mean of a population, but this progress eventually slows down and stops. This result, known as a selection plateau, occurs when the additive genetic variance for the trait has been completely used up. At this point, the population has become genetically uniform for the selected trait, and no further gain can be made without new variation.

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158. (B) Distance, recombination, and effective population size
Linkage disequilibrium within a population is influenced by several factors that determine how alleles at different loci are associated. The physical distance between the loci and the rate of meiotic recombination are key drivers of the decay of this association over time. Additionally, the effective population size plays a role, as smaller populations tend to maintain higher levels of disequilibrium due to genetic drift.

159. (B) 1:1 ratio, simplifying the estimation of recombination frequencies
Backcross populations are a valuable resource for genetic mapping because of their simple and predictable segregation patterns. In a backcross between a hybrid and a homozygous parent, the alleles at a single locus segregate in a one-to-one ratio. This balanced distribution makes it much easier for researchers to estimate the recombination frequencies between markers and accurately determine their physical positions on the chromosome.

160. (B) P-IV, Q-I, R-II, S-III
Different statistical models provide unique metrics for evaluating the stability and adaptation of genotypes in multi-environment trials. The Finlay-Wilkinson model uses regression coefficients, while the Eberhart and Russell model adds a deviation parameter. AMMI analysis uses principal components to interpret complex interaction patterns, and

125. (A) Increase
The predicted response to selection, or genetic advance, is directly influenced by the accuracy of the selection process. Higher accuracy means that the estimated breeding values are more closely correlated with the true genetic merit of the individuals. Therefore, any improvement in the methods used to evaluate breeding values will lead to an increase in the expected genetic gain for the next generation.

126. (A) Multi-trait index and aggregate breeding value
The selection index developed by Smith and Hazel is a sophisticated tool for improving multiple traits simultaneously. It functions by creating a single value for each individual that represents its overall genetic merit for the breeding goal. The index is mathematically optimized to maximize the correlation between the calculated index value and the true aggregate breeding value, leading to the most efficient selection progress.

127. (B) Heritability is low and common environmental effects are negligible
Family selection is most beneficial for improving traits that have low heritability and where individual performance is heavily influenced by random environmental noise. By selecting whole families based on their average performance, breeders can reduce this noise and obtain a more accurate estimate of the underlying genetic merit. This method is particularly effective when there are no significant shared environmental effects that would bias the family means.

128. (B) Shifted to a lower value (closer to the mean)
In the threshold model for disease resistance, the incidence of a trait in the population is determined by the position of the threshold on the liability scale. If the environment becomes more challenging, leading to an increase in the number of affected individuals, the threshold effectively shifts closer to the population mean. This change reflects the increased susceptibility of the population under the new conditions.

129. (B) Population admixture or epistasis
Linkage disequilibrium can occur even between genes that are located on different chromosomes or are far apart on the same chromosome. One major cause of this association is population admixture, where the mixing of two distinct populations creates new combinations of alleles. Additionally, epistatic interactions that favor specific combinations of alleles can also maintain linkage disequilibrium through the process of natural or artificial selection.

130. (A) Both A and R are true and R is the correct explanation of A.
Self-fertilization and full-sib mating are both forms of inbreeding, but they lead to homozygosity at very different rates. Self-fertilization is much faster because it reduces the proportion of heterozygotes by fifty percent in every generation. In contrast, full-sib mating is less intense, and the reduction in heterozygosity is approximately nineteen percent per generation, requiring many more generations to reach the same level.

131. (B) Have high dominance variance and are related to fitness
Inbreeding depression is most frequently observed in traits that are closely related to the biological fitness and survival of an organism. These traits often have a significant amount of dominance variance, where the expression of the phenotype is influenced by interactions between alleles at a locus. As inbreeding increases homozygosity, the loss of these heterozygous advantages leads to a significant decline in overall performance.

132. (B) Adapted to poor environments with stress resistance
In the Finlay-Wilkinson method of stability analysis, the regression coefficient measures how a genotype responds to environmental quality. A genotype with a coefficient significantly less than one is less responsive to environmental changes, meaning it maintains relatively consistent performance across a range of conditions. This characteristic often indicates that the variety is specifically adapted to poor or stressful environments where it can still yield reliably.

133. (B) Principal Component axes (IPCA)
The additive main effects and multiplicative interaction model is used to analyze the results of multi-environment trials in breeding programs. This model first fits the main effects of genotypes and environments using standard ANOVA techniques. The remaining variation, which represents the complex interaction between the two, is then partitioned into several principal component axes. This allows breeders to identify and visualize patterns of adaptation.

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another. Identifying these patterns is essential for breeders to develop varieties that are either broadly adapted or specifically suited to certain target growing areas.

170. (A) I and II
Different methods for estimating herizability rely on the degree of resemblance between various types of relatives. Parent-offspring regression is generally preferred because it provides a relatively unbiased estimate of narrow-sense herizability. In contrast, full-sib correlations can be influenced by shared dominance effects and common environmental factors that are present within a family, which often leads to an overestimation of the true genetic inheritance.

171. (B) Selection intensity (i)
In the breeder's equation, the selection differential is a measure of the selection pressure applied to a trait. It is mathematically related to the selection intensity, which is the differential expressed in units of phenotypic standard deviation. This relationship allows breeders to predict the genetic advance by combining the intensity of selection with the heritability and the existing phenotypic variation in the breeding population.

172. (B) Superior traits cannot compensate for deficient ones
Independent culling levels is a straightforward method for multi-trait selection, but it has a major logical limitation. Because every trait is judged against a fixed minimum standard, an individual that is truly exceptional in one trait will still be discarded if it falls slightly below the threshold for another. This lack of compensation can be inefficient compared to index selection, which balances all traits together.

173. (A) Increase generation interval, reducing annual gain
Progeny testing is a highly accurate method for evaluating the breeding value of a parent, but it has significant practical drawbacks. The main limitation is the time required for offspring to grow and be evaluated, which significantly increases the length of the generation interval. Even though the selection is more accurate, the slow turnaround can reduce the overall rate of genetic progress achieved per year.

174. (B) Combined genetic and environmental values
The threshold model for categorical traits assumes that there is an underlying continuous scale called liability. This scale represents the combined influence of all genetic factors and environmental effects that contribute to the expression of the trait. The population follows a normal distribution on this scale, and individuals only express the discrete phenotype if their total liability exceeds a specific point, known as the threshold.

175. (B) Lead to progressive decay as recombination breaks linkage
Linkage disequilibrium can create a temporary genetic association between traits that are controlled by genes located close to each other on a chromosome. However, this correlation is not permanent because meiotic recombination will gradually separate these alleles over successive generations of random mating. As the linkage is broken, the disequilibrium decays, and the traits will eventually appear to be inherited independently of one another.

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176. (B) Increased expression of deleterious recessive alleles
Inbreeding depression is the decline in performance and fitness observed when related individuals are mated. The primary genetic cause of this phenomenon is the increase in homozygosity, which unmasks harmful recessive alleles that were previously hidden in heterozygous individuals. As these deleterious genes are expressed more frequently, the overall health and vigor of the population decrease, particularly for complex traits related to survival.

177. (B) Overdominance hypothesis
The overdominance hypothesis is a key theory used to explain the biological basis of heterosis, or hybrid vigor. It proposes that the heterozygous genotype is fundamentally superior in performance or fitness to either of the homozygous genotypes. This advantage is thought to arise from unique physiological or biochemical processes that occur only when two different alleles are present at a locus, leading to improved growth.

178. (B) Cause rank changes where best genotype in one environment is inferior in others
Non-linear genotype by environment interactions are a major challenge for plant and animal

genetic distribution can have significant impacts on the fitness and evolutionary potential of the breeding population.

143. (A) $\sqrt{\frac{u}{s}}$
A genetic equilibrium is reached when the introduction of new deleterious recessive alleles through mutation is balanced by their removal through natural selection. The frequency of the allele at this point depends on the mutation rate and the selection coefficient. For a recessive allele, the equilibrium frequency is equal to the square root of the mutation rate divided by the strength of the selection pressure.

144. (B) 0.50
The selection coefficient measures the proportional reduction in the fitness of a specific genotype compared to the most fit genotype in the population. It is calculated by subtracting the relative fitness of the genotype from one. In this scenario, the fitness of the homozygous recessive genotype is half that of the most successful genotype, resulting in a selection coefficient of point five.

145. (B) 36
The effective population size is influenced by the number of breeding males and females in the group. When the sex ratio is unequal, the rate of genetic drift increases, and the effective size is smaller than the total census size. The specific formula calculates this value based on the contributions of each sex, showing how the genetic diversity is restricted in such skewed populations.

146. (B) Variance of breeding values, the transmissible portion
Additive genetic variance is a critical component of the total phenotypic variation in quantitative genetics. It represents the variance of the breeding values and is the only portion of the genetic variation that is directly transmissible from parents to their offspring. Because it determines the response to selection, understanding this variance is essential for breeders trying to improve traits in their populations.

147. (A) Environmental variance (V_E) and non-additive genetic variances approach zero
Narrow-sense heritability is defined as the proportion of the total phenotypic variation that is due to additive genetic effects. Therefore, the value of heritability is maximized when all other sources of variation are minimized. When environmental noise and non-additive genetic effects such as dominance are near zero, the phenotype becomes an almost perfect indicator of the individual's additive genetic merit for that trait.

148. (A) Intensity and interval, as accuracy needs time
Maximizing the annual rate of genetic progress requires a careful balance of several factors in a breeding program. Increasing the intensity of selection and the accuracy of evaluation both help to boost gain, but they often require more time, which increases the generation interval. Therefore, breeders must optimize these parameters together to ensure the highest possible rate of improvement over a given period.

149. (B) A strong negative genetic correlation
Index selection is generally more efficient than tandem selection when multiple traits are being improved at the same time. This advantage is most pronounced when there is a strong negative genetic correlation between the traits, meaning that improving one trait tends to make the other worse. The selection index uses the genetic relationships to balance these opposing effects and achieve the best overall progress.

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150. (A) Both A and R are true and R is the correct explanation of A.
Progeny testing is a powerful breeding tool because it provides a more accurate estimate of a parent's breeding value than its own phenotype alone. By averaging the performance of a large number of offspring, the random environmental variations that affect individuals are reduced. This allows the breeder to more clearly see the additive genetic contribution of the parent, significantly increasing the accuracy of the selection.

151. (A) Polygenic inheritance with underlying liability scale
Threshold traits appear as discrete categories but are actually controlled by many different genes and environmental factors. They are characterized by an underlying, continuous liability scale that represents the total susceptibility to expressing the trait. Only when an individual's liability exceeds a specific threshold do they show the

116. (B) Training population
Genomic selection relies on the use of a training population to build a predictive model for breeding values. This population consists of individuals that have been both genotyped and phenotyped for the traits of interest. The statistical algorithm estimates the effects of all marker loci based on this data, which are then used to calculate breeding values for selection candidates that have only been genotyped.

117. (A) Differences in mRNA transcript abundance
Expression quantitative trait loci mapping is based on the premise that genetic variation in a trait can be caused by changes in gene regulation. It identifies genomic regions that control the amount of mRNA produced by a gene, which is often a key driver of phenotypic variation. By linking these regulatory variants to transcript abundance, researchers can gain a deeper understanding of the molecular basis of complex traits.

118. (A) $2pq$
In species with XX females, the inheritance of sex-linked loci follows the same rules as autosomal loci for the female population. Under the assumptions of the Hardy-Weinberg equilibrium, the proportion of heterozygous carriers is calculated as two times the product of the allele frequencies. This reflects the randomly mating nature of the group and allows for the prediction of carrier frequencies in the females.

119. (B) Violation of assumptions like selection or migration
When a population shows a statistically significant deviation from the Hardy-Weinberg equilibrium, it implies that one or more of the fundamental assumptions have been violated. This could be due to factors such as natural selection, migration, non-random mating, or the effects of genetic drift in a small population. Such deviations are important for identifying the evolutionary forces that are actively shaping the gene pool.

120. (A) II
The effective population size is a critical parameter that determines the rate of genetic change and loss of diversity in a population. Several factors, such as high variance in reproductive success or fluctuating population sizes, can reduce the effective size relative to the total number of individuals. However, a balanced sex ratio actually helps to maximize the effective population size rather than minimizing it.

121. (A) $q_t = \dfrac{q_0}{1 + tq_0}$
Selection against a recessive lethal allele is a process where homozygous recessive individuals fail to reproduce entirely. The change in the allele frequency over successive generations can be modeled mathematically. This specific formula shows that the frequency of the recessive allele decreases slowly as it becomes rarer, because a larger proportion of the surviving alleles are hidden in phenotypically normal heterozygous individuals.

122. (A) Loss of rare alleles and reduced genetic variance
A population bottleneck represents a severe reduction in the number of individuals, which has profound genetic consequences. During this event, many rare alleles are permanently lost from the gene pool simply due to chance, leading to a significant decrease in the overall genetic variance. This reduction in diversity can limit the population's ability to adapt to future environmental changes and increases the risk of inbreeding.

123. (B) Macroscopic, microscopic, and maternal effects
Environmental variance is a major component of the total phenotypic variation for quantitative traits. It includes a wide range of factors, such as large-scale differences in climate or management, as well as small-scale variations in soil or individual care. Additionally, maternal effects that influence the development of offspring are also considered part of this environmental component, as they are non-genetic from the offspring's perspective.

124. (B) Total genetic variance to phenotypic variance
Broad-sense heritability is a measure of the proportion of the total phenotypic variation in a trait that is attributable to genetic differences among individuals. It is calculated by dividing the total genetic variance, which includes additive, dominance, and epistatic effects, by the total phenotypic variance. This parameter provides an overall indication of the degree of genetic control over the trait in a specific population.

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GGE biplots provide a graphical polygon view to identify the best genotypes for specific target mega-environments.

161. (B) Recombinant selection
Recombinant selection is a specialized technique in marker-assisted breeding aimed at refining the genetic region around an introgressed gene. The goal is to identify individuals that have experienced a crossover event very close to the target locus. By selecting for these recombinations, breeders can minimize the amount of donor DNA that remains in the new variety, effectively reducing the impact of linkage drag.

162. (B) Pyramid multiple minor- and major-effect QTLs
Marker-assisted recurrent selection is a sophisticated breeding strategy designed to improve complex quantitative traits by accumulating favorable alleles from different sources. Unlike backcrossing, which focuses on a single gene, this method aims to combine multiple quantitative trait loci into a single line. By intermating selected individuals across several cycles, breeders can pyramid many small-effect genes to achieve a significant overall improvement in performance.

163. (A) Demonstrate if the gene is necessary for the phenotype
Gene knock-outs are considered the definitive method for validating the function of a candidate gene in controlling a trait. By specifically disabling the gene, researchers can directly observe if the corresponding phenotypic trait is lost or significantly altered. This provide clear evidence of a causal relationship between the gene and the trait, which is more rigorous than simple statistical association mapping results.

164. (B) Each genotype has a distinct phenotype
Codominant molecular markers are highly useful in genetic studies because they allow for the direct identification of every individual's genotype. In such systems, the heterozygous individuals have a phenotype that is distinct from both homozygous parents. This transparency means that genotypic frequencies can be determined simply by counting individuals, which simplifies the process of checking for Hardy-Weinberg equilibrium and estimating allele frequencies.

165. (A) Decrease in heterozygotes and increase in homozygotes
Assortative mating is a non-random mating pattern where individuals choose partners that have similar phenotypes to their own. This process has a significant impact on the genetic structure of a population by increasing the frequency of homozygous genotypes across generations. While it does not change the overall allele frequencies, it leads to a systematic reduction in the proportion of heterozygous individuals in the group.

166. (C) 0.0
Recurrent mutation is an evolutionary force that can eventually drive a specific allele to extinction if there is no counter-acting pressure. If an allele mutations at a constant rate into a different form without any backward mutation, its frequency will slowly decline in every generation. Over an immense number of generations, this process will result in the allele being completely replaced by the new version.

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167. (B) Selection against heterozygotes (underdominance)
Underdominance occurs when the heterozygous genotype has a lower fitness than either of the homozygous genotypes. This type of selection pressure creates an unstable equilibrium where the allele frequency will tend to move towards either zero or one depending on its initial value. Any slight deviation from the equilibrium point will cause the population to rapidly lose one of the alleles, reducing genetic diversity.

168. (A) $N_e = \frac{4N-2}{V_k+2}$
The effective population size is a theoretical measure that describes the rate of genetic drift in a population. It is often much smaller than the actual number of individuals, particularly when there is significant variation in reproductive success among parents. When family sizes are not equal, the genetic contribution to the next generation is uneven, which reduces the effective size and accelerates the loss of variation.

169. (B) Genotype differences vary across environments
Genotype by environment interaction is a statistical term used to describe when different varieties do not perform consistently across a range of conditions. This interaction is present whenever the phenotypic difference between two genotypes changes from one environment to

as the proportional contribution of a specific genotype to the next generation's gene pool compared to other genotypes. High fitness indicates greater reproductive success, which is the primary driver of natural selection and changes in allele frequencies over time.

99. (B) Random and unpredictable in magnitude and direction
Genetic drift is an evolutionary force that causes random fluctuations in allele frequencies due to chance events in finite populations. Unlike selection, which is deterministic and directional, drift is unpredictable in both its magnitude and the direction of the change. It is considered a dispersive force because it causes identical populations to diverge from one another and eventually leads to the loss of alleles.

100. (A) I and III
Quantitative genetics provides a framework for understanding the inheritance of complex traits through the partitioning of variance. Total phenotypic variance is the sum of various genetic and environmental components, including additive and dominance effects. Additive variance is particularly important because it determines the degree of resemblance between parents and their offspring, which is the basis for the response to artificial selection.

101. (B) One quarter of the additive genetic variance
In quantitative genetic analysis using a nested mating design, the variance observed between different sires is used to estimate heritability. This component represent one-quarter of the total additive genetic variance because each sire contributes only half of the genetic material to its offspring. This method allows researchers to isolate the genetic contribution of the male parents while minimizing the influence of maternal effects.

102. (B) 5.8 kg
The response to selection is calculated by multiplying the selection differential by the narrow-sense heritability of the trait. In this example, the difference between the selected breeders and the population mean is two kilograms. Multiplying this by the heritability of point four gives a predicted genetic gain of point eight kilograms, which is then added to the original population mean value.

103. (A) Decrease in narrow-sense heritability and increased inbreeding
Applying intense selection pressure in a small, closed population can lead to several long-term genetic risks. As fewer individuals are chosen for breeding, the level of inbreeding inevitably increases, which can reduce the overall fitness and performance of the herd. Furthermore, consistent selection for the same alleles will eventually exhaust the additive genetic variance, leading to a decline in heritability and genetic gain.

104. (D) Narrow-sense heritability is high ($h^2 > 0.5$)
Mass selection, where individuals are chosen based solely on their own phenotypic performance, is most effective for traits that are highly heritable. When a large portion of the phenotypic variation is due to additive genetic effects, the individual's appearance is a reliable indicator of its breeding value. In such cases, mass selection is simpler and more efficient than more complex family-based selection methods.

105. (A) An unobservable, underlying latent variable
The inheritance of threshold traits is modeled using the concept of liability, which represents the combined influence of all genetic and environmental factors affecting the trait. This liability is an unobservable latent variable that follows a continuous normal distribution. While we can see the resulting discrete phenotypes, the actual values of liability for specific individuals cannot be measured directly, requiring statistical conversion for analysis.

106. (B) Linear and mediated by additive genetic covariance
The mathematical prediction of how selecting for one trait affects another depends on the genetic relationship between them. This model assumes that the two traits are linearly related through their shared additive genetic covariance. By understanding this relationship, breeders can calculate the expected correlated response, which is essential when traits are difficult to measure or are genetically linked to other important characteristics.

107. (A) Exact copies of a single ancestral allele due to inbreeding
Two alleles at a locus are considered identical by descent if they are both exact physical copies derived from the same DNA molecule

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breeders. These interactions often lead to rank changes, meaning that a variety that performs exceptionally well in a high-yielding environment might be very poor under stress. This inconsistency makes it difficult to select a single variety that is universally superior, often requiring the development of specialized lines for different regions.

179. (A) Adapted to high-yielding, favorable environments
In stability analysis models, the regression coefficient describes how a variety responds to changes in environmental quality. A genotype with a coefficient significantly greater than one is considered to be highly responsive. This means its performance improves much more rapidly than average as the environment gets better, indicating that it is specifically adapted to high-yielding and favorable conditions where it can maximize its potential.

180. (B) I and II
Natural selection acts on the phenotypic distribution of quantitative traits in different ways. Disruptive selection favors extreme phenotypes and increases the overall variance within the population. In contrast, directional selection shifts the population mean towards one extreme and, over time, reduces the amount of additive genetic variance available. Both processes are essential for the evolutionary adaptation of species to their changing environments.

181. (A) At least one of four gametic haplotypes is absent
Linkage disequilibrium measures the non-random association between alleles at different loci. When the standardized measure D prime reaches its maximum value of one, it indicates a complete association between specific alleles. Biologically, this means that some of the possible combinations of alleles are entirely missing from the population. This pattern is common in recently formed populations or those where recombination has not yet occurred.

182. (A) Homozygous lines ensuring stable phenotyping
Doubled haploid lines are an important tool in genetic research because they are completely homozygous and true breeding. This genetic uniformity means that every individual in a line is identical, allowing for highly stable and repeatable phenotyping across multiple locations and seasons. This consistency provides a significant statistical advantage over other mapping populations, such as F2 groups, which are genetically segregating and temporary.

183. (B) Show significant statistical association with trait
A Manhattan plot is a graphical representation of the results from a genome-wide association study. It displays the significance of the association between each genetic marker and the trait being studied across the entire genome. Researchers look for tall clusters of points, which represent markers with very small p-values. These peaks identify the specific chromosomal regions that are likely to contain genes.

184. (C) Background selection
In marker-assisted backcrossing, background selection is the most intensive phase in terms of marker usage. The goal is to screen the entire genome of the offspring to identify those that carry the highest percentage of the recurrent parent's DNA. This requires a large number of markers that are evenly distributed across all chromosomes to accurately track the inheritance of the genetic background and speed up variety development.

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185. (B) Manage high dimensionality where markers exceed samples
Genomic selection models often face a statistical challenge where the number of genetic markers is much larger than the number of individuals in the training population. To solve this problem, these models use specialized algorithms that penalize marker effects, preventing the model from becoming over-fitted to the data. This ensures that the predicted breeding values are accurate and can be reliably used to select.

186. (B) Transcriptomics, proteomics, or metabolic pathways
Identifying functional candidate genes requires a multidisciplinary approach that goes beyond simple genetic mapping. Researchers combine location information with data from transcriptomics, which measures gene expression, and proteomics, which looks at proteins. By understanding the metabolic pathways and biological processes involved, they can identify the most likely genes that control the trait,

from the source population, shaping the future evolution.

240. (A) Same-locus alleles deviating from homozygote midpoint
Dominance variance is a component of the total genetic variance that arises from interactions between different alleles at a single locus. It is measured as the extent to which the performance of the heterozygote deviates from the average of the two homozygous genotypes. While important for understanding heterosis and inbreeding depression, dominance variance is not directly transmissible and does not contribute to the response to selection.

241. (A) Narrow-sense heritability (h^2)
Broad-sense herizability is the proportion of the total phenotypic variation that is due to all genetic factors, including additive, dominance, and epistatic effects. Because narrow-sense heritability only considers the additive portion of this genetic variance, it must always be less than or equal to the broad-sense value. Therefore, broad-sense heritability sets the upper possible limit for the transmissible inheritance of a trait.

242. (A) 0 and 1
The accuracy of selection is a critical metric in breeding programs that measures the correlation between the estimated breeding value and the true genetic merit of an individual. As a correlation coefficient, its value is mathematically bounded between zero and one. An accuracy of zero means the selection is no better than chance, while an accuracy of one indicates perfect prediction of the genetic potential.

243. (A) Traits have varying economic weights and compensatory genetic correlations
Index selection is generally the most effective multi-trait selection method because it can handle complex relationships between traits. Its advantage over other methods like independent culling is most significant when traits have different economic values and share genetic correlations. The index allows a superior performance in one trait to compensate for a minor deficiency in another, leading to more efficient overall genetic progress.

244. (A) Reducing environmental variance common to families
Within-family selection is a breeding method where candidates are selected based on their performance relative to their own siblings. This approach is particularly useful when families are raised in different environments that might cause significant variation between them. By focusing on the best individuals within each family, the breeder can eliminate the confounding effects of shared environmental factors, leading to a more accurate selection.

245. (A) Standard normal distribution with mean 0 and variance 1
The threshold model for discrete traits assumes that there is an underlying continuous variable called liability. In quantitative genetics, this liability is typically modeled using a standard normal distribution that has a mean of zero and a variance of one. This mathematical assumption allows researchers to apply standard statistical tools to calculate heritability and predict how many individuals will exceed the threshold for the trait.

246. (A) Traits share a strong negative genetic correlation
A correlated response to selection occurs when selecting for one trait leads to a change in another trait due to genetic linkage or pleiotropy. The direction of this change is determined by the nature of the relationship between the traits. If two traits share a strong negative genetic correlation, then increasing the value of one will predictably lead to a decrease in the other.

247. (A) Probability alleles are copies of same ancestor
Wright's inbreeding coefficient is a measure of the level of relatedness and homozygosity in an individual. It specifically calculates the probability that both alleles at a single locus are identical by descent. This means that the alleles are exact physical copies derived from a single gene in a common ancestor. This coefficient is essential for tracking the accumulation of inbreeding within a breeding population.

248. (A) Heterozygotes decreases, exposing recessive alleles
Inbreeding depression is a decline in performance and vigor that occurs as individuals become more closely related. According to the dominance hypothesis, this happens because the frequency of

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and covariances of the traits being selected. Additionally, the index accounts for the relative economic importance of each trait, ensuring that the selection process leads to the greatest overall increase in value.

196. (A) 1.0
Progeny testing is a method used to estimate the true breeding value of a parent by observing the performance of its offspring. As the number of progeny being evaluated increases, the average of their phenotypic values becomes an increasingly accurate representation of the parent's genetic merit. In a theoretical sense, with a large enough sample of offspring, the accuracy of the estimated breeding value will eventually approach perfection.

197. (A) Correct for incidence, making estimates comparable
Categorical traits that appear in discrete classes are often analyzed using the threshold model, which assumes an underlying continuous liability scale. Converting heritability from the observed binary scale to this normal scale is essential because the observed values are influenced by the trait's incidence. This conversion standardizes the results, allowing researchers to compare genetic parameters across different populations and environments that may have varying frequencies.

198. (A) Genetic correlation and additive variances of both traits
The genetic covariance between two traits is a measure of the extent to which they are influenced by the same genes. This value is essential for predicting the correlated response to selection and can be calculated by combining the genetic correlation with the additive genetic variances of both traits. This information helps breeders understand how selecting for one characteristic will indirectly lead to genetic changes.

199. (C) 0.0
Wright's inbreeding coefficient measures the degree of relatedness in a population by calculating the probability that alleles are identical by descent. In a theoretical base population where individuals are assumed to be unrelated and mating randomly, the average value of this coefficient is zero. This provides a starting point for tracking how inbreeding accumulates over time as the population becomes more closely related.

200. (A) Both A and R are true and R is the correct explanation of A.
Inbreeding depression is a phenomenon where the performance of a population declines as the level of inbreeding increases. This effect is primarily caused by the expression of deleterious recessive alleles in homozygous individuals. For traits that are controlled by additive gene action, there are no dominance effects to be unmasked, and therefore the average performance of the population remains relatively constant despite the change.

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201. (A) Dominance hypothesis
The dominance hypothesis is a leading theory used to explain the biological basis of heterosis, or hybrid vigor. It proposes that the superior performance of hybrids results from the accumulation of favorable dominant alleles from both parents. By crossing two inbred lines, the harmful recessive alleles that became fixed in each line are masked by the functional dominant alleles from the other, leading to improved performance.

202. (A) Measure of interaction; if r_G is near 1, interaction is low
The genetic correlation of performance across different environments is a critical parameter for evaluating genotype by environment interaction. If the correlation is close to one, it indicates that the same genes control the trait in all locations and the relative rankings of genotypes are consistent. A lower correlation suggests that genotypes respond differently to various environments, which signifies a more significant and complex interaction.

203. (A) Best genotypes in specific mega-environments
A GGE biplot is a graphical tool used in plant and animal breeding to analyze the results of multi-environment trials. The "which-won-where" pattern is a specific view of the biplot that divides the testing area into different mega-environments. It allows breeders to identify the specific genotypes that are most productive and best suited for each region, helping in the development of specialized varieties.

222. (A) Incidence of trait classes in population
The threshold model for categorical traits assumes an underlying continuous liability scale that follows a normal distribution. The exact location of the threshold on this scale is determined by the proportion of individuals in the population that express the trait. This incidence value is used to calculate the threshold's position, which is essential for estimating the genetic parameters and heritability of the discrete trait.

223. (A) High genetic correlation and $h^2(X) > h^2(Y)$
Indirect selection involves improving one trait by selecting for another that is genetically linked to it. This strategy can be more efficient than direct selection if the two traits share a high genetic correlation and the secondary trait has a higher heritability. In such cases, the selection on the secondary trait leads to a larger genetic gain in the primary trait of interest.

224. (B) $P_t = P_{t-1}\left[1 - \frac{1}{2N}\right]$
The panmictic index measures the relative heterozygosity in a population compared to a base population. In a finite population, random mating will lead to a predictable decrease in heterozygosity over time due to genetic drift. The mathematical formula shows that the panmictic index in any generation is a function of the index in the previous generation and the size of the breeding population.

225. (A) Increase in inbreeding coefficient
Inbreeding depression results in a decline in the average phenotypic performance of a population for traits related to fitness and vigor. Quantitative genetic theory shows that this reduction is directly and linearly proportional to the increase in the inbreeding coefficient. As relatives mate and homozygosity increases across the genome, the accumulation of deleterious recessive effects leads to a predictable decrease in overall performance.

226. (A) Joint regression like Finlay-Wilkinson
Linear genotype by environment interactions occur when the performance of different varieties changes in a predictable way across environments. These patterns are commonly analyzed using joint regression techniques, which relate the yield of each genotype to an environmental index. This approach allows breeders to characterize varieties based on their stability or their ability to respond to favorable conditions, helping in the selection of widely adapted varieties.

227. (A) Interaction residuals after fitting main effects
The additive main effects and multiplicative interaction model is a powerful tool for analyzing multi-environment trials. It first accounts for the main effects of genotypes and environments through an initial analysis. The remaining variation, consisting of the interaction residuals, is then analyzed using principal components. This decomposition allows researchers to identify the most significant interaction patterns and understand how specific genotypes adapt to different environments.

228. (A) Exhaustion of additive genetic variance
Directional selection is used to change the mean of a trait, but this progress cannot continue indefinitely. Eventually, the population reaches a selection limit or plateau where no further genetic gain is achieved. This typically occurs because the additive genetic variance for the trait has been completely used up, meaning all individuals are genetically similar for the selected alleles and no further progress is possible.

229. (A) $P_{\{AB\}} - p_A p_B$
Linkage disequilibrium measures the non-random association of alleles at different genomic locations. It is quantified as the difference between the observed frequency of a specific pair of alleles occurring together and the frequency expected by chance. This value, represented by the parameter D, provides important information about the historical recombination and genetic structure within a population, which is essential for association mapping.

230. (B) I, II, III
Developing different types of mapping populations requires varying amounts of time and labor. An F2 population is the fastest to create, needing only two generations from the initial cross. Recombinant inbred lines require many more generations of selfing to reach homozygosity. Near isogenic lines are the most time-consuming to develop, as they involve multiple cycles of backcrossing to create genetically similar lines for comparison.

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migration. Under these ideal conditions, allele and genotype frequencies remain constant across generations.

213. (A) $m(q_m - q)$
Migration is an evolutionary force that can change the genetic makeup of a local population by introducing alleles from an external source. The shift in allele frequency in a single generation depends on the rate of migration and the difference in frequencies between the two groups. This change is calculated as the product of these factors, representing the direct impact of gene flow on diversity.

214. (A) $\frac{u}{s}$
A deleterious dominant allele is one that reduces the fitness of an individual even in a single copy. In a population, an equilibrium frequency is reached when the introduction of new alleles by mutation is balanced by their removal through natural selection. For a dominant allele, this frequency is equal to the mutation rate divided by the strength of the selection pressure against it.

215. (C) 0.25
The selection coefficient measures the proportional reduction in the reproductive success of a specific genotype compared to the most successful one. It is calculated by subtracting the relative fitness of the genotype from one. In this example, the genotype's relative fitness is point seventy-five of the maximum possible, resulting in a selection coefficient of point twenty-five, which represents the selective pressure.

216. (A) Small fraction of individuals contributing gametes
The effective population size is a measure of the rate of genetic drift and loss of diversity in a breeding group. It is often much smaller than the actual number of individuals, especially when only a small portion of the population successfully reproduces. This restricted contribution limits the amount of genetic material passed to the next generation, accelerating the accumulation of inbreeding and random changes.

217. (A) Genetic variance and experimental error
In a controlled and uniform environment, the phenotypic variation observed for a quantitative trait consists of two main components. The first is the genetic variance, which arises from the differences in the genetic makeup of the individuals. The second is the experimental error or residual variance, which includes small-scale environmental fluctuations and measurement errors. Together, these factors determine the total phenotypic diversity in the trial.

218. (A) Excludes non-additive genetic variances
Narrow-sense heritability is a more specific measure than broad-sense heritability in quantitative genetics. While broad-sense heritability accounts for all genetic influences, including dominance and epistasis, narrow-sense heritability focuses only on the additive genetic variance. This is the portion of variance that is directly passed from parents to offspring, making it the primary factor determining the response to selection in breeding programs.

219. (A) Narrow-sense heritability is zero
The breeder's equation is used to predict the genetic advance or improvement resulting from a selection cycle. One critical component of this equation is narrow-sense heritability. If heritability is zero, it means that none of the phenotypic variation observed is due to additive genetic effects. In such a situation, selecting the best individuals will not lead to any genetic progress in the next generation.

220. (D) A is false but R is true.
Independent culling levels is a multi-trait selection method that is most effective when only a small number of traits are being improved. When too many traits are selected at once, the total number of individuals that meet every standard becomes very small. This forces the breeder to lower the selection pressure for each trait to maintain enough breeding stock, which significantly reduces the efficiency.

221. (A) Zero or negative
Family selection is a strategy where whole families are chosen based on their average performance, which is particularly effective for traits with low heritability. This method is most efficient compared to mass selection when there are no common environmental effects that make family members look more similar than they are genetically. When the intra-class correlation is zero, the family mean provides a more accurate estimate.

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204. (A) Canalization and reduced phenotypic variance
Stabilizing selection is a type of natural selection that favors individuals with intermediate phenotypes, which are often the most successful in a stable environment. Over long periods, this selective pressure results in canalization, where the developmental pathways are buffered against genetic and environmental changes. This leads to a significant reduction in the total phenotypic variance within the population, keeping the trait mean constant.

205. (A) Directly reflects statistical power to detect an association
The measure r-squared is widely preferred for quantifying linkage disequilibrium in genome-wide association studies. Unlike other metrics, it has a direct relationship with the statistical power of the analysis to detect a significant association between a marker and a trait. By understanding the r-squared values, researchers can determine the number of markers and individuals needed to achieve a successful and accurate mapping.

206. (B) Precise localization of QTL without background noise
Composite interval mapping is an advanced statistical method that improves the accuracy of identifying quantitative trait loci. It functions by including other genetic markers as cofactors in the model to account for the effects of QTLs located elsewhere in the genome. By controlling for this background genetic variance, the model reduces noise and allows for more precise localization and estimation of the target locus.

207. (A) Associations from population structure correlations
Population structure is a common source of false positive associations in genome-wide association studies. If individuals from different ancestral groups are included, any trait that varies between these groups may appear associated with markers that also differ in frequency. Using a Q-matrix allows the statistical model to account for these underlying group differences, ensuring that identified associations are truly due to genetic linkage.

208. (A) Tracking target allele without phenotypic expression
Foreground selection is a specialized application of molecular markers in breeding that allows for the selection of specific target genes. It is particularly useful when the trait is difficult to measure or is only expressed later in life. By using markers that are tightly linked to the gene, breeders can identify and track the desired allele across generations without the need for time-consuming phenotyping.

209. (A) Captures small effects of many loci without thresholds
Genomic selection is more effective than traditional marker-assisted selection for complex traits like yield because of its comprehensive approach. While traditional methods rely on identifying a few major-effect genes that pass strict statistical thresholds, genomic selection uses all markers simultaneously. This allows it to capture the cumulative contribution of many minor genes, which collectively determine most of the variation observed in complex characteristics.

210. (A) P-III, Q-II, R-IV, S-I
Population genetics utilizes several key parameters to describe the genetic health and evolutionary trajectory of a breeding group. The selection coefficient and relative fitness measure the reproductive success of different genotypes, while the effective population size determines the rate of genetic drift. Additionally, the inbreeding coefficient quantifies the level of relatedness and the probability that alleles are identical by descent due to shared ancestry.

211. (A) mRNA abundance of specific genes
In eQTL mapping studies, researchers treat the expression levels of individual genes as quantitative traits. This approach identifies genomic regions that regulate the amount of mRNA produced by those genes. By linking genetic markers to transcript abundance, scientists can discover regulatory variants that influence biological pathways and contribute to the variation observed in complex morphological and physiological traits within the population.

212. (A) Population is mating randomly without evolution
When the genotype frequencies of a population satisfy the Hardy-Weinberg principle, it indicates that the gene pool is in a state of genetic equilibrium. This means the population is large enough to avoid genetic drift, is mating randomly, and is not being influenced by evolutionary forces like selection, mutation, or

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231. (A) Resolution down to individual genes or nucleotides
Genome-wide association studies take advantage of historical recombination events that have occurred in natural populations over many centuries. This characteristic provides much higher resolution for mapping than traditional linkage studies, which only capture the recombination in a few recent generations. By analyzing these ancient associations, researchers can pinpoint the specific genes or even individual nucleotides that are responsible for the variation in complex traits.

232. (A) Highest proportion of recurrent parent alleles
In marker-assisted backcrossing, background selection is used to identify individuals that carry the largest percentage of the desired parent's genome. By using molecular markers distributed throughout the genome, breeders can select those progeny that have most rapidly recovered the recurrent parent's genetic background. This process significantly reduces the number of backcross generations required to develop a new variety while maintaining the target gene.

233. (A) Pyramiding multiple favorable QTLs via intermating
Marker-assisted recurrent selection is a modern breeding strategy used to improve complex traits by accumulating beneficial alleles from various parents. It involves first identifying several quantitative trait loci and then systematically intercrossing the best individuals to combine these alleles into a single line. This approach allows for the efficient pyramiding of genetic effects, leading to a much larger overall improvement than selecting for single genes.

234. (A) Regulatory polymorphisms affect transcript levels
eQTL mapping is a functional genomics technique based on the idea that variation in traits can be driven by differences in how genes are regulated. It identifies genetic variants that influence the amount of mRNA produced by a gene, which in turn affects the phenotype. By linking these regulatory polymorphisms to transcript levels, researchers can confirm the role of specific candidate genes in biological pathways.

235. (A) 1
For a single autosomal locus, the Hardy-Weinberg equilibrium describes a stable state where genotype frequencies remain constant over time. If a population is not in equilibrium, it will reach this balanced state in just one single generation of random mating, provided that no evolutionary forces are acting upon it. This rapid shift to equilibrium is a fundamental property of population genetics in large mating groups.

236. (A) $\frac{(\text{Observed} - \text{Expected})^2}{\text{Expected}}$
The chi-square goodness-of-fit test is a statistical method used to evaluate whether observed data matches a theoretical model. In population genetics, it is used to test for deviations from the Hardy-Weinberg equilibrium by comparing actual genotype counts with those predicted from allele frequencies. The test statistic is calculated by summing the squared differences between observed and expected values, weighted by the expected counts themselves.

237. (A) Limited dispersal distance of species
The neighborhood model of migration, or isolation by distance, describes how the limited movement of individuals within a large population creates a genetic structure. Because individuals tend to mate with those nearby, local neighborhoods become more genetically similar and more inbred than the overall population. This degree of relatedness and inbreeding is directly influenced by the dispersal distance and movement patterns of the species.

238. (A) Ratio of selection against two homozygotes
Heterozygote advantage, or overdominance, occurs when the heterozygous genotype is the most fit in the population. This selective pressure prevents any single allele from being lost, leading to a stable balanced polymorphism. The exact frequency of each allele at equilibrium is determined by the relative strength of selection acting against each of the two homozygous genotypes in the current environment.

239. (A) Allele frequencies that differ from original population due to sampling error
The founder effect is a type of genetic drift that occurs when a new population is started by a very small group from a larger population. Because the founders are few in number, they carry only a small sample of the original genetic diversity. This random sampling leads to new allele frequencies that can be very different

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providing a more complete picture of the genetic architecture.

187. (A) 0.0025
The frequency of sex-linked traits in a population differs between males and females due to their different numbers of X chromosomes. In males, the frequency of an X-linked recessive trait is equal to the frequency of the allele itself. In females, who have two X chromosomes, the trait is only expressed in those who are homozygous for the allele, which is calculated as the square of the frequency.

188. (B) Reject null; population deviates from HWE
The chi-square test is used to compare observed genetic data with the proportions expected under the Hardy-Weinberg equilibrium. If the calculated test value is larger than the critical value for a given level of significance, the null hypothesis of equilibrium is rejected. This result provides statistical evidence that the population is currently being influenced by evolutionary forces like selection, mutation, or non-random mating.

189. (B) 1
In the island model of population genetics, migration acts to counteract the effects of genetic drift in small subpopulations. Mathematical models show that a relatively small amount of gene flow is sufficient to prevent these groups from becoming completely genetically distinct. Even one migrant per generation is typically enough to maintain a basic level of genetic similarity and prevent the fixation of different alleles.

190. (A) Allele is hidden in phenotypically normal heterozygotes
Selection against a recessive lethal allele is a very slow process once the allele becomes rare in the population. This occurs because the majority of these harmful alleles are carried by heterozygous individuals who appear perfectly normal and healthy. Since selection only acts against the homozygous recessive individuals, the hidden alleles can persist in the population for many generations, making them very difficult to eliminate.

191. (A) Random mating, equal sex ratio, Poisson family variance
The effective population size is a theoretical concept that assumes an idealized population where every individual has an equal chance of contributing to the next generation. This ideal state requires random mating, a perfectly balanced sex ratio, and consistent reproductive success among parents. In real-world populations, these conditions are rarely met, which usually results in an effective size that is much smaller than the actual census.

192. (B) Non-allelic interactions across different loci
Epistatic variance is a component of the total genetic variation that arises from complex interactions between genes. It occurs when the effect of an allele at one genomic location depends on the specific alleles present at one or more other locations. These non-allelic interactions are part of the broader genetic architecture of quantitative traits and can influence both the phenotype and the response to selection.

193. (B) Fixable, transmissible average effects of alleles
Narrow-sense heritability is the most important measure for predicting the results of a breeding program. It quantifies the proportion of the total phenotypic variation that is due to additive genetic effects, which are the average effects of individual alleles. These effects are transmissible and can be fixed through selection, making them the primary drivers of genetic improvement in animal and plant populations over generations.

194. (A) 6.0
The expected genetic advance from a selection cycle can be calculated using a standardized formula that combines several parameters. By multiplying the selection intensity, the phenotypic standard deviation, and the narrow-sense heritability, breeders can predict the shift in the population mean. In this specific case, the combination of these values leads to an expected genetic gain of six units in the next generation.

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195. (A) Genetic variances, covariances, and economic weights
The Smith-Hazel selection index is an advanced method for improving multiple traits simultaneously in a breeding program. It requires a set of equations that integrate detailed genetic information, including the variances

heterozygous genotypes decreases as inbreeding increases. This loss of heterozygosity leads to the expression of harmful recessive alleles in their homozygous state, which were previously hidden and protected, causing a reduction in the overall health of the group.

249. (A) Intersect, causing rank changes
A crossover genotype by environment interaction occurs when different varieties respond inconsistently to a range of testing locations. This type of interaction is characterized by the reaction norms of the genotypes crossing each other, which leads to a change in their relative rankings. Identifying these patterns is important for breeders, as it indicates that the best genotype in one environment may be inferior.

250. (A) I, II, III, IV
Implementing a genomic selection program involves a specific series of steps to accurately predict and select for breeding values. First, a training population is both genotyped and phenotyped to estimate the effects of every genetic marker. Next, the selection candidates are genotyped. Finally, their genomic estimated breeding values are calculated by summing the estimated marker effects, allowing for selection without the need for immediate phenotyping.

251. (A) Phenotypic variance
Canalization is a biological process that buffers a population's development against both genetic and environmental disturbances. By ensuring that a standard phenotype is produced even under varying conditions, canalization effectively narrows the range of variation observed in the trait. Consequently, the long-term result of this process is a significant reduction in the total phenotypic variance within the population for the canalized characteristic.

252. (A) $D_t = D_0(1 - c)^t$
Linkage disequilibrium measures the non-random association between alleles at different genomic loci. Over successive generations of random mating, this association naturally diminishes as meiotic recombination breaks the physical linkage between the alleles. The rate of this decay is determined by the recombination fraction, with higher rates of crossover leading to a faster loss of disequilibrium and a return to random independent assortment.

253. (C) 1000 times more likely than its absence
In quantitative trait loci mapping, the LOD score is a statistical measure of the strength of the evidence for a linkage between a marker and a trait. It is calculated as the base ten logarithm of the likelihood ratio. Therefore, a LOD score of three indicates that the existence of a QTL at that specific location is one thousand times more likely.

254. (A) Significant statistical association with trait
A Manhattan plot is a standard tool used in association studies to visualize the importance of genetic markers across the entire genome. Each point represents a single marker, and its height on the vertical axis indicates the significance of its association with the trait. A tall peak signifies a region where markers show a very strong statistical association, pinpointing the location of genes.

255. (A) 1-5 cM of target gene
Recombinant selection is used in marker-assisted backcrossing to minimize the amount of donor DNA that remains around an introgressed gene. The goal is to identify individuals that have experienced a crossover event very close to the target locus. By selecting for these recombinations within a few centimorgans, breeders can effectively eliminate undesirable linkage drag while ensuring the target gene is maintained.

256. (A) Captures effects of QTLs failing significance tests
Genomic selection is a modern breeding technique that overcomes many of the limitations of traditional marker-assisted selection. While traditional methods focus on a few significant genes, genomic selection uses every marker across the genome simultaneously. This comprehensive approach allows it to capture the small effects of many genes that may not pass strict statistical tests but collectively contribute to most of the variation.

257. (A) Differential transcript correlating with phenotype
Functional candidate genes identified through mapping are validated by examining their expression patterns under specific conditions. For a trait like drought tolerance, a gene is confirmed as a strong candidate if its mRNA transcript levels show a significant change

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in response to stress that correlates with the observed phenotype. This differential expression provides direct evidence that the gene is active in the biological pathway.

258. (A) Allele frequency itself (p or q)
In species where males are hemizygous for sex-linked loci, they only carry a single copy of genes located on the X chromosome. Therefore, the frequency of a particular genotype among males is exactly equal to the frequency of that allele in the population's gene pool. This simplifies the genetic analysis of sex-linked traits, as male phenotypes directly reflect their allele frequencies.

259. (A) Sampling variance, resulting in genetic drift
The Hardy-Weinberg equilibrium is a theoretical model that assumes an infinite population size to prevent random changes in allele frequencies. In real biological populations, which are finite, sampling variance occurs because only a limited number of gametes are passed to the next generation. This process, known as genetic drift, leads to random fluctuations in allele frequencies and causes deviations from the predicted equilibrium state.

260. (A) I and II
Migration models describe different ways that gene flow can influence the genetic structure of a population. The island model assumes that individuals move between discrete subpopulations at a constant rate. In contrast, the neighborhood model assumes a continuous distribution where mating is restricted by distance. Both models show how migration can introduce new genetic variation and reduce the divergence between different groups over time.

261. (A) 0.2
Relative fitness is a measure of the reproductive success of a genotype compared to the most successful one in the population. The selection coefficient is the mathematical complement of this fitness value, calculated by subtracting it from one. If a genotype has a fitness of point eight, its selection coefficient is point two, representing the proportional reduction in its contribution to the next generation.

262. (A) Smallest generation size (bottleneck effect)
The effective population size of a breeding group that varies in number over time is heavily influenced by the generations with the fewest individuals. Mathematically, it is determined by the harmonic mean of the census sizes, which is always closer to the minimum value than to the larger sizes. This means that a temporary population bottleneck can have a long-lasting impact on genetic diversity.

263. (A) Genotype expression varies across environments
Genotype by environment interaction is a statistical term indicating that different varieties do not respond uniformly to a range of environmental conditions. When this interaction is significant, the performance of a genotype relative to others will change depending on where it is grown. This complexity requires breeders to evaluate varieties across multiple locations to ensure they are either broadly adapted or specifically suited.

264. (A) $\frac{1}{2}h^2$
The degree of resemblance between a single parent and its offspring can be used to estimate the heritability of a quantitative trait. When the phenotypes of the offspring are regressed on those of one parent, the resulting slope of the regression line is equal to half of the narrow-sense heritability. This relationship reflects the fact that each parent contributes only half of its genes.

265. (A) Increase intensity while minimizing generation interval
Maximizing the annual rate of genetic progress is a central goal for any breeding program. To achieve this, breeders must increase the selection intensity and accuracy while also trying to keep the generation interval as short as possible. By reducing the time it takes for animals to reach reproductive age, the genetic gain achieved in each cycle is realized more frequently, increasing the overall gain.

NODIA

266. (A) Integrates covariances to balance trait correlations
The Smith-Hazel selection index is a sophisticated method for improving multiple traits simultaneously by creating a single value for overall genetic merit. It is more efficient than simpler methods like tandem selection because it incorporates the genetic variances and covariances between the traits. By accounting for these correlations, the index ensures that

progress in one trait is not unnecessarily hindered by selection.

267. (A) Intra-class correlation for trait is negative or zero
Individual selection, based solely on a candidate's own phenotype, is generally the most efficient method for traits that are highly heritable. It outperforms within-family selection particularly when there are no shared environmental factors that make family members look more similar than their genetics would suggest. When the intra-class correlation is zero or negative, the individual's appearance is a reliable and accurate indicator.

268. (A) Uses normal distribution probability functions
For traits that are recorded in discrete categories but have a polygenic basis, heritability must be converted from the observed binary scale to an underlying continuous scale. This conversion utilizes mathematical functions based on the normal distribution to account for the incidence of the trait. This process standardizes the heritability estimates, allowing them to be used in standard breeding equations and compared across.

269. (A) Additive genetic variances of both traits
The genetic correlation between two traits is a measure of the extent to which the same genes influence both phenotypes. It is calculated by dividing the additive genetic covariance between the traits by the square root of the product of their individual additive genetic variances. This parameter is essential for predicting how selection for one characteristic will lead to a correlated genetic change.

270. (A) Both A and R are true and R is the correct explanation of A.
Interval mapping is an advanced statistical technique that is preferred over single marker analysis for identifying quantitative trait loci. It functions by systematically evaluating the entire chromosomal interval between two adjacent markers, rather than just the markers themselves. By accounting for the recombination frequencies within these intervals, interval mapping provides a much more precise and accurate estimate of the position.

271. (A) $\left(\frac{1}{2}\right)^n$
Strict self-fertilization is the most rapid way to increase homozygosity in a population. In every generation of selfing, the proportion of heterozygous individuals is reduced by exactly half as they produce homozygous progeny. After a specific number of generations, the remaining heterozygosity is a simple function of this constant rate of reduction, eventually leading to the development of nearly pure breeding lines.

272. (A) Fixed for opposite alleles at dominant loci
According to the dominance hypothesis, heterosis is maximized when the parental lines are homozygous for different alleles at many loci. When these lines are crossed, the resulting hybrid will be heterozygous at all of those locations, allowing the favorable dominant alleles from each parent to mask the harmful recessive alleles from the other. This results in superior performance and vigor in the hybrid.

273. (A) 1.0
In the Finlay and Wilkinson model for evaluating stability, the regression coefficient measures a variety's responsiveness to environmental changes. An ideal and widely adapted genotype is characterized by a high average performance across all locations and a regression coefficient of exactly one. This indicates that the variety responds to environmental improvements at an average rate, making its performance predictable and stable.

274. (A) Genotype x Environment interaction effects
A GGE biplot is a graphical representation used in multi-environment trial analysis to evaluate the performance of varieties. The biplot combines the main effects of genotypes with the complex interaction effects between genotypes and their environments. By visualizing these two components together, breeders can easily identify which varieties are most productive and stable, and which ones are specifically adapted to certain locations.

275. (A) Bimodal distribution favoring trait extremes
Disruptive selection is a form of natural selection that favors individuals with extreme phenotypes at both ends of the distribution while acting against intermediate variants. Over time, this selective pressure can lead to a bimodal distribution, where the population splits into two distinct groups. This process increases the total

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294. (A) $\frac{1}{8}(5)+\frac{1}{8}(50)=0.0275$

The rate of inbreeding in a closed population is determined by the number of breeding males and females contributing to the next generation. It is calculated by summing the reciprocal values of the number of individuals for each sex, multiplied by a constant. This formula shows how small numbers of sires or dams can lead to a rapid increase in relatedness.

295. (A) 0.6

The panmictic index is a measure of the relative heterozygosity in a population compared to a base population where mating is random. It is mathematically related to Wright's inbreeding coefficient, such that the two values always sum to one. As the level of inbreeding increases, the panmictic index decreases proportionally, reflecting the loss of genetic diversity due to the mating.

296. (A) Significantly less than 1.0

A non-linear crossover genotype by environment interaction occurs when different varieties do not perform consistently across a range of locations. This type of interaction indicates that the genetic correlation between the same trait measured in two different environments is significantly less than perfect. This means that different genes may be controlling the trait in each environment, complicating the selection process.

297. (A) General stability with no specific interaction

In the additive main effects and multiplicative interaction model, the IPCA score describes how a genotype interacts with its environment. If a genotype has an interaction score of zero, it means its performance is consistent across all test locations according to the main effects. Such a genotype is considered generally stable, as it lacks any specific positive or negative environmental adaptations.

298. (A) Overall mean of population

Stabilizing selection is a type of natural selection that acts to maintain an optimal phenotype by favoring intermediate variants and acting against extremes. Over time, this selective pressure leads to a significant reduction in the total phenotypic variance within the population. However, because the selection is balanced on both sides of the average, the overall population mean remains relatively constant and unchanged.

NODIA

299. (A) Sample size needed for statistical power in GWAS

The measure r-squared is a critical parameter in genome-wide association studies for quantifying the degree of linkage disequilibrium between markers. It is highly valued because it has a direct relationship with the statistical power of the analysis. By understanding the r-squared values, researchers can calculate the necessary sample size and marker density required to successfully identify the genes controlling the trait.

300. (A) Immortal homozygous genomes for multi-environment trials

Recombinant inbred lines are a valuable type of mapping population because they are completely homozygous and true breeding. This genetic stability means they can be multiplied and tested in multiple environments and over several years, which is essential for accurately measuring complex traits. Their immortal nature allows for repeated experiments, significantly increasing the statistical power and accuracy of the mapping.

****

generation. Higher rates of gene flow lead to a faster shift in the local genetic makeup.

285. (A) Proceed toward fixation (frequency = 1)
When selection acts on codominant alleles and one allele provides a fitness advantage in every genotype, its frequency will systematically increase in the population. Because the heterozygote has a fitness level between the two homozygotes, the favorable allele is always favored by natural selection. Over many generations, this process will lead to the complete replacement of the less fit allele, resulting in fixation.

286. (A) $\frac{pq}{2N}$
In a finite population, genetic drift causes allele frequencies to fluctuate randomly in each generation. The magnitude of this fluctuation, or the variance of the change, is inversely proportional to twice the size of the breeding population. This relationship shows that smaller populations experience much larger random shifts in their genetic makeup, which can lead to a faster loss of variation over time.

287. (A) Breeding values for all individuals in population
Additive genetic variance is a fundamental concept in quantitative genetics that describes the proportion of total phenotypic variance due to the cumulative effects of alleles. It is formally defined as the variance of the breeding values of all individuals within the breeding population. This component is crucial because it determines the response to selection and the degree of resemblance between parents and offspring.

288. (A) Genetic variance plus permanent environmental variance
Repeatability is a measure used for traits that can be recorded multiple times on the same individual throughout its life. It quantifies the correlation between successive measurements and includes both the total genetic variance and any permanent environmental effects that influence the individual. Because it accounts for these permanent factors, repeatability always sets the upper theoretical limit for the broad-sense heritability.

289. (A) Phenotypic standard deviation (σ_P)
In predicting the response to selection, the selection intensity is a standardized measure of the selection pressure being applied. It is calculated by dividing the selection differential by the phenotypic standard deviation of the trait. This parameter allows breeders to compare the rigor of selection across different populations and traits, and it is a key component of the breeder's equation.

290. (A) Both A and R are true and R is the correct explanation of A.
The Smith-Hazel selection index is a highly efficient method for improving multiple traits simultaneously because it optimizes the overall genetic progress. By weighting each trait according to its economic value and its genetic parameters, the index accounts for the variances and correlations among the traits. This balanced approach ensures that the selection process results in the greatest possible increase in total value.

291. (A) High
Within-family selection is a method where candidates are chosen based on their performance relative to their siblings. This approach is particularly advantageous when there is a high environmental correlation among family members, such as when they are raised in the same pen or by the same mother. By focusing on within-family differences, the breeder can eliminate these common environmental influences, improving accuracy.

NODIA

292. (A) Discrete, masking polygenic nature
Threshold traits appear as simple discrete categories, but they are actually influenced by the combined effects of many different genes and environmental factors. This underlying polygenic inheritance is masked by the fact that the trait is only expressed once a certain susceptibility level is reached. The threshold model provides a mathematical framework to analyze these traits as if they followed a continuous distribution.

293. (A) Simultaneous improvement in correlated trait
When two traits share a high positive genetic correlation, it means that they are influenced by many of the same genes in the same way. Consequently, any selection pressure applied to improve the first trait will also lead to a predictable increase in the second trait. Breeders can use this relationship to achieve simultaneous improvement in multiple important characteristics with less effort.

(A) Inability to freeze semen of indigenous breeds for long-term storage
(B) Inadequate milk recording systems within unorganized rural herds
(C) Absence of qualified veterinary surgeons for mandatory vaccinations
(D) Farmers' refusal to utilize artificial insemination under any circumstances

2021

28. A significant socio-economic bottleneck in the implementation of livestock breeding policies in India is:
(A) High literacy rates among rural farmers causing resistance to change
(B) Small herd sizes and fragmentation preventing organized data collection
(C) Excessive availability of grazing land reducing the need for improvement
(D) Over-commercialization of native breeds leading to genetic homogenization

2001

29. Grading-up is a breeding strategy primarily used to:
(A) Improve the genetic merit of a non-descript population by continuously mating them with sires of a pure breed
(B) Create a new synthetic breed by crossing two purebreds
(C) Increase homozygosity in a closed herd to fix specific traits
(D) Exploit maximum heterosis in the terminal generation

2014

30. Consider the following statements regarding crossbreeding in Indian cattle:
I. It introduces exotic germplasm to rapidly increase milk production.
II. It reduces the need for high-quality feed and management.
III. It takes advantage of heterosis.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I, II and III

2011

31. Selective breeding of indigenous non-descript cattle is most appropriate when:
(A) The goal is to immediately double milk production within one year
(B) Artificial insemination with exotic semen is cheaply and readily available
(C) The market exclusively demands high fat milk regardless of total yield
(D) High-stress environments cannot support exotic crossbred individuals

2006

32. In the extensive sheep production systems of arid regions, which trait is generally prioritized in breeding programs?
(A) High twinning rate
(B) Rapid growth rate for heavy carcass weight
(C) Survivability and adaptation to scarce pasture
(D) High milk yield for human consumption

2001

33. The Magra breed of sheep is primarily conserved and bred for which specific utility?
(A) Fine apparel wool
(B) High-quality lustrous carpet wool
(C) High fecundity and prolificacy
(D) Dual-purpose milk and meat

2006

34. Which breeding strategy is predominantly recommended for improving the dual-purpose utility of sheep in favorable agro-climatic zones?
(A) Inbreeding with desert-adapted breeds to fix local adaptation genes
(B) Terminal crossing with Boer goats to enhance meat carcass yield
(C) Continuous grading up with non-descript rams to maintain diversity
(D) Crossing indigenous ewes with exotic dual-purpose rams like Corriedale

2010

35. Pashmina fiber in India is primarily obtained from which breed of goat?
(A) Changthangi
(B) Gaddi
(C) Barbari
(D) Black Bengal

2023

36. For improving meat production in Indian goats through selective breeding, which breed is often utilized for its excellent prolificacy and meat quality in the eastern region?
(A) Sirohi
(B) Osmanabadi
(C) Black Bengal
(D) Malabari

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CHAPTER 06
Genetic Strategies

2003

1. The selection index method, developed by Hazel and Lush, combines multiple traits into a single value based on which of the following?
(A) Equal weighting of all phenotypic traits regardless of heritability values
(B) Genetic and phenotypic parameters combined with trait economic values
(C) Selection focused solely on the single trait having the highest weight
(D) Independent culling levels applied sequentially to every identified trait

2008

2. When selection is applied to a trait with a normal distribution, the difference between the mean of the selected parents and the mean of the entire unselected population is known as:
(A) Genetic gain
(B) Selection intensity
(C) Standardized selection response
(D) Selection differential

2022

3. In a closed herd, which method of selection evaluates an individual's genetic worth based on the performance of its ancestors?
(A) Pedigree selection
(B) Individual selection
(C) Progeny testing
(D) Family selection

2023

4. Which of the following conditions is most appropriate for utilizing family selection rather than individual selection?
(A) When the heritability of the trait is observed to be very high
(B) When the environmental variance is negligible for all candidates
(C) When the trait is sex-limited and possesses low heritability
(D) When the trait is heavily influenced by non-additive gene action

2021

5. The expected genetic progress per year (ΔG) in a breeding program is correctly calculated by which formula?
(A) $\frac{\text{Heritability} \times \text{selection differential}}{\text{generation interval}}$
(B) Repeatability multiplied by phenotypic standard deviation values
(C) Selection differential multiplied by the total generation interval
(D) Heritability divided by the calculated selection intensity value

2006

6. Assortative mating is defined as the mating of individuals that are:
(A) More closely related than the average of the general population
(B) Less closely related than the average of the general population
(C) From completely different distinct breeds within a single species
(D) Phenotypically more similar than expected by random chance

2004

7. Which of the following mating systems is primarily utilized to maximize heterosis in commercial livestock production?
(A) Inbreeding
(B) Crossbreeding
(C) Linebreeding
(D) Negative assortative mating

2019

8. Inbreeding depression is most severely observed in which category of traits?
(A) Highly heritable traits such as specific coat color patterns
(B) Carcass quality traits including marbling and fat thickness
(C) Traits related to fitness, survival, and reproductive ability
(D) Morphological traits such as horn shape or skeletal structure

NODIA

controlled genetic drift

2017

46. Community-based conservation of Animal Genetic Resources (AnGR) relies heavily on:
(A) Storing embryos in government-funded liquid nitrogen facilities
(B) Relocating herds to high-tech research institutions for study
(C) Local pastoralist participation and ownership in native tracts
(D) Mandatory sterilization of indigenous sires to prevent random mating

2025

47. Which traditional institution in India plays an important, informal role in the in-situ conservation of indigenous cattle breeds?
(A) Commercial hatcheries
(B) Semen banks
(C) Abattoirs
(D) Gaushalas

2013

48. Ex-situ conservation of AnGR involves which of the following practices?
(A) Encouraging pastoralists to maintain traditional migratory routes
(B) Formation of local breed societies
(C) Cryopreservation of semen, embryos, and somatic cells
(D) Establishing grazing reserves in the native tract

2015

49. In cryopreservation of semen, what is the primary function of glycerol in the extender?
(A) To provide an energy source for sperm motility during the process
(B) Preventing intracellular ice formation as a cryoprotectant
(C) To buffer the pH of the semen throughout the freezing stages
(D) To inhibit bacterial growth within the extended semen samples

2003

50. Match the following semen evaluation parameters in List I with their primary assessment tools in List II.
List I: (Evaluation Parameters)
P. Sperm motility
Q. Sperm concentration
R. Sperm viability
S. Sperm morphology
List II: (Assessment Tools)
1. Eosin-Nigrosin stain
2. Phase-contrast microscopy
3. Haemocytometer / Spectrophotometer
4. Rose Bengal stain
(A) P-2, Q-3, R-1, S-4
(B) P-3, Q-2, R-1, S-4
(C) P-2, Q-4, R-1, S-3
(D) P-2, Q-1, R-3, S-4

2004

51. The most common hormone used for inducing superovulation in cattle during MOET protocols is:
(A) Follicle Stimulating Hormone (FSH)
(B) Prostaglandin F2α
(C) Oxytocin
(D) Progesterone

2023

52. In a standard MOET program for cattle, non-surgical embryo recovery (flushing) is typically performed on which day after estrus?
(A) Day 2 or 3
(B) Day 10 or 12
(C) Day 6 or 7
(D) Day 14 or 15

2023

53. The advanced reproductive biotechnology known as Ovum Pick-Up (OPU) involves:
(A) Ultrasound-guided transvaginal aspiration of oocytes from live animals
(B) Surgical removal of the entire ovary for laboratory processing
(C) Flushing the uterus for unfertilized eggs using specialized catheters
(D) Harvesting embryos post-slaughter only from high-merit beef cattle

2021

54. Intracytoplasmic Sperm Injection (ICSI) is an advanced IVF technique primarily used when:
(A) The female has a blocked reproductive tract preventing natural conception
(B) Embryos need to be sexed prior to transfer to a recipient animal
(C) Cloning of the male is desired through somatic cell nuclear transfer
(D) Poor sperm quality or motility prevents standard in-vitro fertilization

2006

55. Quantitative Trait Loci (QTL) mapping is fundamentally based on identifying the statistical association between:
(A) Animal age and feed conversion efficiency

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(B) Gujarat Plains and Hills Region
(C) Trans-Gangetic Plains Region
(D) Southern Plateau and Hills Region

2008

18. Which buffalo breed is characterized by its high butterfat content, often exceeding 8%, and is native to Uttar Pradesh?
(A) Murrah
(B) Surti
(C) Nili-Ravi
(D) Bhadawari

2021

19. Identify the incorrect pair regarding sheep breeds and their primary utility.
(A) Magra – Purely dairy purposes
(B) Chokla – Fine carpet wool
(C) Nellore – Mutton production
(D) Garole – Prolificacy (multiple births)

2006

20. The following question consists of two statements, one labeled as Assertion (A) and the other as Reason (R). Examine these two statements carefully and select the correct answer using the codes given below.
Assertion (A): The Jamunapari goat is known as the best dairy goat breed of India.
Reason (R): It has a pendulous udder and typically grazes on tall bushes in the Etawah district of Uttar Pradesh.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2002

21. Which indigenous pig breed is native to the North-Eastern region of India and is valued for its specific adaptation to the local climate?
(A) Niang Megha
(B) Ghungroo
(C) Agonda Goan
(D) Tenyi Vo

2012

22. The Double-humped (Bactrian) camel in India is exclusively found in which region?
(A) Rann of Kutch, Gujarat
(B) Thar Desert, Rajasthan
(C) Spiti Valley, Himachal Pradesh
(D) Nubra Valley, Ladakh

2001

23. The Key Village Scheme (KVS), launched during the First Five Year Plan, primarily focused on:
(A) Establishing highly mechanized dairy processing plants in rural areas
(B) Comprehensive cattle development via AI and healthcare in compact areas
(C) Distributing exotic poultry breeds to landless laborers for income
(D) Setting up commercial feed manufacturing units across rural India

2014

24. A major limitation observed in the implementation of the Intensive Cattle Development Project (ICDP) was:
(A) Over-emphasis on indigenous draft breeds rather than milk production
(B) Complete reliance on natural service instead of artificial insemination
(C) Insufficient feed and fodder to support crossbred requirements
(D) Failure to include veterinary healthcare services in the project scope

2017

25. Arrange the following genetic improvement initiatives in India in chronological order from earliest to most recent.
I. Intensive Cattle Development Project (ICDP)
II. Key Village Scheme (KVS)
III. National Dairy Plan (NDP)
IV. All India Coordinated Research Project (AICRP) on Cattle
(A) II, I, IV, III
(B) I, II, III, IV
(C) II, IV, I, III
(D) IV, I, II, III

NODIA

2005

26. The National Dairy Plan (NDP) implemented by NDDB focuses heavily on:
(A) Producing high genetic merit bulls using testing and pedigree selection
(B) Producing genetically engineered dairy cattle for increased efficiency
(C) Banning the use of indigenous semen in all participating rural areas
(D) Shifting milk production entirely to corporate-owned dairy farms

2013

27. Which technical bottleneck most severely affects the success of field-level progeny testing programs in India?

phenotypic variance and is often an important step in the divergence of new species.

276. (A) Allele frequencies at both loci
Linkage disequilibrium measures the non-random association of alleles at different genomic locations. The maximum possible value of the disequilibrium parameter D is not constant but is mathematically constrained by the frequencies of the alleles at the two loci being studied. This relationship is important for researchers to understand, as it affects the interpretation of disequilibrium levels and the power of association.

277. (A) Locate QTLs precisely by removing background variance
Composite interval mapping is a sophisticated method for identifying quantitative trait loci that improves upon simpler techniques. It works by including other genetic markers as cofactors in the analysis to account for the effects of other genes located elsewhere in the genome. By removing this background genetic variation, the model reduces noise and allows for more precise mapping and estimation of effects.

278. (A) Fitting MLM with population structure and kinship
Genome-wide association studies are prone to false positive results if the underlying population structure and relatedness are not properly addressed. To solve this, researchers use mixed linear models that incorporate matrices representing both the ancestral population structure and the pairwise kinship among individuals. These adjustments ensure that the identified associations are truly due to genetic linkage with the trait being studied.

279. (A) Unintentional introgression of undesirable genes linked to target gene
Linkage drag is a common challenge in backcross breeding where a desired gene is being transferred from a donor parent. Because the target gene is physically linked to other genes on the chromosome, these neighboring segments of donor DNA are often inherited along with it. If these linked genes have undesirable effects on performance, they can hinder the overall success of the breeding program.

280. (A) P-III, Q-I, R-IV, S-II
Different statistical methodologies are used to map quantitative trait loci and predict breeding values. Single marker analysis uses basic tests to identify associations at individual loci, while simple interval mapping evaluates the areas between markers. Composite interval mapping adds cofactors to control for background genetic noise. Finally, genomic selection uses every marker across the entire genome simultaneously to estimate breeding values without significance testing.

281. (A) Functional expression or known biochemical pathways
The candidate gene approach identifies specific genes that may control a trait by combining genetic mapping data with biological knowledge. Researchers look for genes within a mapped chromosomal region that have functions related to known biochemical or physiological pathways. By integrating this functional information with genetic location, they can prioritize the most likely genes for further validation through expression analysis or knock-outs.

282. (A) More frequently in males
In species with XY sex determination, males have only one copy of genes located on the X chromosome. This means that a single recessive allele on their X chromosome will be expressed in the phenotype, whereas females require two copies to show the trait. As a result, rare sex-linked recessive characteristics appear much more frequently in males than they do in females.

283. (A) A decrease in homozygosity and an increase in heterozygosity
Disassortative mating is a non-random mating pattern where individuals choose partners with different phenotypes than their own. This process has a significant impact on the genetic structure of the population by increasing the frequency of heterozygous genotypes across successive generations. While it does not alter the overall allele frequencies, it actively promotes genetic diversity and counteracts the effects of inbreeding within the group.

284. (A) m
Continuous migration from a large source population into a smaller local group will eventually cause the local allele frequencies to match the source. The rate at which this convergence occurs is directly proportional to the migration rate, which is the percentage of new individuals entering the group in each

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2024

37. Which strategy is most effective for improving milk yield in native goats while retaining adaptability?
(A) Upgrading with Jamunapari or Beetal within their adaptable zones
(B) Crossbreeding with Boer goats to enhance meat and milk traits
(C) Continuous inbreeding to fix the lactation traits in small herds
(D) Importing Alpine purebreds and replacing native stock entirely

2005

38. The primary focus of genetic improvement of swine in India currently involves:
(A) Eradicating all indigenous breeds to make way for exotic purebreds
(B) Using transgenic pigs for commercial pork production units
(C) Promoting vegetarianism, thus halting swine breeding initiatives
(D) Crossing indigenous pigs with exotic breeds like Large White Yorkshire

2023

39. A major challenge in conserving indigenous swine germplasm in India is:
(A) Their extremely high maintenance costs compared to exotic breeds
(B) Dilution of native genetics due to indiscriminate crossbreeding
(C) Their complete lack of disease resistance in tropical environments
(D) Their inability to scavenge for food in traditional rearing systems

2019

40. Consider the following statements regarding equine and camel conservation in India:
I. The Spiti pony is found in high-altitude regions.
II. The Kathiawari horse is known for its inward curving ear tips.
III. Bactrian camels are bred extensively for dairy production in the Thar desert.
IV. The Marwari horse is native to Rajasthan.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and III
(C) III only
(D) I, II and IV

2006

41. The donkey breed known for its white color, superior draught power, and adaptation to the arid regions of Gujarat is:
(A) Spiti
(B) Zanskari
(C) Manipuri
(D) Halari

2016

42. In poultry breeding, a "synthetic parent line" refers to:
(A) A population created by crossing multiple established lines and selecting
(B) A line developed exclusively through artificial gene editing techniques
(C) Birds that are fed purely synthetic diets to maximize growth potential
(D) Cloned copies of a single high-yielding layer for commercial use

NODIA

2006

43. Breeding for backyard poultry strains in India emphasizes which set of traits?
(A) Extreme body weight, white plumage, and strict confinement adaptation
(B) Colored plumage, dual-purpose utility, hardiness, and predator evasion
(C) High egg production only, with no emphasis on survivability traits
(D) Production of extremely large eggs at the expense of hatchability rates

2021

44. Compared to a Closed Nucleus Breeding System, an Open Nucleus Breeding System (ONBS) allows for:
(A) Strict restriction of gene flow into the nucleus from the base
(B) Selecting top females from the base population into the nucleus
(C) Elimination of all selection pressures in the base population herds
(D) The use of natural mating only for all tiers of the breeding scheme

2004

45. What is the primary genetic advantage of an ONBS?
(A) Higher genetic gain and lower inbreeding than closed systems
(B) It eliminates inbreeding entirely across all generations of the herd
(C) It removes the need for maintaining any pedigree or performance records
(D) It fixes recessive traits more rapidly through

2023

9. Linebreeding is considered a specialized form of:
(A) Crossbreeding
(B) Outcrossing
(C) Species hybridization
(D) Inbreeding

2022

10. Match the following mating systems in List I with their genetic consequences in List II.
List I: (Mating Systems)
P. Inbreeding
Q. Crossbreeding
R. Positive assortative mating
S. Negative assortative mating
List II: (Genetic Consequences)
1. Increases heterozygosity and heterosis
2. Increases homozygosity and exposes recessive alleles
3. Increases phenotypic variance but maintains intermediate gene frequencies
4. Decreases phenotypic variance and increases intermediate phenotypes
(A) P-2, Q-1, R-3, S-4
(B) P-1, Q-2, R-4, S-3
(C) P-2, Q-3, R-1, S-4
(D) P-3, Q-1, R-4, S-2

2012

11. Heritability in the narrow sense is defined as the ratio of:
(A) Total genetic variance to phenotypic variance
(B) Additive genetic variance to phenotypic variance
(C) Dominance variance to phenotypic variance
(D) Epistatic variance to genetic variance

2007

12. If a trait has a repeatability of 0.80, what does this indicate about the trait?
(A) Multiple records on an individual will not improve selection accuracy
(B) One record accurately predicts future performance of the animal
(C) The environmental influences are highly variable and unpredictable
(D) The trait is primarily controlled by non-additive genetic effects

2017

13. Which genetic parameter is crucial for predicting the correlated response to selection when selecting for a primary trait?
(A) Genetic correlation between the primary and secondary traits
(B) Heritability of the primary trait alone
(C) Repeatability of the secondary trait
(D) Phenotypic variance of the primary trait

2019

14. Which of the following best describes a negative genetic correlation between milk yield and fat percentage in dairy cattle?
(A) Selecting for higher milk yield will simultaneously increase fat percentage
(B) The two traits are controlled by completely different, independent sets of genes
(C) Increased milk yield selection tends to lower fat percentage
(D) Environmental factors affect milk yield but not fat percentage

2019

15. Select the correct sequence of steps involved in the NBAGR guidelines for the registration of a new livestock breed.
(A) Phenotypic characterization → Application submission → Evaluation by Breed Registration Committee → Molecular characterization → Gazette notification
(B) Application submission → Phenotypic characterization → Molecular characterization → Evaluation by Breed Registration Committee → Gazette notification
(C) Application submission → Phenotypic characterization → Evaluation by Breed Registration Committee → Molecular characterization → Gazette notification
(D) Phenotypic characterization → Molecular characterization → Application submission → Evaluation by Breed Registration Committee → Gazette notification

2002

16. Which of the following is an essential requirement for registering a new breed of livestock under standard guidelines?
(A) The population must be an exact synthetic mix of two exotic breeds
(B) The breed must be present in at least five different states of India
(C) Documentation of unique phenotypes and a defined native tract
(D) The population size must be less than 1,000 individuals to ensure conservation priority

2002

17. The Kankrej breed of cattle is primarily distributed in which agro-climatic zone of India?
(A) Eastern Himalayan Region

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(B) Phenotypic variation and molecular markers
(C) Environmental temperature and milk yield
(D) Coat color and horn length

2009

56. Which type of molecular marker is highly polymorphic, co-dominant, and consists of short tandem repeats?
(A) RFLP
(B) RAPD
(C) Microsatellites
(D) AFLP

2010

57. In Marker-Assisted Introgression, the primary objective is to:
(A) Remove all molecular markers from the genome to increase uniformity
(B) Create a new synthetic breed using equal parts of four different breeds
(C) Cloning the donor breed using somatic cell nuclear transfer techniques
(D) Transfer a specific gene or QTL while recovering the recipient background

2009

58. Genomic Selection (GS) differs from traditional Marker-Assisted Selection (MAS) in that GS:
(A) Uses whole-genome marker panels to predict breeding values
(B) Relies on a few significant QTLs for selection in small populations
(C) Completely ignores phenotypic data from the reference population groups
(D) Can only be applied to monogenic traits with simple inheritance patterns

2024

59. The reference population in a Genomic Selection program must have:
(A) Only genotypic data for all individuals within the breeding herd
(B) Genotypic data combined with accurate phenotypic records or EBVs
(C) Only phenotypic data recorded over multiple lactations or generations
(D) Neither genotypic nor phenotypic data, relying only on pedigree records

2025

60. The following question consists of two statements, one labeled as Assertion (A) and the other as Reason (R). Examine these two statements carefully and select the correct answer using the codes given below.
Assertion (A): Somatic Cell Nuclear Transfer (SCNT) allows for the production of genetically identical copies of an elite farm animal.
Reason (R): SCNT involves transferring the nucleus of a somatic cell into an enucleated oocyte, followed by embryo development.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2018

61. The revolutionary gene-editing technology CRISPR/Cas9 utilizes a guide RNA to direct the Cas9 enzyme to a specific genomic location to induce:
(A) Double-strand DNA breaks
(B) Random genome duplication in all somatic cells of the organism
(C) Complete destruction of mitochondrial DNA within the target cell
(D) Reverse transcription of RNA to DNA for insertion of new genes

2010

62. The Karan Swiss cattle breed was developed at NDRI, Karnal by crossing which two breeds?
(A) Holstein Friesian and Sahiwal
(B) Jersey and Red Sindhi
(C) Brown Swiss and Sahiwal
(D) Brown Swiss and Tharparkar

2019

63. The Frieswal cattle project is a collaborative effort between:
(A) NDRI and NDDB
(B) NBAGR and IVRI
(C) BAIF and State Animal Husbandry Departments
(D) ICAR-CIRC and Military Farms

2021

64. The Sunandini breed, developed in Kerala, is a result of grading up local non-descript cattle with:
(A) Exclusively pure Holstein Friesian sires for maximum milk production
(B) Sahiwal and Red Sindhi bulls to maintain indigenous adaptability
(C) A mix of Brown Swiss, Jersey, and Holstein Friesian inheritance
(D) Brahman cattle to enhance heat tolerance and disease resistance

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2004

142. Fertility optimization in artificial insemination programs heavily depends on:
(A) Inseminating the cow immediately at the first sign of estrus
(B) Using semen with the highest possible volume regardless of concentration
(C) Following the AM-PM rule for timing the insemination relative to estrus
(D) Inseminating during the luteal phase of the cycle

2021

143. Prostaglandin F2α (PGF2α) is used in estrus synchronization protocols primarily to:
(A) Induce ovulation directly
(B) Stimulate follicular wave emergence
(C) Maintain pregnancy
(D) Cause luteolysis (regression of the corpus luteum)

2024

144. In embryo transfer, the recipient cow must be synchronized to match the exact stage of the estrous cycle of the donor cow. Why is this critical?
(A) To ensure the recipient's immune system does not attack the embryo
(B) To trigger superovulation in the recipient
(C) To provide the appropriate uterine environment for the embryo
(D) To allow the embryo to change its sex

2005

145. The most reliable method for sexing bovine embryos prior to transfer is:
(A) Visual inspection under a light microscope
(B) PCR amplification of Y-chromosome specific DNA sequences
(C) Weighing the embryo
(D) Staining with eosin-nigrosin

2004

146. Which DNA marker relies on the variation in the presence or absence of specific restriction enzyme cleavage sites?
(A) Microsatellites
(B) SNPs
(C) RAPD
(D) RFLP

2017

147. A Quantitative Trait Locus (QTL) is fundamentally a:
(A) Region of DNA associated with a particular phenotypic trait
(B) Single gene with a major dominant effect
(C) Recessive mutation that causes lethality
(D) Protein expressed in milk

2010

148. Marker-Assisted Introgression is most useful for which of the following scenarios?
(A) Improving an already highly heritable trait like coat color
(B) Creating identical clones of an animal
(C) Transferring a disease-resistance gene from a wild relative
(D) Estimating phenotypic variance

2004

149. The accuracy of Genomic Estimated Breeding Values (GEBVs) in dairy cattle primarily depends on:
(A) Size of the reference population and herizability of the trait
(B) The physical size of the SNP chip
(C) The number of years the breed has existed
(D) The color of the cattle

2009

150. Match the following institutions in List I with their focal animal species or discipline in List II.
List I: (Institutions)
P. NBAGR
Q. CSWRI
R. CIRG
S. DPR
List II: (Focal Species/Discipline)
1. Poultry
2. Goats
3. Animal Genetic Resources
4. Sheep
(A) P-3, Q-4, R-2, S-1
(B) P-4, Q-3, R-2, S-1
(C) P-3, Q-2, R-4, S-1
(D) P-1, Q-4, R-2, S-3

2015

151. Which genetic phenomenon poses a major risk when using highly selected elite sires extensively across a large population via AI?
(A) Rapid increase in generation interval
(B) Inbreeding depression and reduced genetic diversity
(C) Complete loss of additive genetic variance
(D) Hybrid vigor

NODIA

2001

152. Gene editing via CRISPR/Cas9 has been experimentally used in pigs to introduce resistance against which economically devastating disease?

2021

75. Repeatability sets the upper limit for which genetic parameter?
(A) Selection intensity
(B) Heritability (broad sense)
(C) Epistatic variance
(D) Environmental variance

2013

76. The concept of "generation interval" in animal breeding is best defined as:
(A) The time taken for a young animal to reach its sexual maturity
(B) Average age of parents when offspring replacing them are born
(C) The lifespan of an animal from birth to its natural death
(D) The duration of pregnancy in a specific livestock species

2009

77. Phenotypic characterization of indigenous breeds includes all of the following EXCEPT:
(A) Whole genome sequencing data for molecular mapping
(B) Body biometry including length, height, and girth measurements
(C) Coat color patterns and specific horn orientation features
(D) Production and reproduction performance data in the field

2024

78. Which of the following Indian cattle breeds is renowned for its excellent draught capacity and is characterized by a prominent forehead and majestic gait?
(A) Sahiwal
(B) Gir
(C) Kankrej
(D) Red Sindhi

2024

79. The Toda breed of buffalo is uniquely adapted to which specific region?
(A) The arid deserts of Rajasthan
(B) The Himalayan foothills
(C) The coastal plains of Odisha
(D) The Nilgiri hills of Tamil Nadu

2016

80. Consider the following statements concerning Indian goat breeds:
I. The Beetal goat is highly prevalent in Punjab.
II. The Barbari goat is known for its stall-feeding adaptability and small size.
III. The Changthangi goat is primarily bred for meat in southern India.
IV. The Osmanabadi goat is well-adapted to the harsh conditions of Maharashtra.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) II, III and IV
(C) I, III and IV
(D) I, II and III

2022

81. Which breed of sheep is famously known as the "Merino of Rajasthan" due to its fine wool quality?
(A) Marwari
(B) Chokla
(C) Malpura
(D) Sonadi

2001

82. Which indigenous pig breed, found in the Dooars region of West Bengal, is highly prolific and forms a vital part of the tribal economy?
(A) Tenyi Vo
(B) Doom
(C) Zovawk
(D) Ghungroo

2015

83. The major constraint identified in the All India Coordinated Research Project (AICRP) on Cattle was:
(A) Farmers' poor adoption of crossbred males for draught work
(B) The excessive funding which led to project misallocation issues
(C) The complete failure of crossbred females to produce any milk
(D) Rapid extinction of all indigenous breeds due to project focus

2013

84. Which institutional factor frequently hinders the successful execution of breeding programs in rural areas?
(A) Overabundance of highly trained veterinary geneticists in villages
(B) Excessive availability of purebred bulls on every smallholder farm
(C) Lack of a synchronized cold chain for storing frozen semen
(D) Strict adherence to pedigree recording by all illiterate farmers

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2009

103. In vitro maturation (IVM) is a critical step following which reproductive biotechnology?
(A) Artificial Insemination
(B) Ovum Pick-Up (OPU)
(C) Natural mating
(D) Non-surgical embryo flushing

2016

104. Which technique involves physically injecting a single spermatozoon directly into the cytoplasm of an oocyte?
(A) IVF
(B) MOET
(C) ICSI
(D) SCNT

2010

105. Single Nucleotide Polymorphisms (SNPs) are highly useful in Genomic Selection because:
(A) They are extremely rare throughout the bovine genome
(B) They only occur in the mitochondrial DNA of the animal
(C) They always cause severe phenotypic mutations in the breed
(D) They are dense and abundant across the entire genome

2016

106. Genomic Estimated Breeding Values (GEBVs) are calculated using:
(A) Prediction equations derived from effects in a reference group
(B) Only the individual's own phenotypic record for that trait
(C) Phenotypic data of parents and offspring without genetic markers
(D) Random number generation based on global breed averages

2009

107. The first cloned buffalo calf produced using the hand-guided cloning technique at NDRI, Karnal was named:
(A) Garima
(B) Samrupa
(C) Pratham
(D) Mahima

2018

108. The transgenic application in farm animals aiming to produce human pharmaceutical proteins in milk is commonly referred to as:
(A) Gene knock-out techniques for trait elimination
(B) Pharming
(C) Xenotransplantation for organ donor production
(D) Marker introgression from wild to domestic breeds

2018

109. Karan Fries is a crossbred cattle strain developed by crossing Tharparkar cows with bulls of which exotic breed?
(A) Holstein Friesian
(B) Jersey
(C) Brown Swiss
(D) Ayrshire

2014

110. The following question consists of two statements, one labeled as Assertion (A) and the other as Reason (R). Examine these two statements carefully and select the correct answer using the codes given below.
Assertion (A): Crossbreeding indigenous cattle with exotic breeds leads to an immediate increase in milk production in the F1 generation.
Reason (R): The F1 generation expresses maximum heterosis and combines the high milk yield genes of the exotic breed with the adaptability of the indigenous breed.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

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2001

111. Which crossbred sheep was specifically developed for fine apparel wool in India by crossing Chokla ewes with Rambouillet rams?
(A) Bharat Merino
(B) Avikalin
(C) Hissardale
(D) Avivastra

2019

112. The most significant advantage of maintaining a closed nucleus breeding system is:
(A) Rapid increase in genetic diversity within the breeding herd
(B) Absolute elimination of inbreeding in all future generations
(C) Strict health control and precise trait recording in the herd
(D) Dependence on external germplasm for periodic improvement

2024

94. The genetic gain in an ONBS is generally higher than in a closed nucleus scheme primarily because:
(A) The mutation rate is artificially increased through chemicals
(B) Generation interval is doubled to allow for better trait expression
(C) Female selection intensity increases by using the large base
(D) Heritability magically increases due to the open flow of genes

2013

95. Community-based management of animal genetic resources focuses on:
(A) The complete replacement of indigenous breeds with exotic breeds
(B) Confining local breeds to zoological parks for public display
(C) Banning the sale of animal products from all local native breeds
(D) Empowering local keepers to manage and conserve local breeds

2022

96. Embryo freezing in cattle relies heavily on the use of permeating cryoprotectants. Which of the following is most commonly used?
(A) Sodium chloride solutions
(B) Distilled water
(C) Ethylene glycol
(D) Liquid nitrogen alone without additives

2010

97. Artificial vagina (AV) preparation for bull semen collection requires careful regulation of:
(A) Only the internal pressure within the device
(B) Internal pressure and temperature levels
(C) Only the temperature of the inner lining
(D) The ambient lighting in the collection room

2006

98. In a semen extender, egg yolk is primarily added to provide:
(A) An acidic environment to immobilize sperm for storage
(B) A substitute for seminal plasma proteins in the mixture
(C) Antibacterial properties to protect the sample from infection
(D) Protection to spermatozoa against the effects of cold shock

2015

99. The ideal storage temperature for cryopreserved bull semen in liquid nitrogen is:
(A) $-273^{\circ}C$
(B) $-196^{\circ}C$
(C) $-100^{\circ}C$
(D) $-79^{\circ}C$

2010

100. Match the following biotechnological tools in List I with their primary applications in List II.
List I: (Biotechnological Tools)
P. Marker-Assisted Selection
Q. Embryo Sexing
R. Somatic Cell Nuclear Transfer
S. CRISPR/Cas9
List II: (Primary Applications)
1. Precise editing of specific genomic sequences
2. Producing offspring of a predetermined gender
3. Cloning an adult animal
4. Early selection based on DNA variations linked to traits
(A) P-4, Q-2, R-3, S-1
(B) P-1, Q-4, R-2, S-3
(C) P-4, Q-1, R-3, S-2
(D) P-3, Q-2, R-1, S-4

2024

101. Which grading system is commonly used to evaluate bovine embryos before transfer or freezing?
(A) Grade A, B, C based on color alone observed under light
(B) Numerical grades from 1 (excellent) to 4 (dead/degenerating)
(C) The Apgar score used for assessing newborn calf vitality
(D) The Body Condition Score of the donor cow at flushing time

2015

102. In MOET, flushing of embryos is typically performed using a specialized catheter known as:
(A) Standard Foley catheter used in human medical procedures
(B) Urethral catheter designed for small animal veterinary use
(C) Intravenous cannula used for fluid administration in cattle
(D) Two-way or three-way foley-like catheter for embryo recovery

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2009

65. Avikalin, a synthetic sheep breed developed at CSWRI, is a cross between:
(A) Rambouillet and Chokla
(B) Rambouillet and Malpura
(C) Merino and Nali
(D) Corriedale and Sonadi

2018

66. ILI-80 is a high-yielding synthetic commercial layer poultry bird developed by:
(A) Project Directorate on Poultry (now DPR), Hyderabad
(B) Kerala Veterinary and Animal Sciences University
(C) Venkateshwara Hatcheries
(D) Central Avian Research Institute (CARI)

2016

67. The phenomenon where the phenotypic value of crossbred offspring exceeds the average of the parental breeds is termed:
(A) Heterosis
(B) Inbreeding depression
(C) Epistasis
(D) Recombination loss

2003

68. Which of the following formulas correctly calculates Selection Differential (S)?
(A) $S = \dfrac{\text{Mean of population}}{\text{Mean of selected parent sin the group}}$
(B) S = Heritability multiplied by the phenotypic standard deviation value
(C) S = Mean of selected parents − Mean of the unselected population
(D) S = Generation interval divided by the total genetic variance value

2019

69. Progeny testing is highly justified for traits that:
(A) Are sex-limited, such as milk production in dairy cattle
(B) Can be measured early in the life of the animal candidate
(C) Are observed to be highly heritable in the specific population
(D) Have extremely high penetrance and simple mendelian inheritance

2008

70. Consider the following statements regarding genetic progress:
I. Decreasing the generation interval increases genetic progress per year.
II. Increasing selection intensity increases genetic progress.
III. High environmental variance maximizes genetic progress.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I only

2003

71. Outbreeding is fundamentally defined as mating individuals that:
(A) Belong to the same immediate family or close genetic lineage
(B) Are less related than the average relationship of the population
(C) Share exactly the same phenotype for all commercially relevant traits
(D) Have been cloned from the same embryo in a laboratory setting

2005

72. Crisscrossing is a crossbreeding system that typically involves:
(A) Three or more breeds used in a rotational manner over time
(B) Mating a crossbred female back to a non-descript male sire
(C) Two breeds alternated continuously over subsequent generations
(D) Mating purebred parents only once for terminal market production

2014

73. Which of the following traits in poultry is typically least affected by inbreeding depression?
(A) Hatchability
(B) Egg production
(C) Early chick survival
(D) Comb type

2002

74. If the genetic correlation between Trait X and Trait Y is positive and high, selecting for Trait X will:
(A) Simultaneously increase the value of Trait Y in the offspring
(B) Decrease the value of Trait Y through negative pleiotropy effects
(C) Have no effect on Trait Y due to independent gene assortment
(D) Reduce the heritability of both traits in the subsequent generation

NODIA

2012

113. The main technical bottleneck in implementing Marker-Assisted Selection (MAS) for quantitative traits like milk yield is:
(A) Lack of DNA extraction methods for large scale field testing
(B) Many genes with small effects make robust marker ID difficult
(C) Markers mutate too rapidly within a single animal generation
(D) Ethical bans on DNA testing for all commercial livestock species

2011

114. Why is the adoption of pure exotic cattle breeds like Holstein Friesian challenging in the rural Indian context?
(A) They produce less milk than indigenous breeds in all trials
(B) They are highly aggressive and difficult for farmers to handle
(C) Their milk contains toxic proteins unfit for human consumption
(D) They require high inputs and are susceptible to heat and disease

2005

115. A farmer wishes to calculate the selection index for a boar based on growth rate, backfat thickness, and feed conversion ratio. This method ensures:
(A) Economic improvement across all multiple traits simultaneously
(B) Maximum improvement in a single trait while ignoring others
(C) Selection based entirely on visual appeal of the male animal
(D) That only non-additive genetic variance is utilized in selection

2015

116. Which of the following is a classic genetic consequence of intensive inbreeding?
(A) Masking of deleterious recessive alleles from phenotypic expression
(B) Increase in the frequency of heterozygotes in the population
(C) Fixation of alleles and increased homozygosity levels
(D) Introduction of novel genetic variation through targeted mutation

2011

117. When the phenotypic correlation between two traits is low but the genetic correlation is highly positive, what does this imply?
(A) Environment masks the true genetic relationship of the traits
(B) Pleiotropy does not exist for these specific traits in the herd
(C) Selecting for one trait will severely decrease the other trait
(D) Both traits have extremely high heritability in this population

2001

118. The concept of "repeatability" is highly applicable to traits such as:
(A) Birth weight
(B) Coat color
(C) Pre-weaning mortality
(D) Milk yield across multiple lactations

2019

119. A breed of livestock is generally defined as a group of animals that:
(A) Have identical genomes across all individuals in the group
(B) Share common ancestry and distinct, uniform, heritable traits
(C) Live in the exact same geographical location regardless of look
(D) Belong to completely different species but interbreed successfully

2013

120. Consider the following statements concerning genetic parameters:
I. Heritability values range from 0 to 1.
II. A genetic correlation can range from -1 to +1.
III. Repeatability is always less than heritability.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I, II and III

2018

121. Under the NBAGR classification, a breed is considered "endangered" primarily based on:
(A) Its milk production potential dropping below the national average
(B) Its crossbreeding with exotic breeds in commercial dairy units
(C) Its migration to a neighboring state for better grazing lands
(D) Drastic reduction in breeding individuals within the native tract

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2006

85. The term "non-descript" cattle refers to animals that:
(A) Lack distinct breed features and have mixed genetic backgrounds
(B) Are highly purebred but lack official registration documents
(C) Cannot vocalize or moo due to a specific genetic mutation
(D) Have been genetically edited for increased production traits

2019

86. When grading-up a non-descript population, what percentage of the exotic breed's inheritance is expected in the third generation (F3) offspring?
(A) 50%
(B) 75%
(C) 87.5%
(D) 93.75%

2018

87. For the genetic improvement of milk production in buffaloes, which breed is most extensively used as an improver breed across India?
(A) Surti
(B) Murrah
(C) Jaffarabadi
(D) Toda

2014

88. Under the intensive sheep production system, breeding programs primarily prioritize traits related to:
(A) Walking long distances between grazing sites in arid regions
(B) Resistance to prolonged starvation during seasonal drought periods
(C) Rapid growth rate and efficient conversion of high-quality feed
(D) Extremely fine wool for hand-spinning by traditional artisans

2003

89. The Garole sheep, originating from the Sundarbans region, contributed which important gene to the development of prolific sheep strains worldwide?
(A) The Myostatin gene related to double muscling in meat breeds
(B) The Callipyge gene associated with increased hindquarter muscle
(C) The Halothane gene linked to stress susceptibility in swine
(D) The Booroola (FecB) gene for increased ovulation rate

2015

90. Consider the following statements regarding the conservation of Animal Genetic Resources:
I. In-situ conservation maintains the breed within its natural habitat.
II. Semen cryopreservation is an in-situ method.
III. Breed societies facilitate ex-situ conservation exclusively.
IV. Ex-situ in-vivo conservation involves maintaining live herds outside their native tract.
V. DNA banking provides immediate live animals for commercial farming.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and IV
(C) II, III and V
(D) I, IV and V

2019

91. Synthetic parent lines in poultry are generated by crossing multiple lines to:
(A) Reduce total genetic variance within the breeding population
(B) Combine desirable traits and maintain a broad genetic base
(C) Ensure all offspring are perfectly homozygous for all traits
(D) Produce sterile layers for commercial egg production markets

2013

92. The Vanaraja bird, developed by DPR Hyderabad, is best characterized as:
(A) A pure White Leghorn strain designed for intensive caging
(B) A dual-purpose, colored bird for free-range backyard farming
(C) A highly inbred line of indigenous Aseel for conservation
(D) A commercial broiler requiring climate-controlled housing units

2008

93. In an Open Nucleus Breeding System (ONBS), how are the best females in the base population utilized?
(A) They become dams of nucleus sires by moving to the nucleus herd
(B) They are immediately culled to prevent competition with the nucleus
(C) They are exclusively used for natural service in the base herd only
(D) They are sterilized and sold for meat production in the local market

NODIA

(D) Coat color inheritance

2008

132. The Marwari horse is distinctly recognized by its:
(A) Exceptionally short legs
(B) Heavy draft capability
(C) Inwardly curved and touching ear tips
(D) Pure white coat color at birth

2024

133. Which organization is primarily responsible for the conservation and research of equines in India?
(A) NRCE, Hisar
(B) CSWRI, Avikanagar
(C) NDRI, Karnal
(D) CARI, Izatnagar

2025

134. Poultry breeding for meat production (broilers) utilizes a selection index heavily weighted toward:
(A) Egg mass and shell thickness
(B) Age at sexual maturity
(C) Plumage color
(D) Six-week body weight and feed conversion ratio

2012

135. Arrange the following breeding milestones in the development of a synthetic poultry line in the correct procedural order:
I. Multi-generation random mating to stabilize the synthetic population
II. Crossing of selected founder lines
III. Evaluation of founder lines for combining ability
IV. Intensive selection within the synthetic population for desired traits
(A) II, III, I, IV
(B) III, II, I, IV
(C) III, I, II, IV
(D) I, II, III, IV

2023

136. An essential requirement for the success of an Open Nucleus Breeding System (ONBS) is:
(A) Complete ban on AI
(B) Restricting the nucleus herd to less than 10 animals
(C) Accurate identification and recording in the base population
(D) Preventing any movement of animals out of the nucleus

2006

137. Which of the following defines an in-situ conservation strategy for AnGR?
(A) Storing embryos in a central repository
(B) Keeping animals in urban zoos
(C) Preserving DNA samples in a laboratory
(D) Maintaining breeds in their native environments by local communities

2010

138. The primary objective of establishing "Breed Societies" in India is to:
(A) Bring together farmers to maintain purity and record performance
(B) Sell imported exotic semen
(C) Promote the slaughter of non-descript animals
(D) Monopolize the milk market in urban areas

2011

139. Liquid nitrogen (LN_2) used in semen cryopreservation maintains a stable temperature due to its:
(A) High boiling point
(B) Boiling point of $-196^{\circ}C$ at atmospheric pressure
(C) Endothermic expansion properties
(D) Chemical reaction with the semen extender

2004

140. Consider the following statements regarding Ex-situ conservation:
I. Semen cryopreservation captures only half the genetic diversity of an individual.
II. Embryo banking captures the entire genetic makeup of both parents.
III. Somatic cell banking is a viable path for breed restoration via cloning.
IV. DNA repositories are helpful for future genomic studies.
V. Cryopreservation halts all biological degradation processes.
Which of the above statement(s) is/are correct?
(A) I, II, III, IV and V
(B) III only
(C) IV and V
(D) II and III

NODIA

2016

141. The CASA system used in modern andrology laboratories stands for:
(A) Computer-Assisted Sperm Analysis
(B) Cyto-Analytical Semen Assessment
(C) Centrifugation And Sperm Aspiration
(D) Cryogenic Application for Semen Archiving

2014

122. The Vechur cattle, known for being one of the smallest cattle breeds in the world, belongs to which state?
(A) Kerala
(B) Tamil Nadu
(C) Karnataka
(D) Andhra Pradesh

2013

123. The indigenous chicken breed Kadaknath is famous for its:
(A) Exceptional egg-laying capacity surpassing White Leghorn birds
(B) Black meat valued for nutritional and medicinal properties
(C) Extremely heavy body weight for rapid broiler production units
(D) Pure white plumage and blue eggshells found in wild types

2006

124. The failure of several initial crossbreeding programs in India was partly due to ignoring the importance of:
(A) Artificial insemination training for local village technicians
(B) Adjusting management and feeding to suit crossbred needs
(C) The color of the crossbred animals in relation to heat absorption
(D) Building massive concrete barns in every small village center

2008

125. Select the correct chronological sequence of steps in a standard MOET protocol in cattle:
(A) Superovulation → AI → Embryo recovery → Embryo evaluation → Transfer to recipients
(B) AI → Superovulation → Embryo recovery → Transfer to recipients → Embryo evaluation
(C) Embryo recovery → Superovulation → AI → Embryo evaluation → Transfer to recipients
(D) Superovulation → Embryo recovery → AI → Embryo evaluation → Transfer to recipients

2019

126. A serious institutional bottleneck for genomic selection in Indian dairy cattle is:
(A) The lack of high-performance computing facilities globally today
(B) The high cost of liquid nitrogen for long-term sample storage
(C) Lack of large, well-recorded reference populations with phenotypes
(D) The illegality of DNA extraction from bovines in several states

2017

127. Grading-up is generally recommended up to what level of exotic inheritance to balance production and adaptability in tropical climates?
(A) 100%
(B) 87.5%
(C) 50% to 62.5%
(D) 12.5%

2010

128. For breeding programs in harsh, extensive grazing systems, the best strategy for indigenous sheep is:
(A) Continuous crossbreeding with highly demanding exotic breeds
(B) Feeding them strictly on concentrated feed blocks in confinement
(C) Selecting for adaptability and survival within indigenous breeds
(D) Selecting solely for maximum adult body weight in all rams

2002

129. The Deccani breed of sheep is primarily classified as:
(A) A fine wool breed
(B) A mutton and coarse carpet wool breed
(C) An exclusive dairy breed
(D) A pelt breed

2003

130. Consider the following statements concerning Indian goat breeding strategies:
I. Upgrading local stock with purebred sires of larger breeds improves meat yield.
II. Artificial insemination is as widely successful and easy in goats as in cattle.
III. Conservation of the Black Bengal goat focuses on maintaining its prolificacy.
IV. Exotic breeds like Saanen are highly resilient to tropical heat stress.
Which of the above statement(s) is/are correct?
(A) I and III
(B) II and IV
(C) I and II
(D) III and IV

2023

131. In the context of swine breeding, heterosis is usually most pronounced in which category of traits?
(A) Reproductive traits (e.g., litter size)
(B) Carcass traits (e.g., backfat thickness)
(C) Highly heritable morphological traits

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(A) Foot and Mouth Disease
(B) Swine Brucellosis
(C) Porcine Reproductive and Respiratory Syndrome (PRRS)
(D) Classical Swine Fever

2024

153. The term "synthetic breed" refers to a population that:
(A) Has been artificially synthesized in a lab without parents
(B) Is fed entirely on synthetic diets
(C) Results from cloning
(D) Is formed by crossing breeds and inter-se mating stabilization

2003

154. The Frieswal cattle was stabilized at what level of Holstein Friesian inheritance?
(A) 50%
(B) 62.5%
(C) 75%
(D) 87.5%

2025

155. Which calculation determines the Response to Selection (R)?
(A) $R = \frac{S}{h^2}$
(B) $R = h^2 \times S$
(C) $R = h^2 \times \sigma_p$
(D) $R = S \times \sigma_g$

2024

156. If a breeder culls all animals falling below a certain threshold for milk yield, and separately culls those falling below a threshold for fat percentage, this method is called:
(A) Tandem selection
(B) Independent culling levels
(C) Selection index
(D) Family selection

2015

157. Tandem selection is generally considered less efficient than a selection index because:
(A) Improving one trait at a time may cause regression in others
(B) It applies selection to all traits simultaneously
(C) It requires complex mathematical equations
(D) It only works on qualitative traits

2025

158. Under Hardy-Weinberg equilibrium, the genotypic frequencies remain constant from generation to generation provided there is:
(A) Strong directional selection
(B) Frequent mutations
(C) Random mating in a large population
(D) High rates of migration

2022

159. The primary reason outbreeding produces heterosis is because it:
(A) Eliminates all recessive alleles
(B) Decreases the environmental variance
(C) Causes mutations to occur at a higher rate
(D) Increases heterozygosity masking deleterious recessive alleles

2018

160. The following question consists of two statements, one labeled as Assertion (A) and the other as Reason (R). Examine these two statements carefully and select the correct answer using the codes given below.
Assertion (A): The genetic correlation between traits can change over multiple generations of intense selection.
Reason (R): Selection alters allele frequencies, changing the pleiotropic effects and linkage disequilibria that underpin genetic correlations.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

NODIA

2021

161. Estimation of heritability via the paternal half-sib correlation method requires:
(A) Mating identical twins
(B) A hierarchical mating design with sires mated to multiple dams
(C) Only measuring the performance of the dams
(D) Completely random mating with no pedigree records

2017

162. The standard error of a heritability estimate generally decreases when:
(A) The number of sires and progeny per sire decreases
(B) The environmental variance increases dramatically
(C) Pedigree errors are introduced

(B) $75\mu m$
(C) $500\mu m$
(D) $1mm$

2021

229. Ovum Pick-Up (OPU) can be performed on pregnant cows during the first trimester. This is advantageous because:
(A) It maximizes superior female utility even during gestation
(B) It induces abortion safely
(C) The oocytes are larger during pregnancy
(D) The oocytes do not require fertilization

2004

230. A major technical limitation of In-Vitro Fertilization (IVF) in farm animals compared to in-vivo embryo production is:
(A) The inability to use frozen semen
(B) The requirement of millions of oocytes per session
(C) The resulting embryos always being male
(D) Lower pregnancy rates and incidence of large offspring syndrome

2006

231. The primary advantage of using Microsatellite markers over RFLPs in early genetic diversity studies was that microsatellites are:
(A) Monomorphic
(B) Highly polymorphic and multi-allelic
(C) Bi-allelic
(D) Composed entirely of RNA

2006

232. In QTL mapping, the term "LOD score" refers to:
(A) Level of Dominance, indicating gene action
(B) Length of DNA sequenced
(C) Logarithm of Odds, a statistical estimate of linkage
(D) Limit of Detection for a trait

2012

233. The application of Marker-Assisted Selection (MAS) has been particularly successful in dairy cattle for traits influenced by a few major genes, such as:
(A) Somatic cell score
(B) Overall milk volume
(C) Heat tolerance
(D) Milk protein variants like Kappa-casein alleles

2007

234. Genomic selection effectively bypasses the need for which traditional, time-consuming breeding step in dairy cattle?
(A) Progeny testing of young sires
(B) Artificial Insemination
(C) Measuring milk yield of cows
(D) Recording pedigree

2019

235. The reliability of Genomic Estimated Breeding Values (GEBV) drops significantly if applied to:
(A) Animals highly related to the reference population
(B) Animals of a completely different breed from the reference
(C) Traits with high heritability
(D) Large reference populations

2013

236. The first successful mammalian clone from an adult somatic cell was Dolly the sheep. Which cell type was used as the nuclear donor?
(A) Embryonic stem cell
(B) Mammary gland epithelial cell
(C) Fibroblast from the ear
(D) Sperm cell

2019

237. In CRISPR/Cas9 gene editing, the "Cas9" component functions as:
(A) An endonuclease that cleaves the target DNA
(B) A guide RNA
(C) A DNA ligase
(D) A reverse transcriptase

2001

238. The ILI-80 poultry strain is primarily utilized for:
(A) Commercial broiler production
(B) Cockfighting
(C) High volume commercial egg production
(D) Ornamental exhibition

2003

239. The Frieswal cattle breed was developed with the objective of stabilizing the population to produce a minimum milk yield of:
(A) 1000 kg per lactation
(B) 2000 kg per lactation
(C) 4000 kg per lactation
(D) 10000 kg per lactation

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2001

174. Which indigenous goat breed is predominantly recognized as a dual-purpose breed (meat and milk) found in the semi-arid tracts of Rajasthan?
(A) Black Bengal
(B) Ganjam
(C) Sirohi
(D) Chegu

2007

175. What is the major genetic advantage of using the Large White Yorkshire in swine crossbreeding programs in India?
(A) High adaptability to scavenging
(B) Dark skin color preventing sunburn
(C) Small mature body size suitable for smallholdings
(D) Large litter size, high growth, and excellent mothering

2025

176. The conservation of the double-humped camel is critical primarily because:
(A) They are the highest milk-producing camels globally
(B) Their population has exploded to unmanageable numbers
(C) They are the only draught animals in the cold Nubra valley
(D) They carry genes for extreme heat tolerance

2006

177. The term "sex-linked trait" in poultry breeding refers to a trait that:
(A) Only appears in females
(B) Is controlled by genes located on the sex chromosomes (Z or W)
(C) Is expressed differently depending on ambient temperature
(D) Can be altered by feeding specific hormones

2014

178. A classic example of utilizing a sex-linked trait in commercial poultry production is:
(A) Selecting for maximum breast meat yield
(B) Controlling eggshell color
(C) Improving resistance to Marek's disease
(D) Auto-sexing of day-old chicks based on feather or color

2013

179. In an ONBS, the base population provides which of the following to the nucleus herd?
(A) Selected superior females
(B) Selected superior males only
(C) All unselected cull animals
(D) Extender fluid for AI

NODIA

2007

180. A Gaushala acting as an in-situ conservation center is most effective when it:
(A) Keeps only aged, unproductive, mixed-breed animals
(B) Castrates all males on the premises
(C) Maintains purebred indigenous herds with scientific recording
(D) Avoids any veterinary intervention

2025

181. For establishing a DNA repository for long-term conservation, the most common source material collected from farm animals is:
(A) Blood samples or hair follicles
(B) Hair clippings without roots
(C) Hoof trimmings
(D) Horn clippings

2013

182. A critical property of a good semen extender is its ability to:
(A) Rapidly decrease the pH to 4.0
(B) Provide a hyperosmotic environment to shrink sperm cells permanently
(C) Maintain motility through excessive volume
(D) Provide energy, buffer pH, and protect against cold shock

2025

183. The process of gradually cooling semen from room temperature to 5°C before freezing is called:
(A) Thawing
(B) Equilibration
(C) Vitrification
(D) Pasteurization

2023

184. Vitrification is an alternative cryopreservation technique for embryos that differs from slow-freezing by:
(A) Using extremely low concentrations of cryoprotectants
(B) Using boiling water instead of liquid nitrogen
(C) Ultra-rapid cooling to form a glass-like state
(D) Taking several days to complete the cooling process

2023

185. To recover embryos from a donor cow, the flushing medium must be:
(A) Highly acidic
(B) Pure distilled water

2008

206. An indigenous sheep breed highly valued for producing fine quality carpet wool and possessing a characteristic black or brown face is the:
(A) Nellore
(B) Gaddi
(C) Marwari
(D) Mandya

2013

207. Which native pig breed of India is primarily reared by the Mising tribe in Assam and is characterized by a relatively smaller body size and early sexual maturity?
(A) Mali
(B) Niang Megha
(C) Agonda Goan
(D) Doom

2012

208. A major objective of the National Dairy Plan Phase I (NDP-I) was to:
(A) Export live indigenous cattle to Europe
(B) Replace all buffaloes with exotic cows
(C) Meet demand via improved bulls and scientific rations
(D) Eradicate artificial insemination

2011

209. The implementation of field progeny testing faces the primary challenge of:
(A) Procuring enough semen from the bulls
(B) Recording daughter milk yields across numerous smallholder farms
(C) Farmers rejecting the use of frozen semen
(D) Bulls failing to reach puberty

2005

210. The following question consists of two statements, one labeled as Assertion (A) and the other as Reason (R). Examine these two statements carefully and select the correct answer using the codes given below.
Assertion (A): In India, crossbreeding of cattle is generally restricted to areas with adequate feed, fodder, and healthcare infrastructure.
Reason (R): Crossbred cattle have higher maintenance requirements and lower disease resistance compared to indigenous cattle.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2011

211. When formulating a breeding strategy for indigenous draft cattle breeds like Nagori, the most appropriate approach is:
(A) Selective breeding for traits related to draught power and endurance
(B) Crossbreeding with Holstein Friesian
(C) Upgrading with Murrah buffaloes
(D) Selecting solely for milk yield

2023

212. Grading-up non-descript sheep in Rajasthan using purebred Rambouillet rams aimed to improve:
(A) Mutton quality only
(B) The milk production of the ewes
(C) Fine wool yield and quality for apparel
(D) The size of the horns

2014

213. The strategy of crossing two indigenous sheep breeds to combine the fast growth of one and the adaptability of another to create a new synthetic strain is an example of:
(A) Crossbreeding for synthesis
(B) Grading-up
(C) Outcrossing
(D) Linebreeding

2017

214. Which goat breed is frequently utilized as an improver breed in grading-up programs for milk production in the North-Western semi-arid zones of India?
(A) Black Bengal
(B) Barbari
(C) Ganjam
(D) Jamunapari

2009

215. The "Chegu" and "Changthangi" goat breeds are predominantly maintained for the production of:
(A) High-quality leather
(B) Pashmina fiber
(C) Heavy meat carcasses
(D) Commercial cheese

2004

216. In swine breeding, the creation of a three-way cross (e.g., mating a Yorkshire $\times$ Landrace crossbred sow to a Duroc boar) maximizes:
(A) Individual heterosis only
(B) Maternal heterosis only
(C) Both maternal and individual heterosis
(D) Inbreeding coefficient

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trait threshold
(D) Ignoring all economic weights

2005

196. The expected response to selection will be zero if:
(A) The selection intensity is very high
(B) The generation interval is short
(C) The heritability of the trait is zero
(D) The phenotypic variance is large

2018

197. Pedigree selection is generally preferred over individual selection when:
(A) The individual is young or the trait is sex-limited
(B) The trait has very high heritability
(C) The individual has already completed its productive life
(D) The pedigree records are completely unknown

2006

198. In breeding coefficient (F) is defined as the probability that:
(A) An animal will be born with a defect
(B) The animal is related to the sire
(C) A population will become extinct
(D) Alleles at a locus are identical by descent

2021

199. Crossbreeding Bos taurus (exotic) with Bos indicus (indigenous) cattle generally yields higher heterosis than crossing two Bos taurus breeds because:
(A) Bos taurus and Bos indicus belong to different species entirely
(B) Greater genetic divergence leads to higher non-additive effects
(C) Bos indicus possesses no dominant genes
(D) Bos taurus is highly inbred

2004

200. Match the trait category in List I with its typical level of heritability in List II.
List I: (Trait Category)
P. Reproductive traits
Q. Production traits
R. Product quality traits
S. Morphological traits
List II: (Heritability Level)
1. Low (< 0.2)
2. Moderate ($0.2 - 0.4$)
3. High (> 0.4)
4. Very High (often qualitative/mendelian)
(A) P-1, Q-2, R-3, S-4
(B) P-2, Q-3, R-1, S-4
(C) P-1, Q-3, R-2, S-4
(D) P-3, Q-2, R-1, S-4

2025

201. Which formula is utilized to calculate the genetic correlation (r_g) between trait X and trait Y?
(A) $\dfrac{\text{Covariance}(X, Y)}{\text{Variance}(X) \times \text{Variance}(Y)}$
(B) $\dfrac{\text{Heritability}(X)}{\text{Heritability}(Y)}$
(C) $\text{Phenotypic Variance}(X) + \text{Phenotypic Variance}(Y)$
(D) $\dfrac{\text{Genetic Covariance}(X, Y)}{\sqrt{\text{Gen.Var.}X \times \text{Gen.Var.}Y}}$

NODIA

2023

202. Repeatability provides an estimate of:
(A) Future performance based on past performance of an individual
(B) The performance of offspring
(C) The degree of inbreeding
(D) The probability of mutation

2003

203. For evaluation and characterization of animal genetic resources, descriptors are used. What are descriptors?
(A) The names of the farmers owning the animals
(B) Standardized phenotypic, reproductive, and geographic parameters
(C) The monetary value of the breed
(D) The list of diseases the animal is immune to

2024

204. The Siri breed of cattle, adapted to the steep slopes and cold climate, is predominantly found in:
(A) Rajasthan
(B) Sikkim and Darjeeling
(C) Kerala
(D) Punjab

2021

205. Which breed of buffalo, originating from the swamps of North-East India, is characterized by 48 chromosomes instead of the standard 50 found in riverine buffaloes?
(A) Luit
(B) Chilika
(C) Murrah
(D) Banni

(C) Rich in heavy metals
(D) Isotonic, sterile, and supplemented with protein

2003

186. Which of the following defines an oocyte graded as suitable for In-Vitro Fertilization (IVF)?
(A) Oocyte with compact cumulus layers and homogenous cytoplasm
(B) Naked oocyte completely stripped of cumulus cells
(C) Oocyte with fragmented cytoplasm
(D) Oocyte that has already divided into two cells

2014

187. The identification of a QTL implies that the marker being used is:
(A) The exact gene causing the trait variation
(B) Linked in close physical proximity to the controlling gene(s)
(C) Completely unlinked to the trait but statistically similar by chance
(D) A dominant allele

2022

188. A major benefit of Marker-Assisted Selection (MAS) is most evident when selecting for traits that are:
(A) Highly heritable and easy to measure in both sexes
(B) Difficult to measure, sex-limited, or late-expressed
(C) Expressed early in life with high heritability
(D) Controlled entirely by environmental factors

2010

189. Genomic Selection utilizes a statistical model trained on the reference population. The key equation essentially estimates:
(A) The sum of the additive effects of all SNPs across the genome
(B) The exact number of genes an animal has
(C) The degree of inbreeding in the population
(D) The environmental variance only

2025

190. Consider the following statements regarding reproductive biotechnology:
I. ICSI bypasses the need for sperm to penetrate the zona pellucida naturally.
II. Embryo splitting can produce identical twins.
III. OPU can be performed repeatedly on live animals.
IV. SCNT requires an enucleated recipient oocyte.
V. IVM stands for In Vitro Maturation.
Which of the above statement(s) is/are correct?
(A) I and II
(B) III only
(C) I, II, III, IV and V
(D) II and III

2019

191. Somatic Cell Nuclear Transfer (SCNT) has a notoriously low efficiency rate. A major cause of this inefficiency is:
(A) Complete absence of DNA in somatic cells
(B) The extreme size of the somatic cell compared to the oocyte
(C) Rejection by the recipient mother's immune system
(D) Aberrant epigenetic reprogramming of the somatic nucleus

2015

192. Transgenic animals have been successfully created using which of the following classical methods?
(A) Artificial insemination with normal semen
(B) Feeding genetically modified crops to pregnant females
(C) Pronuclear microinjection of DNA into a zygote
(D) Selective breeding

2021

193. The synthetic sheep breed "Bharat Merino" was primarily developed to:
(A) Produce extremely coarse carpet wool
(B) Serve as a substitute for imported fine wool
(C) Produce heavy carcasses for export
(D) Thrive in the extremely hot and humid coastal plains

2013

194. The Karan Fries cattle breed typically contains what percentage of exotic inheritance?
(A) 25%
(B) 50%
(C) 62.5%
(D) 100%

2025

195. What is the fundamental principle behind calculating a Selection Index?
(A) Maximizing correlation between index and breeding value
(B) Selecting based on the physical appearance of the animal only
(C) Eliminating animals that fail a single specific

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2007

217. The primary conservation strategy for the rare Zanskari pony involves:
(A) Exporting them to desert climates
(B) Crossbreeding them with heavy draft horses
(C) Utilizing them exclusively for meat
(D) In-situ preservation and selective breeding in Ladakh

2002

218. The "RIR" (Rhode Island Red) chicken breed is historically classified as a:
(A) Dual-purpose breed
(B) Light breed for egg production only
(C) Heavy breed for meat production only
(D) Game bird

2019

219. In poultry breeding, "reciprocal recurrent selection" is designed specifically to improve:
(A) Additive genetic variance only
(B) Combining ability to maximize crossbred performance
(C) Plumage color consistency
(D) Adult bird survivability to old age

2024

220. The concept of an Open Nucleus Breeding System (ONBS) was primarily developed to counter which specific disadvantage of a Closed Nucleus Breeding System?
(A) High cost of feeding
(B) Accumulation of inbreeding and lower female selection intensity
(C) The necessity of natural mating
(D) The inability to use artificial insemination

2001

221. Under an ONBS scheme, if the top 10% of females from the base population are brought into the nucleus, and the top males from the nucleus are used in the base, this gene flow is described as:
(A) Unidirectional downward
(B) Unidirectional upward
(C) Bidirectional
(D) Horizontal

2006

222. Gaushalas can significantly enhance in-situ conservation efforts if they transition from merely being hospices for old cattle to:
(A) Abattoirs
(B) Factories for synthetic milk
(C) Centers for scientific breeding and superior germplasm distribution
(D) Storage facilities for exotic semen

2021

223. Somatic cell banking for animal genetic resource conservation involves the cryopreservation of which cell type?
(A) Spermatozoa
(B) Unfertilized oocytes
(C) Red blood cells
(D) Fibroblasts derived from skin or ear cartilage biopsies

2003

224. During semen evaluation, the presence of "primary abnormalities" (e.g., coiled tails, pyriform heads) generally indicates a defect originating in the:
(A) Epididymis during transport
(B) Accessory sex glands
(C) Testes during spermatogenesis
(D) Artificial vagina during collection

2003

225. The most critical temperature zone where irreversible damage ("cold shock") occurs to unprotected spermatozoa during cooling is between:
(A) $37^{\circ}C$ and $25^{\circ}C$
(B) $15^{\circ}C$ and $5^{\circ}C$
(C) $0^{\circ}C$ and $-10^{\circ}C$
(D) $-100^{\circ}C$ and $-196^{\circ}C$

2015

226. In artificial insemination of cattle, the preferred site for semen deposition to optimize conception rates is the:
(A) Vagina
(B) External cervical os
(C) Tip of the uterine horn
(D) Body of the uterus past the internal cervical os

2018

227. In a superovulation protocol, FSH is typically administered via:
(A) Twice daily IM injections in declining doses over 4-5 days
(B) A single massive intravenous injection
(C) Oral feed additives
(D) Subcutaneous implants lasting a year

2013

228. During MOET, the flush fluid recovered from the donor cow is passed through a micro-filter with a pore size of approximately:
(A) $10\mu m$

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(C) The animals from becoming too small
(D) The horns from falling off

2010

252. The breeding strategy for improving wool quality in indigenous coarse-wool sheep generally involves crossing them with:
(A) Corriedale rams
(B) Rambouillet or Merino rams
(C) Suffolk rams
(D) Dorset rams

2013

253. Corriedale is often used in crossbreeding programs in India to improve which specific utility in sheep?
(A) Dual-purpose (mutton and wool)
(B) Pure fine apparel wool
(C) Prolificacy (multiple births)
(D) Milk production

2012

254. The Sirohi goat is an excellent breed for meat production, primarily native to:
(A) Kerala
(B) Assam
(C) Rajasthan
(D) Kashmir

2021

255. The Landrace pig is widely used in crossbreeding programs worldwide because of its distinct characteristics, which include:
(A) Black coat color and short body
(B) Erect ears and extreme muscling
(C) Slow growth and poor feed conversion
(D) White coat, long body, and maternal traits

2022

256. A significant challenge in conserving the local dromedary camel population in India is:
(A) Their extremely high fertility rates
(B) Their inability to survive in the desert
(C) Replacement by mechanized transport reducing functional use
(D) Their aggressive nature towards humans

2006

257. Which modern application has emerged as a potential economic savior for camel breeders in Rajasthan?
(A) Camel racing for international betting
(B) Promoting anti-diabetic therapeutic properties of camel milk
(C) Using camels for ploughing wet paddy fields
(D) Exporting camel meat to Europe

2006

258. Poultry developed for "backyard" farming must possess which critical behavioral trait that is often bred out of commercial broilers?
(A) Flightlessness
(B) Extreme docility
(C) Inability to brood
(D) Foraging ability and predator evasion

2001

259. A key advantage of using a "synthetic" breed over continuous crossbreeding is that the synthetic breed:
(A) Can be bred inter-se without maintaining parent lines
(B) Requires constantly maintaining two purebred parent lines
(C) Exhibits 100% heterosis indefinitely
(D) Never suffers from inbreeding

NODIA

2008

260. The genetic gain in an Open Nucleus Breeding System relies on the fundamental assumption that:
(A) The base population is genetically inferior in every aspect
(B) Mutation rates are higher in the base population
(C) Some base females exceed average nucleus merit
(D) AI is less effective in the nucleus

2013

261. Ex-situ conservation in the form of a live animal herd outside its natural habitat is termed:
(A) Ex-situ in-vivo
(B) Ex-situ in-vitro
(C) In-situ in-vitro
(D) Cryoconservation

2014

262. During the cryopreservation of semen, adding antibiotics to the extender is standard protocol primarily to:
(A) Enhance sperm motility
(B) Act as a cryoprotectant
(C) Buffer the pH
(D) Prevent venereal disease and control bacterial growth

2003

263. When evaluating frozen-thawed semen for AI, the minimum acceptable post-thaw progressive motility for bovine semen is typically:
(A) 10%
(B) 25%

2016

240. Which of the following best explains why "generation interval" is shorter in poultry compared to cattle?
(A) Cattle undergo a faster rate of mutation
(B) Poultry lay eggs rather than giving live birth
(C) Poultry have shorter sexual maturity and incubation periods
(D) Selection intensity is lower in poultry

2012

241. Genetic drift is a random change in allele frequencies that is most pronounced in:
(A) Very large, random-mating populations
(B) Small, isolated populations
(C) Populations undergoing intense directional selection
(D) Populations with high mutation rates

2010

242. In a progeny test for a dairy sire, the accuracy of his estimated breeding value for milk yield depends primarily on:
(A) The milk yield of his dam
(B) The physical size of the sire
(C) The number of sons he produces
(D) The number of daughters and heritability of the trait

2010

243. The mating of half-siblings results in offspring with an inbreeding coefficient (F) of:
(A) 0.50
(B) 0.25
(C) 0.125
(D) 0.0625

2023

244. When comparing the phenotypic correlation between two traits with their genetic correlation, it is possible for them to have:
(A) Exactly identical values always
(B) Only positive values
(C) Opposite signs
(D) A sum of exactly 1

2008

245. Which of the following factors does NOT affect the rate of genetic progress in a closed breeding herd?
(A) Importation of live animals from another country
(B) Heritability of the trait
(C) Selection differential
(D) Generation interval

2012

246. The Poda Thurpu cattle breed, recognized by NBAGR, is primarily known for its draught power and adaptation to the drylands of:
(A) West Bengal
(B) Himachal Pradesh
(C) Assam
(D) Telangana

2002

247. The Banni buffalo, bred by the Maldhari community in Gujarat, is specifically renowned for its:
(A) Resistance to foot and mouth disease
(B) Desert production and night grazing behavior
(C) Extraordinarily short horns
(D) Pure white_coat_color

2001

248. The primary utility of the indigenous equine breed "Spiti" is:
(A) Racing in derby events
(B) Polo matches in urban centers
(C) Carrying loads in high-altitude mountainous terrains
(D) Agricultural plowing

2016

249. Which of the following correctly describes the "Nucleus" in a structured breeding program?
(A) The commercial herds that solely produce milk or meat
(B) The abattoir where culled animals are sent
(C) The veterinary clinic managing herd health
(D) The elite herd for intensive recording and sire generation

2018

250. Which bottleneck heavily restricts the widespread adoption of MOET in Indian village conditions?
(A) Infrastructure, hormone, and synchronization requirements
(B) The low cost of the procedure
(C) The fact that indigenous cattle produce hundreds of embryos naturally
(D) A religious ban on handling embryos

2011

251. When a non-descript cattle population is graded up using Jersey bulls, the breeding policy usually aims to cap exotic inheritance at 50% to 75% to prevent:
(A) A decrease in fat percentage
(B) Breakdown in adaptability and heat tolerance

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(D) Sample size of families and individuals increases

2008

163. The Malvi breed of cattle is best classified under which utility group?
(A) Draught breed
(B) Milch breed
(C) Dual-purpose breed
(D) Exotic beef breed

2019

164. The Hallikar cattle breed, renowned for its draught capability, is native to:
(A) Gujarat
(B) Rajasthan
(C) Karnataka
(D) Uttar Pradesh

2023

165. Which of the following buffalo breeds possesses distinctive sickle-shaped horns?
(A) Surti
(B) Murrah
(C) Mehsana
(D) Nili-Ravi

2005

166. A critical reason for the decline of the purebred indigenous cattle population in India is:
(A) Their lack of draught capability
(B) The high cost of indigenous semen compared to exotic semen
(C) Their inability to adapt to the Indian climate
(D) Socio-economic shifts and mechanization reducing functional utility

2025

167. Which indigenous sheep breed of South India is widely known for its excellent meat quality and high growth rate, often used in grading up programs?
(A) Nilgiri
(B) Mandya (Bannur)
(C) Nellore
(D) Coimbatore

2024

168. The "Key Village Scheme" was eventually phased out and superseded by which more comprehensive program?
(A) Operation Flood
(B) RKVY
(C) Intensive Cattle Development Project (ICDP)
(D) National Gokul Mission

2013

169. What is a primary objective of the National Gokul Mission launched in India?
(A) To eradicate all indigenous cattle breeds
(B) To solely promote the import of Holstein Friesian cows
(C) To ban the consumption of milk
(D) To conserve indigenous bovine breeds scientifically

2018

170. Which socio-economic factor is a major bottleneck in establishing large-scale ONBS for sheep in India?
(A) Nomadic rearing practices make organized recording difficult
(B) Sheep farmers possess exceptionally large, fenced pastures
(C) There is no market demand for mutton
(D) The complete lack of indigenous sheep breeds

2018

171. A breeding policy aiming to cross non-descript cattle in hilly, high-altitude regions of India typically recommends which exotic breed for its hardiness?
(A) Holstein Friesian
(B) Jersey
(C) Brahman
(D) Charolais

2012

172. The term "grading up" implies continuous backcrossing. When is this process typically considered complete (i.e., the population is treated as purebred)?
(A) After 1 generation
(B) After 2 generations
(C) After 5 to 6 generations (reaching $> 98\%$ exotic inheritance)
(D) It is never considered complete

2001

173. Breeding programs for dual-purpose sheep in intensive systems face the challenge of:
(A) Negative correlation between wool quality and meat yield
(B) High heritability of both traits
(C) Extreme ease in measuring both traits simultaneously
(D) Lack of available exotic breeds for crossing

NODIA

(C) 40% to 50%
(D) 90%

2002

264. Superovulation in cattle primarily targets which physiological event in the ovary?
(A) Luteinization of thecal cells
(B) Destruction of the corpus luteum
(C) Rescue of follicles from atresia to reach pre-ovulatory size
(D) Halting of all follicular waves

2010

265. Embryos for transfer are ideally recovered at which developmental stage to ensure the highest survival rate post-transfer?
(A) 2-cell stage
(B) 8-cell stage
(C) Hatched blastocyst
(D) Morula to blastocyst stage

2009

266. "Sex-sorted semen" in dairy cattle is produced by utilizing flow cytometry to separate sperm based on:
(A) Differences in DNA content between X and Y sperm
(B) The difference in motility between X and Y bearing sperm
(C) The difference in the length of the sperm tail
(D) The response of sperm to acidic environments

2021

267. What is the main drawback of using sex-sorted semen in cattle?
(A) It guarantees 100% male calves
(B) Lower conception rates compared to conventional semen
(C) It causes severe genetic mutations
(D) It requires surgical insemination

2017

268. Single Nucleotide Polymorphisms (SNPs) are the preferred markers for Genomic Selection because they are:
(A) Found exclusively in coding regions
(B) Abundant, stable, and easily genotyped via chips
(C) Highly unstable and mutate rapidly
(D) Only found in ex-situ conserved breeds

2023

269. The "reference population" in genomic selection is crucial because it is the group where:
(A) Genotypes and phenotypes are used to estimate SNP effects
(B) Only genotypes are collected
(C) Only phenotypes are collected
(D) Embryos are flushed and stored

2019

270. CRISPR/Cas9 differs from older gene editing technologies primarily in its:
(A) Reliance on proteins to find the target DNA sequence
(B) Inability to cause double-strand breaks
(C) Use of a customizable RNA guide for targeting
(D) Restriction to only working in plant cells

2025

271. Transgenic animals engineered to secrete valuable pharmaceuticals in their milk use promoters specific to which tissue?
(A) Liver
(B) Skeletal muscle
(C) Kidney
(D) Mammary gland

2025

272. The crossbred cattle strain "Sunandini" was created as part of the bilateral project between the Government of India and:
(A) Denmark
(B) The Netherlands
(C) Switzerland
(D) Australia

2018

273. The "Avikalin" sheep breed synthesizes the fine wool characteristics of Rambouillet with the hardiness and carpet wool traits of the:
(A) Chokla
(B) Malpura
(C) Nali
(D) Magra

2005

274. In quantitative genetics, the total phenotypic variance (V_P) is partitioned primarily into:
(A) Additive variance and Dominance variance only
(B) Epistatic variance and Mutation variance
(C) Selection variance and Drift variance
(D) Genetic variance (V_G) and Environmental variance (V_E)

2022

275. A high selection intensity implies that:
(A) A very small, top proportion of the population is selected
(B) A very large proportion of the population is

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46. (C) Local pastoralist participation and ownership in native tracts
Community-based conservation of animal genetic resources relies on the active participation and ownership of local pastoralists within their native tracts. This approach recognizes that the survival of indigenous breeds is closely linked to the traditional knowledge and livelihoods of the communities that keep them. It focuses on empowering local people to manage their animals sustainably in their environments.

47. (D) Gaushalas
Gaushalas are traditional Indian institutions that play an informal but important role in the in-situ conservation of indigenous cattle. Many of these centers maintain purebred herds of native breeds like Gir, Sahiwal, or Tharparkar. When managed scientifically, they serve as valuable repositories of indigenous germplasm and contribute to the preservation of genetic diversity within the local cattle population.

48. (C) Cryopreservation of semen, embryos, and somatic cells
Ex-situ conservation of animal genetic resources involves preserving genetic material outside the natural habitat of the breed. This is primarily achieved through cryopreservation, where semen, embryos, or somatic cells are stored in liquid nitrogen. This method provides a long-term backup of the breed's genetic diversity, ensuring its availability even if the live population in the field declines.

49. (B) Preventing intracellular ice formation as a cryoprotectant
In semen cryopreservation, glycerol is a crucial permeating cryoprotectant. Its primary function is to lower the freezing point of the cytoplasm and prevent the formation of lethal intracellular ice crystals during the cooling process. By dehydrating the cells and stabilizing the membranes, glycerol ensures that the spermatozoa remain viable and functional after thawing for artificial insemination.

50. (A) P-2, Q-3, R-1, S-4
Semen evaluation involves various tools to assess fertility potential. Phase-contrast microscopy is standard for determining sperm motility, while a haemocytometer or spectrophotometer measures concentration. Sperm viability is typically checked using eosin-nigrosin stain, which identifies dead cells. Morphology is examined using stains like Rose Bengal to detect abnormalities. These parameters collectively ensure the quality of semen used in artificial insemination.

51. (A) Follicle Stimulating Hormone (FSH)
Follicle Stimulating Hormone is the most common hormone used to induce superovulation in cattle. It stimulates the rescue of multiple follicles from atresia, allowing them to reach pre-ovulatory size simultaneously. In standard protocols, it is administered twice daily in declining doses over several days to mimic the natural physiological surge required for multiple follicle development and eventual ovulation.

52. (C) Day 6 or 7
In a standard multiple ovulation and embryo transfer program, non-surgical embryo recovery is typically performed six or seven days after the first artificial insemination. At this stage, the embryos have reached the morula or blastocyst stage and have moved from the oviduct into the uterus. This timing is ideal for successful recovery and subsequent transfer to recipient animals.

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53. (A) Ultrasound-guided transvaginal aspiration of oocytes from live animals
Ovum Pick-Up is an advanced reproductive technology that involves the ultrasound-guided transvaginal aspiration of oocytes from live donor animals. This technique allows for the repeated collection of oocytes without the need for surgical intervention. OPU can be performed frequently, providing a continuous supply of oocytes for in-vitro fertilization and accelerating the genetic improvement of high-merit females.

54. (D) Poor sperm quality or motility prevents standard in-vitro fertilization
Intracytoplasmic Sperm Injection is a specialized in-vitro fertilization technique where a single spermatozoon is directly injected into the cytoplasm of an oocyte. It is primarily used when the sperm quality or motility is too poor to achieve fertilization through standard methods. This technology enables the use of limited or low-quality germplasm to produce offspring from genetically valuable individuals.

55. (B) Phenotypic variation and molecular markers
Quantitative Trait Loci mapping is based on identifying statistical associations between phenotypic variation and molecular markers

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2021

288. To overcome the shortage of progeny-tested indigenous bulls, which modern technology is currently advocated to rapidly multiply superior genetics?
(A) Selective culling
(B) Importation of live exotic bulls
(C) Genomic selection combined with MOET
(D) Natural service using non-descript bulls

2025

289. The term "grading up" is synonymous with:
(A) Crisscrossing
(B) Top-crossing
(C) In-and-in breeding
(D) Outcrossing

2008

290. When designing a crossbreeding program for rural backyards, why are three-way crosses preferred over two-way crosses?
(A) They are cheaper to feed
(B) They eliminate the need for an exotic breed
(C) They prevent any dominant genes from expressing
(D) They exploit maternal heterosis while maintaining high individual merit

2023

291. "Rotational crossbreeding" is highly practical in commercial swine production because it:
(A) Allows farms to produce replacement gilts with heterosis
(B) Requires buying replacement females every generation
(C) Involves intense inbreeding
(D) Completely eliminates genetic variance

2019

292. In camel breeding, the Bikaneri breed is predominantly utilized for:
(A) High milk production exclusively
(B) Racing over short distances
(C) Heavy draught and transport purposes
(D) Fine wool production

2019

293. The primary reason for utilizing synthetic parent lines in modern commercial broiler production is to:
(A) Capitalize on heterosis for growth and efficiency
(B) Preserve ancient breed purity
(C) Reduce the body weight of the birds
(D) Slow down the growth rate

2002

294. Compared to other livestock species, why is genomic selection particularly highly adopted and successful in commercial dairy cattle breeding?
(A) Cows have very small genomes
(B) Cattle do not exhibit quantitative traits
(C) SNPs only exist in bovine species
(D) It drastically reduces testing costs and generation intervals

2018

295. Which chemical is the most commonly used cryoprotectant for the deep freezing of bull semen?
(A) Dimethyl sulfoxide (DMSO)
(B) Glycerol
(C) Propylene glycol
(D) Methanol

2010

296. In standard bovine artificial insemination, a single insemination dose typically contains approximately how many progressively motile spermatozoa post-thaw?
(A) 1 million
(B) 10 to 15 million
(C) 100 million
(D) 1 billion

2012

297. The process of capacitation, which sperm must undergo to successfully fertilize an oocyte, naturally occurs in the:
(A) Epididymis
(B) Seminal vesicles
(C) Testes
(D) Female reproductive tract

2012

298. Embryo transfer technology can significantly increase the selection intensity of which pathway in a breeding program?
(A) Dams to breed Sires and Dams to breed Dams
(B) Sires to breed Sires
(C) Sires to breed Dams
(D) It does not affect selection intensity

2016

299. Somatic Cell Nuclear Transfer (SCNT) involves electrofusion. What is the purpose of providing an electrical pulse during this procedure?
(A) To kill any bacteria present in the medium
(B) Cell fusion and simultaneous oocyte activation

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(C) To extract the DNA from the oocyte
(D) To sex the embryo

2016

300. Consider the following statements regarding Marker-Assisted Selection (MAS):

I. It is highly effective for monogenic traits.
II. It is least effective for traits with complex polygenic nature with many small effects.
III. It can be used for sex-limited traits.
IV. It is useful for traits that are difficult to measure phenotypically.

Which of the above statement(s) is/are correct?
(A) I and III
(B) II only
(C) II, III and IV
(D) I, II, III and IV

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****

ANSWERS

1. (B) Genetic and phenotypic parameters combined with trait economic values
The selection index method integrates multiple traits into a single numerical value to facilitate simultaneous improvement. It utilizes genetic and phenotypic parameters, including heritability and correlations, along with the relative economic importance of each trait. This approach maximizes the genetic gain of the aggregate breeding value by weighting traits according to their total economic contribution.

2. (D) Selection differential
Selection differential represents the phenotypic superiority of the chosen parents over the unselected population mean. It is a critical parameter for calculating the response to selection within a single generation. A larger differential typically leads to greater genetic progress, assuming the trait is heritable. This value is influenced by the proportion of the population selected for breeding.

3. (A) Pedigree selection
Pedigree selection involves evaluating an individual's breeding value by analyzing the performance records of its ancestors. This method is particularly valuable for traits that are not yet expressed in young animals or are sex-limited. It allows for early selection decisions before individual performance or progeny data become available, thereby reducing the generation interval within a breeding program.

4. (C) When the trait is sex-limited and possesses low heritability
Family selection is most effective when the heritability of a trait is low and the environmental variance is high. It is also particularly useful for sex-limited traits, such as milk production, where the individual itself may not express the phenotype. By using family averages, breeders can more accurately estimate the breeding value than by individual performance alone.

5. (A) $\frac{\text{Heritability} \times \text{selection differential}}{\text{generation interval}}$
Genetic progress per year is determined by multiplying the heritability of a trait by the selection differential and then dividing by the generation interval. This formula highlights that progress is maximized by selecting individuals with high phenotypic superiority and shortening the time between generations. Accurate estimation of these parameters is essential for planning efficient and sustainable livestock improvement.

6. (D) Phenotypically more similar than expected by random chance
Assortative mating is a non-random mating strategy where individuals are paired based on their phenotypic similarities or differences. Positive assortative mating involves breeding animals with similar traits, which tends to increase the phenotypic variance in the population. This method does not change gene frequencies but affects the distribution of genotypes, often leading to more extreme phenotypes in offspring.

7. (B) Crossbreeding
Crossbreeding involves mating individuals from different breeds or populations to exploit heterosis, also known as hybrid vigor. This system typically results in offspring that perform better than the average of their parents, especially for traits with low heritability like reproduction and survival. It is a fundamental tool in commercial livestock production for enhancing productivity and overall animal fitness.

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8. (C) Traits related to fitness, survival, and reproductive ability
Inbreeding depression is the reduction in performance and fitness resulting from the mating of closely related individuals. It is most severe for traits related to reproductive efficiency, viability, and survival, which are typically influenced by many genes and have low herizability. This phenomenon occurs because inbreeding increases homozygosity, which allows deleterious recessive alleles to be expressed phenotypically.

9. (D) Inbreeding
Linebreeding is a specific form of inbreeding designed to maintain a high degree of relationship to a particular admired ancestor while keeping the overall inbreeding coefficient low. It involves mating individuals within a specific lineage

28. (B) Small herd sizes and fragmentation preventing organized data collection
The socio-economic landscape of Indian livestock farming is dominated by smallholders with fragmented herd sizes. This structure makes it extremely challenging to implement organized breeding programs that require consistent data collection and pedigree recording. The high cost and logistical difficulty of managing records across millions of tiny, geographically dispersed units hinder the effective implementation of national breeding.

29. (A) Improve the genetic merit of a non-descript population by continuously mating them with sires of a pure breed
Grading-up is a breeding strategy designed to transform a non-descript population into a purebred one over several generations. It involves mating non-descript females with superior purebred sires, and then repeatedly backcrossing the offspring to sires of the same pure breed. This method rapidly increases the proportion of desirable genes from the improver breed within the local population.

30. (C) I and III
Crossbreeding in Indian cattle primarily aims to introduce exotic genes that enhance milk production and growth rates. This strategy effectively utilizes heterosis to improve productivity in the first generation. However, crossbred animals often require better management and high-quality feed compared to native breeds. It is a common method for achieving rapid genetic improvement in favorable environmental conditions.

31. (D) High-stress environments cannot support exotic crossbred individuals
Selective breeding within indigenous non-descript populations is the most appropriate strategy in regions with extreme climates or poor resources. In high-stress environments, exotic crossbred animals often fail to thrive due to poor heat tolerance and high disease susceptibility. Improving the local stock through selection preserves their natural adaptability while gradually enhancing their production potential without requiring intensive management.

32. (C) Survivability and adaptation to scarce pasture
In arid and semi-arid regions, sheep production is characterized by extensive grazing and seasonal resource scarcity. Breeding programs in these systems prioritize survivability and the ability to walk long distances on sparse pasture. Traits like heat tolerance and disease resistance are more critical than maximum growth rates, as the animals must first survive the environmental stressors to produce.

33. (B) High-quality lustrous carpet wool
The Magra sheep is a vital breed native to the Bikaner region of Rajasthan. It is specifically bred for its high-quality, lustrous carpet wool, which is internationally renowned for its durability and texture. Conservation and breeding programs for this breed focus on maintaining the unique fiber characteristics that make it essential for the traditional carpet weaving industry.

34. (D) Crossing indigenous ewes with exotic dual-purpose rams like Corriedale
Improving the dual-purpose utility of sheep in favorable zones often involves crossing indigenous ewes with exotic dual-purpose rams like the Corriedale. This strategy aims to combine the local adaptability of native sheep with the superior wool and mutton qualities of the exotic breed. The resulting crossbreds typically show improved growth rates and finer wool while maintaining reasonable survival.

35. (A) Changthangi
Pashmina fiber, one of the finest natural fibers in the world, is obtained from the undercoat of the Changthangi goat. These goats are native to the high-altitude, cold deserts of Ladakh. The extreme cold stimulates the growth of this soft, warm down, which is essential for the livelihoods of nomadic pastoralists and the traditional shawl-making industry.

36. (C) Black Bengal
The Black Bengal goat is highly regarded for its excellent meat quality and exceptional prolificacy, often producing multiple births. Native to West Bengal and surrounding eastern regions, it is a small-sized breed that matures early and is well-adapted to humid climates. These traits make it an ideal candidate for improving meat production in smallholder farming systems.

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exceeds eight percent. This breed exhibits a characteristic copper-colored coat and is well-adapted to the harsh climatic conditions and traditional management systems of its native tract.

19. (A) Magra – Purely dairy purposes
Indian sheep breeds are classified based on their primary utility in different regions. The Chokla is renowned for fine carpet wool, while the Nellore is a major mutton breed. The Garole is highly valued for its prolificacy and multiple births. However, the Magra breed is primarily utilized for producing high-quality lustrous carpet wool rather than for dairy purposes.

20. (B) Both A and R are true but R is not the correct explanation of A.
The Jamunapari is a premier dairy goat breed of India, native to the Etawah district. While it is highly valued for milk production, its classification as a dairy breed is distinct from its physical characteristics or grazing habits. The breed possesses a unique Roman nose and long, pendulous ears, and is well-adapted to the local environmental conditions.

21. (A) Niang Megha
The Niang Megha is an indigenous pig breed native to the North-Eastern hills region, specifically Meghalaya. It is well-adapted to the local climate and traditional low-input rearing systems. These pigs are valued by local communities for their hardiness and ability to produce quality meat while scavenging, making them an important component of the rural tribal economy.

22. (D) Nubra Valley, Ladakh
The Double-humped or Bactrian camel is a rare species in India, found exclusively in the cold deserts of the Nubra Valley in Ladakh. Unlike the more common dromedary camels of Rajasthan, these animals are adapted to freezing temperatures and high altitudes. They have historically served as essential pack animals for transport along the ancient Silk Road routes.

23. (B) Comprehensive cattle development via AI and healthcare in compact areas
The Key Village Scheme was the first major organized attempt at cattle development in independent India. It focused on intensive work in compact areas, providing a package of services including artificial insemination, controlled breeding, veterinary healthcare, and fodder development. The primary goal was to increase the productivity of indigenous cattle by providing superior germplasm and improved management practices.

24. (C) Insufficient feed and fodder to support crossbred requirements
The Intensive Cattle Development Project aimed to create large milk shed areas to support urban dairy plants. However, a major limitation was the gap between genetic improvement and nutritional support. Crossbred animals produced through the project had higher nutrient requirements, and the existing feed and fodder resources were often insufficient to allow these animals to reach their full potential.

25. (A) II, I, IV, III
India's livestock improvement initiatives followed a specific chronological order. The Key Village Scheme was launched in the early nineteen-fifties, followed by the Intensive Cattle Development Project in the mid-sixties. The All India Coordinated Research Project on Cattle was established later to evaluate breeding strategies. The National Dairy Plan represents a more recent, comprehensive effort to enhance dairy productivity.

26. (A) Producing high genetic merit bulls using testing and pedigree selection
The National Dairy Plan focuses on increasing milk production to meet growing demand through scientific breeding and nutrition. A central component is the production of high genetic merit bulls via organized progeny testing and pedigree selection programs. These bulls are used to produce superior semen for artificial insemination, ensuring that genetic improvement reaches millions of smallholder dairy farmers.

27. (B) Inadequate milk recording systems within unorganized rural herds
Progeny testing requires accurate performance data from the daughters of bulls being evaluated. In India, the lack of systematic milk recording in unorganized rural herds is a major technical bottleneck. Without reliable data on milk yield and lactation length, it is difficult to accurately estimate the breeding value of sires, which slows down the genetic improvement process.

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to fix desirable traits and increase uniformity. Although it is more conservative than close inbreeding, it still increases homozygosity and requires careful selection.

10. (A) P-2, Q-1, R-3, S-4
Mating systems significantly influence the genetic structure of populations. Inbreeding increases homozygosity and can expose harmful recessive alleles. Crossbreeding enhances heterozygosity and heterosis, improving fitness. Positive assortative mating pairings of similar individuals increase phenotypic variance. Conversely, negative assortative mating between dissimilar individuals reduces phenotypic variance, leading to more intermediate phenotypes while maintaining genetic diversity within the breeding herd.

11. (B) Additive genetic variance to phenotypic variance
Narrow-sense heritability is a critical genetic parameter that measures the proportion of total phenotypic variation attributable to additive genetic effects. These effects are predictable and passed directly from parents to offspring, making them the primary focus of selection programs. A higher value indicates that the phenotype is a reliable indicator of the animal's breeding value for that trait.

12. (B) One record accurately predicts future performance of the animal
Repeatability measures the correlation between multiple records of the same trait in an individual over its lifetime. A high value, such as eighty percent, indicates that the first record is a very reliable predictor of future performance. In such cases, taking additional measurements provides little extra information, allowing breeders to make accurate selection decisions early in life.

13. (A) Genetic correlation between the primary and secondary traits
Genetic correlation describes the degree to which the same genes or linked genes influence two different traits. It is essential for predicting how selection for a primary trait will indirectly change a secondary trait. This relationship helps breeders understand if improving one characteristic will lead to a desirable or undesirable correlated response in another commercially important trait.

14. (C) Increased milk yield selection tends to lower fat percentage
A negative genetic correlation between two traits indicates that genes favoring one trait tend to have an opposing effect on the other. In dairy cattle, selection focused solely on increasing total milk yield often results in a reduction of the fat percentage. Breeders must account for this antagonistic relationship when designing selection programs to maintain balanced production performance.

15. (D) Phenotypic characterization → Molecular characterization → Application submission → Evaluation by Breed Registration Committee → Gazette notification
The registration of a new livestock breed follows a rigorous protocol established by the National Bureau of Animal Genetic Resources. The process begins with comprehensive phenotypic and molecular characterization in the native tract. Once characterization is complete, an application is submitted for evaluation by the Breed Registration Committee. Successful evaluation leads to the official gazette notification of the breed.

16. (C) Documentation of unique phenotypes and a defined native tract
Registering a new breed requires clear evidence of its distinctiveness and stability over generations. Essential requirements include the documentation of unique phenotypic characteristics that differentiate it from existing breeds and the identification of a defined native tract. This process ensures that the population represents a stable genetic resource that is locally adapted and culturally significant to the region.

17. (B) Gujarat Plains and Hills Region
The Kankrej cattle breed is a heavy, majestic draught and milch breed native to the arid regions of Gujarat. It is primarily distributed within the Gujarat Plains and Hills agro-climatic zone. Known for its powerful gait and resistance to harsh conditions, it is a vital genetic resource for farmers in the Rann of Kutch and surrounding areas.

18. (D) Bhadawari
The Bhadawari buffalo is a unique indigenous breed native to the Agra and Etawah regions of Uttar Pradesh. It is highly valued for its exceptional milk fat content, which frequently

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37. (A) Upgrading with Jamunapari or Beetal within their adaptable zones
To improve milk yield in native goats while retaining environmental resilience, the most effective strategy is upgrading with superior indigenous dairy breeds like Jamunapari or Beetal. These breeds possess higher genetic potential for milk production compared to non-descript goats and share similar adaptations to the Indian climate. This approach ensures sustainable genetic gain without compromising health.

38. (D) Crossing indigenous pigs with exotic breeds like Large White Yorkshire
Genetic improvement of swine in India currently emphasizes crossing indigenous pigs with exotic breeds like the Large White Yorkshire. This strategy aims to enhance the growth rate, litter size, and feed conversion efficiency of the local stock. The resulting crossbreds are better suited for commercial pork production while still retaining some of the hardiness of the indigenous parentage.

39. (B) Dilution of native genetics due to indiscriminate crossbreeding
A major challenge in the conservation of indigenous swine is the loss of genetic purity through indiscriminate crossbreeding. Many local populations are being diluted as farmers cross them with exotic breeds to achieve faster growth without a systematic plan. This process threatens the unique genetic adaptations of native pigs, which are essential for survival in traditional low-input systems.

40. (D) I, II and IV
The Spiti pony and Marwari horse represent vital indigenous equine resources in India, adapted to high-altitude and desert regions respectively. The Kathiawari horse is specifically noted for its unique inward-curving ears. Conversely, Bactrian camels are rare and confined to the cold deserts of Ladakh, where they serve as draught animals rather than being bred for dairy production.

41. (D) Halari
The Halari donkey is a distinct breed native to the Jamnagar and Dwarka districts of Gujarat. It is characterized by its white color, superior draught power, and adaptation to arid environments. These donkeys are traditionally used by local communities for transport and heavy work, making them an important part of the rural economy in their native tract.

42. (A) A population created by crossing multiple established lines and selecting
In poultry breeding, a synthetic parent line is developed by crossing several distinct lines to combine their desirable characteristics. After the initial crosses, the population is managed through inter-se mating and intensive selection over several generations to stabilize the performance. This method creates a broad genetic base and allows for the simultaneous improvement of multiple commercially important traits.

43. (B) Colored plumage, dual-purpose utility, hardiness, and predator evasion
Breeding for backyard poultry in India focuses on traits that ensure survival and productivity in low-input environments. Key priorities include colored plumage for camouflage, dual-purpose utility for meat and eggs, and high hardiness. Additionally, behavioral traits like foraging ability and predator evasion are essential, as these birds are often reared in free-range systems with minimal protection.

44. (B) Selecting top females from the base population into the nucleus
An Open Nucleus Breeding System differs from a closed system by allowing the flow of superior genetic material from the base population back into the nucleus. This involves identifying and selecting the highest-performing females from the larger base population to be used as dams in the nucleus. This strategy increases the selection intensity and reduces the rate of inbreeding.

45. (A) Higher genetic gain and lower inbreeding than closed systems
The primary genetic advantage of an open nucleus breeding system is the potential for higher genetic gain and reduced inbreeding. By incorporating superior individuals from the base population, the scheme maintains a larger effective population size and increases the overall selection pressure. This flexibility helps in sustaining genetic progress over many generations compared to a restricted closed system.

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selected
(C) Selection is done completely at random
(D) All animals are allowed to breed

2005

276. The "generation interval" for males in a traditional dairy progeny testing scheme is typically long because:
(A) Bulls take 10 years to reach puberty
(B) Semen freezing takes several years
(C) Sires wait for daughter lactation data to prove merit
(D) Bulls must undergo extensive physical training

2013

277. The term "nick" in animal breeding refers to:
(A) Specific crosses yielding better offspring than expected
(B) A physical cut on the animal
(C) A deleterious mutation
(D) The loss of an allele due to drift

2014

278. Which of the following is a classic sign of inbreeding depression in a dairy herd?
(A) An exponential increase in milk yield
(B) A sudden change in breed color
(C) Increased adult body size
(D) Reduced conception rates and calf survivability

2024

279. The Khillar cattle breed, highly regarded for its fast, powerful draft ability, is native to the arid regions of:
(A) Punjab
(B) Maharashtra and Karnataka
(C) Odisha
(D) Tamil Nadu

2016

280. The National Bureau of Animal Genetic Resources (NBAGR) is headquartered in:
(A) New Delhi
(B) Hyderabad
(C) Karnal
(D) Izatnagar

2025

281. Phenotypic correlation (r_P) is a composite of:
(A) Additive correlation and dominance correlation
(B) Heritability and repeatability
(C) Selection differential and generation interval
(D) Genetic correlation and environmental correlation

2017

282. For a trait with a heritability of 0.10 (low), the most effective selection method is:
(A) Family selection or progeny testing
(B) Mass selection (individual phenotypic selection)
(C) Random mating
(D) Selecting solely on coat color

2008

283. The Gaddi sheep, found in Himachal Pradesh and Uttarakhand, is renowned for producing:
(A) High volumes of milk
(B) Lustrous carpet wool in migratory systems
(C) Extremely heavy mutton carcasses
(D) Pelt for luxury garments

2021

284. Which indigenous buffalo breed has a relatively lighter body and is known for its peculiar copper-colored coat?
(A) Purely dairy purposes
(B) Bhadawari
(C) Nili-Ravi
(D) Jaffarabadi

2023

285. A major bottleneck in applying systematic breeding programs for Indian swine is:
(A) Marginalized rearing with little capital for infrastructure
(B) The lack of any indigenous pig breeds
(C) Pigs do not exhibit heterosis
(D) Inability of exotic pigs to breed with indigenous pigs

2003

286. What is the fundamental goal of conserving the native "Ghungroo" pig breed?
(A) It produces completely fat-free pork
(B) It has the thickest backfat of any breed
(C) Exceptional prolificacy with large litter sizes
(D) It is an excellent draft animal

2002

287. Which institutional framework coordinates the systematic evaluation and genetic improvement of various livestock species across different states in India?
(A) World Health Organization
(B) Food and Agriculture Organization
(C) Central Zoo Authority
(D) All India Coordinated Research Projects (AICRP)

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across the genome. By studying populations with known pedigrees and phenotypes, researchers can pinpoint chromosomal regions that influence complex traits like milk yield or growth. This mapping is the foundation for marker-assisted selection, allowing breeders to identify superior animals at the DNA level.

56. (C) Microsatellites
Microsatellites are short tandem repeats of DNA that are highly polymorphic and co-dominantly inherited. They were widely used in early genetic characterization and diversity studies because they are abundant and easy to analyze via PCR. These markers allow for accurate parentage testing and the assessment of genetic variation within and between different livestock breeds and populations.

57. (D) Transfer a specific gene or QTL while recovering the recipient background
Marker-assisted introgression is a breeding strategy designed to transfer a specific desirable gene or quantitative trait locus from a donor breed into a recipient breed. The goal is to incorporate the target trait, such as disease resistance, while using molecular markers to rapidly recover the original genetic background of the recipient breed through successive generations of backcrossing.

58. (A) Uses whole-genome marker panels to predict breeding values
Genomic selection differs from traditional marker-assisted selection by utilizing whole-genome marker panels, such as single nucleotide polymorphism chips. Instead of focusing on a few significant quantitative trait loci, genomic selection estimates the combined effects of all markers across the genome to predict breeding values. This comprehensive approach provides higher accuracy for complex polygenic traits like milk production and fertility.

59. (B) Genotypic data combined with accurate phenotypic records or EBVs
A reference population is essential for genomic selection because it provides the data needed to train the prediction models. This population must have both genotypic data from marker panels and accurate phenotypic records or estimated breeding values for the traits of interest. The statistical relationships established in the reference group are then used to predict values for young candidates.

60. (A) Both A and R are true and R is the correct explanation of A.
Somatic Cell Nuclear Transfer is a sophisticated cloning technique used to produce genetically identical animals. The process involves removing the nucleus from an egg cell and replacing it with a nucleus from a specialized somatic cell. This reconstructed embryo is then stimulated to develop into a clone. It allows for the multiplication of elite individuals with highly desirable genetic traits.

61. (A) Double-strand DNA breaks
CRISPR technology utilizes a guide RNA to direct the Cas9 enzyme to a precise location in the genome. The enzyme then induces a double-strand DNA break at the target site. The cell's natural repair mechanisms can then be harnessed to introduce specific changes, such as gene knockouts or insertions, allowing for the highly precise genetic modification of livestock.

62. (C) Brown Swiss and Sahiwal
The Karan Swiss cattle breed was developed at the National Dairy Research Institute by crossing Brown Swiss bulls with Sahiwal cows. This crossbreeding program aimed to combine the high milk production potential of the Brown Swiss with the heat tolerance and disease resistance of the indigenous Sahiwal. The breed has been stabilized and successfully utilized in intensive dairy systems.

63. (D) ICAR-CIRC and Military Farms
The Frieswal cattle project is a collaborative initiative between the Central Institute for Research on Cattle and the Military Farms of India. The objective was to develop a high-yielding dairy breed suitable for diverse Indian climates by crossing Holstein Friesian with Sahiwal cattle. The project utilized the large, recorded herds at military farms to facilitate systematic breeding and evaluation.

64. (C) A mix of Brown Swiss, Jersey, and Holstein Friesian inheritance
The Sunandini breed, developed in Kerala, resulted from an extensive crossbreeding program involving local non-descript cattle. It incorporates genetic inheritance from multiple exotic dairy breeds, including Brown Swiss, Jersey, and Holstein Friesian. This composite breed was designed to provide high milk production while maintaining the adaptability required for the

NODIA

farmers to collaborate on genetic improvement and marketing.

139. (B) Boiling point of $-196^{\circ}C$ at atmospheric pressure
Liquid nitrogen is used in semen cryopreservation because it maintains a very stable temperature at its boiling point of negative one hundred and ninety-six degrees Celsius. This extreme cold effectively halts all biological activity within the sperm cells. As long as the nitrogen remains in the liquid state, the temperature will not rise, providing a secure environment for long-term storage.

140. (A) I, II, III, IV and V
Ex-situ conservation methodologies provide various levels of genetic preservation. Semen cryopreservation captures half the genetics, while embryo banking preserves the entire genome. Somatic cell banking offers the potential for restoration through cloning, and DNA repositories support genomic research. By halting biological degradation, these techniques collectively ensure that the full range of genetic diversity is available for future generations.

141. (A) Computer-Assisted Sperm Analysis
Computer-Assisted Sperm Analysis is a modern technology used in andrology laboratories to objectively evaluate semen quality. The system uses high-speed cameras and specialized software to measure various sperm parameters, including concentration, total motility, and specific velocity patterns. This provides a more accurate and reproducible assessment of sperm function compared to traditional manual microscopic evaluation by laboratory technicians.

142. (C) Following the AM-PM rule for timing the insemination relative to estrus
Optimizing fertility in artificial insemination programs requires precise timing relative to the onset of estrus. The "AM-PM rule" suggests that cows seen in heat in the morning should be inseminated in the evening, and those seen in the evening should be inseminated the following morning. This timing ensures that viable sperm are present in the reproductive tract when ovulation occurs.

143. (D) Cause luteolysis (regression of the corpus luteum)
Prostaglandin F two alpha is a hormone used in estrus synchronization protocols to induce luteolysis, which is the regression of the corpus luteum. By terminating the luteal phase of the estrous cycle, the hormone triggers a rapid decline in progesterone levels, allowing the cow to return to estrus and ovulate within a predictable timeframe for successful artificial insemination or embryo transfer.

144. (C) To provide the appropriate uterine environment for the embryo
Successful embryo transfer requires precise synchronization between the donor and the recipient cow. The recipient's uterus must be at the exact same stage of the estrous cycle as the embryo's developmental stage. This ensures that the uterine environment provides the correct hormonal and nutritional signals required for the embryo to implant and develop into a successful and healthy pregnancy.

145. (B) PCR amplification of Y-chromosome specific DNA sequences
The most reliable method for sexing bovine embryos involves taking a small biopsy and using the polymerase chain reaction to amplify DNA sequences specific to the Y-chromosome. If the Y-specific sequence is detected, the embryo is male; otherwise, it is female. This highly accurate technology allows breeders to selectively transfer embryos of the desired gender to meet production goals.

146. (D) RFLP
Restriction Fragment Length Polymorphism is a molecular marker based on variations in the DNA sequence that change the recognition sites for specific restriction enzymes. When the DNA is digested with these enzymes, the resulting fragments vary in length between individuals. While largely replaced by newer markers, RFLPs were pioneering tools for genetic mapping and identifying variations linked to important livestock traits.

147. (A) Region of DNA associated with a particular phenotypic trait
A quantitative trait locus is a specific region of the genome that contains genes influencing a complex, measurable trait like milk yield or growth. Identifying QTLs involves finding

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74. (A) Simultaneously increase the value of Trait Y in the offspring
A high positive genetic correlation between two traits implies that many of the same genes influence both. Consequently, selecting for an increase in one trait will automatically result in a simultaneous increase in the other trait. This pleiotropic effect is a valuable tool for breeders, as it allows for the indirect improvement of traits that might be difficult to measure.

75. (B) Heritability (broad sense)
Repeatability sets the upper limit for broad-sense heritability. This is because repeatability includes all genetic variance plus the permanent environmental effects that influence multiple records of an individual. Since heritability only accounts for genetic variance, it cannot exceed the repeatability value. Understanding this relationship helps breeders estimate the potential for genetic improvement through repeated observations of a trait.

76. (B) Average age of parents when offspring replacing them are born
Generation interval is defined as the average age of the parents at the time their offspring, which will replace them in the breeding herd, are born. It is a critical factor in the rate of annual genetic progress. Shorter intervals allow for more cycles of selection per unit of time, thereby accelerating the accumulation of desirable genes within the population.

77. (A) Whole genome sequencing data for molecular mapping
Phenotypic characterization focuses on the observable physical and production characteristics of a breed. This includes body biometry, such as height and girth, as well as coat color patterns and horn shapes. It also involves recording performance data for milk yield or growth. Molecular mapping and whole genome sequencing are considered separate forms of characterization that occur at the DNA level.

78. (C) Kankrej
The Kankrej cattle breed is famous for its powerful draught capacity and its majestic "Sawai Chal" or rhythmic gait. It is characterized by a prominent, broad forehead and large, lyre-shaped horns. This breed is highly resilient and serves as an important dual-purpose animal in the arid regions of Gujarat, valued for both work and milk production.

79. (D) The Nilgiri hills of Tamil Nadu
The Toda buffalo is a unique breed native to the Nilgiri hills of Tamil Nadu. It is exclusively reared by the Toda tribe in high-altitude environments. This breed is well-adapted to the hilly terrain and is characterized by its semi-wild nature and distinct horn shape. It plays a central role in the cultural and religious life of the Toda people.

80. (A) I, II and IV
India possesses diverse goat breeds adapted to specific agro-climatic zones. The Beetal is prevalent in Punjab, while the Barbari is famous for its stall-feeding suitability. The Osmanabadi is hardy and well-suited to the conditions of Maharashtra. However, the Changthangi is a pashmina-producing breed from high-altitude cold deserts, rather than a meat breed from the southern regions of India.

81. (B) Chokla
The Chokla sheep is often referred to as the "Merino of Rajasthan" because it produces the finest quality carpet wool among Indian breeds. Native to the Shekhawati region, it is highly valued for its wool quality, which has good luster and density. Breeders focus on this breed for high-value carpet production due to its superior fiber characteristics compared to other desert sheep.

82. (D) Ghungroo
The Ghungroo pig is a highly prolific indigenous breed found in the Dooars region of West Bengal. It is characterized by its large litter size, often producing more than ten piglets per farrowing. These pigs are integral to the tribal economy and are valued for their ability to thrive on local feed resources and their resistance to common tropical diseases.

83. (A) Farmers' poor adoption of crossbred males for draught work
A significant constraint identified in early crossbreeding projects was the reluctance of farmers to use crossbred males for draught work. There was a widespread perception that crossbred bulls lacked the endurance and temperament required for traditional agricultural operations. This bottleneck slowed the integration of crossbred animals into rural farming systems,

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tropical environment and management systems of southern India.

65. (B) Rambouillet and Malpura
Avikalin is a synthetic sheep breed developed at the Central Sheep and Wool Research Institute. It was created by crossing exotic Rambouillet rams with indigenous Malpura ewes. The breed was specifically designed to improve carpet wool production, combining the finer wool characteristics of the Rambouillet with the hardiness and survival capabilities of the native Malpura sheep.

66. (D) Central Avian Research Institute (CARI)
ILI-80 is a high-yielding synthetic commercial layer poultry bird developed by the Central Avian Research Institute. It was designed to meet the demands of commercial egg production in India, exhibiting high egg numbers and good feed efficiency. CARI has played a major role in developing such specialized poultry strains to support the growth of the domestic industry.

67. (A) Heterosis
Heterosis, or hybrid vigor, refers to the improved performance of crossbred offspring relative to the average of their purebred parents. This phenomenon is most pronounced for traits with low heritability, such as fertility, survival, and general health. It results from increased heterozygosity and the masking of deleterious recessive alleles, making crossbreeding a powerful tool for enhancing overall productivity in livestock.

68. (C) S = Mean of selected parents
− Mean of the unselected population
Selection differential is a measure of the phenotypic superiority of the individuals chosen for breeding. It is calculated as the difference between the mean performance of the selected parents and the average performance of the entire unselected population. This value is a primary driver of genetic progress, as it determines the intensity of the selection pressure applied to the trait.

69. (A) Are sex-limited, such as milk production in dairy cattle
Progeny testing is highly justified for traits that are sex-limited, meaning they are only expressed in one gender, such as milk yield. Since bulls do not produce milk, their genetic merit must be evaluated based on the performance of their daughters. This method ensures that only sires with proven genetic superiority for the target trait are used extensively.

70. (A) I and II
Genetic progress is maximized by increasing selection intensity and shortening the generation interval. Higher intensity involves selecting only the very best individuals, while a shorter interval ensures that genetic improvements are passed on more quickly over time. Conversely, high environmental variance reduces progress because it masks the true genetic potential of individuals, making selection decisions less accurate.

71. (B) Are less related than the average relationship of the population
Outbreeding is a mating system involving individuals that are less closely related than the average relationship within the population. This strategy is used to increase genetic diversity and exploit heterosis. By bringing together divergent alleles, outbreeding tends to improve traits related to fitness and productivity, serving as the opposite of inbreeding which increases homozygosity and relationship levels.

72. (C) Two breeds alternated continuously over subsequent generations
Crisscrossing, also known as two-breed rotational crossing, is a system where two pure breeds are used alternately over subsequent generations. Crossbred females are mated to a sire of the breed not represented by their own sire. This method allows for the continuous maintenance of high levels of heterosis in the offspring while providing a source of replacement females within the herd.

73. (D) Comb type
Inbreeding depression primarily affects complex fitness-related traits like hatchability, egg production, and survival. These traits are typically polygenic and have low heritability. Conversely, qualitative traits like comb type or plumage color are controlled by one or a few genes with simple inheritance. These morphological traits are generally unaffected by the reduction in fitness associated with increased homozygosity from inbreeding.

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93. (A) They become dams of nucleus sires by moving to the nucleus herd
In an Open Nucleus Breeding System, the top-performing females in the base population are periodically identified and transferred to the nucleus herd. These superior females then serve as dams to produce the next generation of nucleus sires. This open flow of genes ensures that the best genetic material from the entire population is captured, maximizing the rate of genetic gain.

94. (C) Female selection intensity increases by using the large base
The open nucleus breeding system achieves higher genetic gain than closed systems primarily by increasing the selection intensity of females. By screening a large base population of animals, breeders can identify and utilize only the most exceptional individuals for the nucleus. This larger pool of candidates allows for a much higher selection pressure than would be possible within a restricted nucleus.

95. (D) Empowering local keepers to manage and conserve local breeds
Community-based management of animal genetic resources focuses on empowering the local livestock keepers who have traditionally managed these breeds. This approach involves providing technical support, establishing breed societies, and improving market access for local products. By making the maintenance of indigenous breeds economically viable and socially rewarding, communities are encouraged to take an active role in their long-term conservation.

96. (C) Ethylene glycol
Ethylene glycol is a commonly used permeating cryoprotectant in the freezing of bovine embryos. It has a low molecular weight, allowing it to penetrate the embryonic cells quickly and prevent the formation of damaging ice crystals. This chemical helps stabilize the cell membranes during the transition to ultra-low temperatures, ensuring high survival rates when the embryos are eventually thawed.

97. (B) Internal pressure and temperature levels
Preparation of the artificial vagina for semen collection requires precise control of internal temperature and pressure. The temperature must mimic the natural physiological state of the cow to stimulate ejaculation, usually between forty-two and forty-five degrees Celsius. Correct pressure ensures adequate contact with the penis. These factors are essential for obtaining a high-quality semen sample from the bull.

98. (D) Protection to spermatozoa against the effects of cold shock
Egg yolk is a standard component of many semen extenders because it contains lipoproteins that protect the sperm cell membranes. These components provide a protective layer that helps prevent damage caused by rapid cooling or "cold shock" during the process of preparing semen for storage. This protection is vital for maintaining sperm motility and fertility during the cryopreservation process.

99. (B) $-196^{\circ}C$
The ideal storage temperature for cryopreserved bull semen is negative one hundred and ninety-six degrees Celsius, which is the temperature of liquid nitrogen at atmospheric pressure. At this ultra-low temperature, all biological and metabolic processes within the spermatozoa are halted. This allows the semen to be stored indefinitely without significant loss of fertility, provided the liquid nitrogen levels are maintained.

100. (A) P-4, Q-2, R-3, S-1
Advanced biotechnological tools enhance livestock improvement through various applications. Marker-assisted selection uses DNA variations to identify superior animals early in life. Embryo sexing allows for the production of offspring of a specific gender to meet production goals. Somatic cell nuclear transfer is used for cloning elite individuals, while CRISPR technology provides a mechanism for the precise editing of genomic sequences.

101. (B) Numerical grades from 1 (excellent) to 4 (dead/degenerating)
Bovine embryos are evaluated before transfer or freezing using a standardized numerical grading system. Grade one represents excellent embryos with homogenous cytoplasm and symmetrical shape, while grade four indicates dead or degenerating embryos. This morphological assessment is crucial for selecting the most viable embryos, which maximizes the chances of a successful pregnancy and high survival rates after cryopreservation.

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which still relied heavily on animal power for cultivation.

84. (C) Lack of a synchronized cold chain for storing frozen semen
The success of breeding programs utilizing artificial insemination depends on the maintenance of a reliable cold chain. In many rural areas of India, the lack of synchronized infrastructure for storing and transporting frozen semen in liquid nitrogen is a major bottleneck. Without proper temperature control, semen quality deteriorates rapidly, leading to low conception rates and poor farmer participation.

85. (A) Lack of distinct breed features and have mixed genetic backgrounds
Non-descript cattle are animals that do not belong to any recognized pure breed and lack distinct, uniform characteristics. These populations typically have mixed genetic backgrounds and are found in various regions across India. While they often have lower productivity than specialized breeds, they possess high adaptability and are the primary focus of grading-up programs for genetic improvement.

86. (C) 87.5%
In the grading-up process, each successive generation of backcrossing increases the proportion of the exotic breed's genes. The first generation contains fifty percent exotic inheritance, and the second contains seventy-five percent. By the third generation, the offspring are expected to have eighty-seven point five percent of the exotic breed's genetic makeup, moving the population closer to the purebred state.

87. (B) Murrah
The Murrah buffalo is the most important dairy buffalo breed in the world and is extensively used as an improver breed across India. Known for its high milk yield and jet-black color, it is native to Haryana and Punjab. Grading-up non-descript buffaloes with Murrah sires is a primary strategy for increasing milk production in various states.

88. (C) Rapid growth rate and efficient conversion of high-quality feed
Intensive sheep production systems prioritize economic efficiency through rapid growth and high-quality mutton production. In these systems, breeding programs focus on selecting for high body weight gain and the ability to efficiently convert concentrate feed into meat. This is distinct from extensive systems where survival on poor pasture is the primary goal, allowing for faster turnover and higher profitability.

89. (D) The Booroola (FecB) gene for increased ovulation rate
The Garole sheep of the Sundarbans is famous for its exceptional prolificacy, frequently producing twins or triplets. This trait is controlled by the Booroola or FecB gene, which increases the ovulation rate. This gene has been widely studied and introduced into other sheep populations worldwide to enhance their reproductive efficiency and increase the number of lambs born per ewe.

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90. (B) I and IV
Conservation of animal genetic resources involves both in-situ and ex-situ methods. In-situ conservation maintains breeds within their natural habitats through community participation. Ex-situ in-vivo conservation involves keeping live herds outside their native tract, such as on research farms. Cryopreservation of semen or embryos is an ex-situ in-vitro method, while DNA banking is useful for research but cannot restore live animals.

91. (B) Combine desirable traits and maintain a broad genetic base
Synthetic parent lines are created by crossing several established lines to combine their best traits, such as egg production and feed efficiency. This process helps in maintaining a broad genetic base while selecting for specific performance targets. These lines are then used in structured crossbreeding programs to produce commercial offspring that exhibit high levels of heterosis and productivity.

92. (B) A dual-purpose, colored bird for free-range backyard farming
The Vanaraja bird is a highly successful poultry strain developed for rural backyard farming. It is a dual-purpose bird that provides both meat and eggs while possessing colored plumage for protection against predators. Vanaraja birds are hardy, can thrive on scavenging, and have better growth rates than local indigenous chickens, making them ideal for improving rural livelihoods.

with exotic Rambouillet rams. The breed was specifically engineered to produce fine quality wool suitable for the apparel industry while maintaining the ability to survive in Indian conditions. It represents a successful effort to reduce India's dependence on imported fine wool by improving local sheep productivity.

112. (C) Strict health control and precise trait recording in the herd
A closed nucleus breeding system maintains a restricted population with no external gene flow. The primary advantage is the ability to exercise strict control over health status and ensure highly precise recording of pedigrees and performance traits. This centralized management allows for very accurate genetic evaluations within the nucleus, although it requires careful monitoring to prevent the rapid accumulation of inbreeding.

113. (B) Many genes with small effects make robust marker ID difficult
Most commercially important traits in livestock, like milk yield, are polygenic and influenced by many genes with small individual effects. This complexity is a major bottleneck for marker-assisted selection because identifying robust markers that explain a large portion of the variance is difficult. Consequently, the accuracy of selection based on only a few markers is often too low for effective improvement.

114. (D) They require high inputs and are susceptible to heat and disease
Pure exotic cattle breeds like the Holstein Friesian are highly productive but face significant challenges in rural India. They are evolved for temperate climates and have high requirements for nutrition and specialized management. In tropical environments, they suffer from heat stress and are more susceptible to local diseases and parasites, making them difficult for smallholder farmers to maintain successfully.

115. (A) Economic improvement across all multiple traits simultaneously
The selection index method allows for the simultaneous improvement of multiple traits by assigning weight to each based on its genetic parameters and economic value. For a boar, this ensures that traits like growth rate and feed conversion are improved together in a way that maximizes overall profitability. This balanced approach is more efficient than selecting for one trait at a time.

116. (C) Fixation of alleles and increased homozygosity levels
Intensive inbreeding leads to a rapid increase in the proportion of homozygous genotypes within a population. This process results in the fixation of alleles, where all individuals carry the same gene at a specific locus. While this increases uniformity, it also leads to inbreeding depression and the expression of deleterious recessive traits that were previously masked by heterozygous gene pairings.

117. (A) Environment masks the true genetic relationship of the traits
When the genetic correlation is high but the phenotypic correlation is low, it suggests that environmental factors are significantly influencing the expression of the traits. The environment may affect the two traits in different or opposite ways, thereby masking their underlying genetic relationship. In such cases, selection based on DNA markers or genetic evaluations is more effective than selecting based on phenotypes alone.

118. (D) Milk yield across multiple lactations
Repeatability is a measure of the consistency of a trait over multiple occurrences in the same individual. It is highly applicable to production traits like milk yield, which can be recorded across several successive lactations. A high repeatability value for milk yield indicates that an animal's performance in its first lactation is a strong indicator of its potential in future lactations.

119. (B) Share common ancestry and distinct, uniform, heritable traits
A livestock breed is defined as a group of animals within a species that share a common ancestry and possess distinct, uniform characteristics. These traits, which may include physical features or production abilities, must be heritable and consistently passed down to offspring. This shared genetic identity differentiates a breed from other populations and forms the basis for organized breeding and conservation.

120. (A) I and II
Heritability and genetic correlations are fundamental parameters in quantitative

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genetics. Heritability values range from zero to one, representing the proportion of variance due to genetics. Genetic correlations range from negative one to positive one, indicating the relationship between two traits. However, repeatability is not always less than heritability; it is generally greater because it includes permanent environmental effects and total genetic variance.

121. (D) Drastic reduction in breeding individuals within the native tract
Under the National Bureau of Animal Genetic Resources classification, a breed is considered endangered primarily when there is a drastic reduction in its population size. A low number of breeding individuals within the native tract increases the risk of genetic drift and extinction. Conservation efforts prioritize these breeds to ensure that their unique genetic adaptations and cultural heritage are not permanently lost.

122. (A) Kerala
The Vechur cattle breed is native to Kerala and is recognized as one of the smallest cattle breeds in the world. Despite its small stature, it is highly productive for its size and produces milk with high medicinal value. The breed is extremely hardy, heat-tolerant, and disease-resistant, making it a valuable genetic resource for sustainable farming in tropical climates.

123. (B) Black meat valued for nutritional and medicinal properties
Kadaknath is a unique indigenous chicken breed from the Jhabua region of Madhya Pradesh. It is famous for its black plumage, black skin, and black meat, a condition known as fibromelanosis. The meat is highly valued for its nutritional content and perceived medicinal properties. This breed is a vital component of the local tribal economy and has received significant conservation focus.

124. (B) Adjusting management and feeding to suit crossbred needs
Initial crossbreeding programs in India often failed because they ignored the higher management requirements of crossbred animals. These animals have higher genetic potential for milk production but require superior nutrition and healthcare to express it. When they were managed under traditional low-input systems meant for indigenous cattle, their performance suffered, and they became highly susceptible to environmental stress and diseases.

125. (A) Superovulation → AI → Embryo recovery → Embryo evaluation → Transfer to recipients
A standard multiple ovulation and embryo transfer protocol involves several sequential steps. First, the donor cow is treated with hormones to induce superovulation. She is then artificially inseminated using high-quality semen. Several days later, the embryos are recovered from the uterus, evaluated for quality, and finally transferred to synchronized recipient cows that will carry the pregnancies to term.

126. (C) Lack of large, well-recorded reference populations with phenotypes
Genomic selection requires a large reference population where both genotypic and phenotypic data are available to train prediction models. In India, the lack of well-organized milk recording systems across large numbers of animals is a major bottleneck. Without accurate performance records linked to genotypes, it is difficult to develop reliable prediction equations for genomic breeding values in indigenous dairy cattle.

127. (C) 50% to 62.5%
In tropical climates, the recommended level of exotic inheritance for crossbred cattle is typically capped between fifty and sixty-two point five percent. This level balances the high productivity genes of the exotic breed with the heat tolerance and disease resistance of the indigenous stock. Maintaining this genetic balance is crucial for ensuring that the animals remain productive and healthy under local conditions.

128. (C) Selecting for adaptability and survival within indigenous breeds
For sheep production in harsh, extensive grazing systems, the best strategy is selecting for adaptability and survival within indigenous breeds. These breeds have evolved to thrive on poor-quality pasture and withstand seasonal drought. By selecting the best-performing individuals within these populations, breeders can gradually improve productivity while ensuring the animals maintain the resilience necessary for their specific environment.

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129. (B) A mutton and coarse carpet wool breed
The Deccani breed of sheep is native to the Deccan Plateau region and is primarily used for

mutton and coarse carpet wool. It is a hardy breed, well-adapted to the semi-arid climate and extensive grazing practices of the region. While its wool is not suitable for fine clothing, it is widely used in the traditional local industry for making blankets.

130. (A) I and III
Goat breeding in India focuses on improving production through various strategies. Upgrading local stock with larger indigenous breeds like Jamunapari can enhance meat yield and growth. The conservation of the Black Bengal goat is a priority due to its exceptional meat quality and prolificacy. However, exotic dairy breeds like the Saanen often struggle with tropical heat stress compared to local resilient populations.

131. (A) Reproductive traits (e.g., litter size)
In swine breeding, heterosis is most pronounced for reproductive traits such as litter size and piglet survival. These traits typically have low heritability and are heavily influenced by non-additive genetic effects. By utilizing crossbreeding, farmers can significantly improve the reproductive efficiency of their herds, resulting in more piglets produced per sow and higher overall economic returns.

132. (C) Inwardly curved and touching ear tips
The Marwari horse is a prestigious indigenous breed from the Marwar region of Rajasthan. It is easily recognized by its unique ear shape, where the tips are inwardly curved and often touch or overlap. This hardy horse is renowned for its loyalty, endurance, and brave temperament, having historically served as a noble war horse for the Rajput warriors.

133. (A) NRCE, Hisar
The National Research Centre on Equines, located in Hisar, is the primary organization responsible for research and conservation of horses, ponies, and donkeys in India. The center focuses on breed characterization, genetic improvement, and the control of equine diseases. Its work is essential for preserving the unique heritage of Indian equines and supporting their continued utility in various sectors.

134. (D) Six-week body weight and feed conversion ratio
Breeding for commercial broiler poultry focuses on maximizing meat production efficiency. The selection index for these birds is heavily weighted toward traits that contribute to rapid growth, such as body weight at six weeks of age. Additionally, feed conversion ratio is prioritized to ensure that the birds efficiently turn feed into muscle, reducing production costs for the broiler industry.

135. (B) III, II, I, IV
Developing a synthetic poultry line involves a structured sequence of steps. First, candidate founder lines are evaluated for their combining ability to identify the best parents. These lines are then crossed, followed by several generations of random mating to stabilize the gene pool. Finally, intensive selection is applied within the new synthetic population to achieve the desired performance for commercial use.

136. (C) Accurate identification and recording in the base population
The success of an open nucleus breeding system depends on the ability to identify superior animals within the large base population. This requires accurate animal identification and systematic recording of performance traits across many smallholder farms. Without reliable data, it is impossible to select the best females to move into the nucleus, which is the primary mechanism for achieving higher genetic gain.

137. (D) Maintaining breeds in their native environments by local communities
In-situ conservation refers to the maintenance of animal genetic resources within their natural habitats. This strategy relies on local communities and pastoralists to continue rearing indigenous breeds using traditional management systems. By keeping the animals in their native tract, they are allowed to continue evolving in response to local environmental pressures, ensuring the preservation of their unique adaptive traits.

138. (A) Bring together farmers to maintain purity and record performance
Breed societies are organizations formed by livestock keepers to promote and protect specific breeds. Their primary objectives include maintaining breed purity, establishing standards, and organizing systematic performance recording. These societies play a crucial role in breed development by facilitating the identification of superior germplasm and providing a platform for

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102. (D) Two-way or three-way foley-like catheter for embryo recovery
For non-surgical embryo recovery in cattle, a specialized two-way or three-way foley-type catheter is used. This device allows for the infusion of flushing medium into the uterine horns and the simultaneous recovery of the fluid containing the embryos. The catheter is designed to be flexible and safe for the uterine environment, ensuring the efficient collection of multiple embryos.

103. (B) Ovum Pick-Up (OPU)
In vitro maturation is a critical laboratory step that follows the collection of immature oocytes, often through techniques like Ovum Pick-Up. During IVM, the oocytes are cultured under specific conditions to allow them to reach the stage of development where they can be successfully fertilized. This process is essential for the production of viable embryos in a laboratory setting.

104. (C) ICSI
Intracytoplasmic sperm injection is a sophisticated micromanipulation technique where a single spermatozoon is physically injected into the center of an oocyte. This method bypasses the need for the sperm to naturally penetrate the outer layers of the egg. It is particularly valuable when using semen with very low motility or when only a limited number of sperm cells are available.

105. (D) They are dense and abundant across the entire genome
Single Nucleotide Polymorphisms are the most common type of genetic variation and are found abundantly across the entire bovine genome. Their high density and stability make them ideal markers for genomic selection. By genotyping thousands of SNPs simultaneously, researchers can create a high-resolution map of the genome, allowing for the accurate prediction of breeding values for complex quantitative traits.

106. (A) Prediction equations derived from effects in a reference group
Genomic Estimated Breeding Values are calculated using complex statistical models and prediction equations. These equations are derived by analyzing the relationships between DNA markers and phenotypic traits in a large reference population. Once the marker effects are estimated, they can be applied to the genotypes of young animals to predict their genetic potential before they express any phenotypes.

107. (B) Samrupa
Samrupa was the name of the first cloned buffalo calf produced in the world using the hand-guided cloning technique. This milestone was achieved by scientists at the National Dairy Research Institute in Karnal, India. The successful birth of Samrupa demonstrated India's advanced capabilities in reproductive biotechnology and opened new possibilities for the multiplication of elite buffalo germplasm through cloning.

108. (B) Pharming
Pharming refers to the use of transgenic farm animals to produce valuable human pharmaceuticals, such as proteins or antibodies, in their milk. This technology utilizes tissue-specific promoters to ensure that the human protein is expressed only in the mammary gland. It provides a cost-effective and scalable method for producing complex biopharmaceuticals that are otherwise difficult to manufacture in laboratories.

109. (A) Holstein Friesian
Karan Fries is a stabilized crossbred cattle strain developed by crossing Tharparkar cows with Holstein Friesian bulls. The goal of this program was to create a high-yielding dairy animal that could withstand the environmental stresses of the Indian plains. The breed combines the massive milk production capacity of the Holstein Friesian with the hardiness and heat tolerance of the Tharparkar.

110. (A) Both A and R are true and R is the correct explanation of A.
Crossbreeding indigenous cattle with exotic breeds aims to rapidly improve milk production by utilizing heterosis. The first generation typically exhibits the highest degree of hybrid vigor, combining the high yield potential of exotic breeds with the environmental adaptability of native stock. This strategy is effective for achieving immediate gains in productivity under favorable management and nutritional regimes in India.

111. (D) Avivastra
Avivastra is a synthetic sheep breed developed through crossing indigenous Chokla ewes

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statistical associations between DNA markers and phenotypic variation. Once a QTL is located, breeders can use linked markers to select for desirable alleles, even if the actual genes involved are not yet known.

148. (C) Transfering a disease-resistance gene from a wild relative
Marker-assisted introgression is most valuable for transferring specific, high-value traits, such as disease resistance, from a donor population into a elite breed. By using DNA markers to monitor the presence of the target gene and the recovery of the recipient's genetic background, breeders can achieve the desired genetic combination much faster than through traditional backcrossing methods without molecular assistance.

149. (A) Size of the reference population and heritability of the trait
The accuracy of genomic estimated breeding values depends primarily on the size of the reference population and the heritability of the trait. A larger reference group with high-quality phenotypic and genotypic data allows for more precise estimation of marker effects. For traits with higher heritability, the genetic markers explain more of the phenotypic variance, leading to more reliable predictions of breeding values.

150. (A) P-3, Q-4, R-2, S-1
India has established specialized research institutions to manage different livestock species. The National Bureau of Animal Genetic Resources focuses on characterizing all indigenous breeds. The Central Sheep and Wool Research Institute and Central Institute for Research on Goats lead improvements in their respective species. Additionally, the Directorate of Poultry Research develops high-yielding strains for commercial and backyard poultry production across regions.

151. (B) Inbreeding depression and reduced genetic diversity
The extensive use of a few elite sires through artificial insemination can lead to a rapid increase in the average relationship within a population. This results in higher levels of inbreeding, which can cause inbreeding depression and a significant reduction in overall genetic diversity. Breeders must monitor and manage these relationship levels to ensure the long-term health and sustainability of the breed.

152. (C) Porcine Reproductive and Respiratory Syndrome (PRRS)
CRISPR technology has been used experimentally to create pigs that are resistant to Porcine Reproductive and Respiratory Syndrome. By editing specific genes that the virus uses to enter host cells, researchers have produced animals that do not become infected when exposed to the pathogen. This demonstrates the potential of gene editing for improving livestock health and reducing economic losses in swine production.

153. (D) Is formed by crossing breeds and inter-se mating stabilization
A synthetic breed is a new population developed by crossing two or more existing breeds and then stabilizing the offspring through several generations of inter-se mating. This process combines the desirable characteristics of the parent breeds while allowing for the expression of heterosis. Once stabilized, the synthetic breed can be maintained as a purebred population with its own unique traits.

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154. (B) 62.5%
The Frieswal cattle breed was developed to achieve a balance between high milk production and tropical adaptability. Through systematic crossbreeding and selection, the population was stabilized at an inheritance level of sixty-two point five percent Holstein Friesian and thirty-seven point five percent Sahiwal. This specific genetic mix was found to provide the best overall performance in the Indian military farm system.

155. (B) $R = h^2 \times S$
The response to selection is the change in the population mean between the current generation and the offspring of the selected parents. It is calculated by multiplying the narrow-sense heritability of the trait by the selection differential. This fundamental formula allows breeders to predict the rate of genetic improvement and evaluate the effectiveness of their selection strategies over time.

156. (B) Independent culling levels
Independent culling levels is a selection method where a minimum threshold is set for each trait independently. Any animal that fails to meet the threshold for even one trait is culled, regardless of its performance in other areas. This method allows for simultaneous selection on multiple

traits and is simpler to implement than a selection index, although it may be less efficient.

157. (A) Improving one trait at a time may cause regression in others
Tandem selection involves selecting for one trait at a time until the desired level is reached, then switching to another trait. This method is less efficient than a selection index because it does not account for the genetic correlations between traits. Improving one characteristic may cause an undesirable correlated response in others, leading to slow overall progress across the whole breeding objective.

158. (C) Random mating in a large population
The Hardy-Weinberg equilibrium states that allele and genotypic frequencies in a population will remain constant from generation to generation in the absence of evolutionary influences. This requires a large population with random mating and no mutation, selection, or migration. It provides a baseline for understanding how breeding and selection processes change the genetic structure of livestock populations over multiple generations.

159. (D) Increases heterozygosity masking deleterious recessive alleles
Outbreeding produces heterosis primarily by increasing the proportion of heterozygous genotypes in the offspring. When genetically divergent individuals are mated, the favorable dominant alleles from one parent can mask the deleterious recessive alleles from the other. This masking effect leads to improved vigor, health, and productivity in crossbred animals compared to the average of their more homozygous parent populations.

160. (A) Both A and R are true and R is the correct explanation of A.
Genetic correlations between traits are not static and can change over generations due to intense selection. Selection processes alter allele frequencies, which in turn modifies the pleiotropic effects and linkage disequilibria between loci. Consequently, the relationship between traits may shift as the population evolves, necessitating periodic reassessment of genetic parameters to maintain the efficiency of livestock breeding programs over time.

161. (B) A hierarchical mating design with sires mated to multiple dams
The paternal half-sib correlation method for estimating heritability requires a hierarchical mating design. In this setup, each sire is mated to several different dams, and each dam produces one or more offspring. By comparing the variation between sire groups to the variation within groups, researchers can estimate the additive genetic variance and calculate the narrow-sense heritability of a trait.

162. (D) Sample size of families and individuals increases
The standard error of a heritability estimate is a measure of its precision. It generally decreases as the total sample size of the study increases. By including more families, such as sire and dam groups, and more individual offspring per family, researchers can obtain more reliable and accurate estimates of heritability, which are essential for making informed selection decisions in breeding programs.

163. (A) Draught breed
The Malvi cattle breed is an indigenous draught breed native to the Malwa region of Madhya Pradesh. It is highly valued for its endurance and strength in heavy agricultural work and transport. The breed is well-adapted to the local environment and traditional management systems, playing a crucial role in the rural economy where animal power is still essential for cultivation.

164. (C) Karnataka
The Hallikar cattle breed is a prestigious indigenous draught breed native to Karnataka. It is renowned for its exceptional power, stamina, and agility in agricultural operations. Hallikar bulls are highly prized for their draught capacity and distinctive long horns. The breed is a symbol of rural heritage and remains an important genetic resource for smallholder farmers in southern India.

165. (A) Surti
The Surti buffalo is an indigenous breed native to the Gujarat region, specifically around Surat and Baroda. It is easily identified by its characteristic sickle-shaped horns, which are flat and grow in a downward and backward direction before curving upwards. These medium-sized buffaloes are valued for their efficient milk production

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and high fat content under traditional rural management systems.

166. (D) Socio-economic shifts and mechanization reducing functional utility
The decline of purebred indigenous cattle populations in India is largely driven by socio-economic shifts and increasing mechanization. As tractors replace animal power for ploughing and transport, the functional utility of traditional draught breeds has decreased. This has led many farmers to either stop keeping these breeds or cross them with exotic dairy breeds to maximize milk yield for commercial markets.

167. (B) Mandya (Bannur)
The Mandya sheep, also known as the Bannur sheep, is an indigenous breed from Karnataka renowned for its excellent meat quality. It has a characteristic compact body and high growth rate compared to other local breeds. Because of its superior mutton characteristics, it is frequently used in grading-up programs to improve meat production in southern Indian sheep populations.

168. (C) Intensive Cattle Development Project (ICDP)
The Key Village Scheme was eventually superseded by the more ambitious Intensive Cattle Development Project in the mid-sixties. While the KVS worked in small pockets, the ICDP was designed to cover much larger areas, providing a comprehensive range of services including breeding, nutrition, healthcare, and marketing. This shift aimed to rapidly increase milk production to supply the growing network of urban dairy plants.

169. (D) To conserve indigenous bovine breeds scientifically
The National Gokul Mission was launched with the primary objective of conserving and developing indigenous bovine breeds in a scientific manner. The mission focuses on enhancing the productivity of native cattle and buffaloes through selective breeding and improved management. It also aims to establish Gokul Grams to promote the use of purebred indigenous bulls and protect India's valuable genetic heritage.

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170. (A) Nomadic rearing practices make organized recording difficult
A major bottleneck for sheep breeding programs in India is the prevalence of migratory and nomadic rearing systems. Many sheep owners move their flocks over long distances in search of pasture, which makes it extremely difficult to maintain systematic performance and pedigree records. Without consistent data, it is challenging to implement organized selection schemes or open nucleus breeding systems effectively.

171. (B) Jersey
In high-altitude and hilly regions of India, the Jersey breed is often recommended for crossbreeding with non-descript cattle. Jersey cattle are smaller, hardier, and better suited to rugged terrain and limited feed resources than larger exotic breeds like the Holstein Friesian. They also produce milk with higher fat content, which is well-suited to the traditional dairy practices in mountain communities.

172. (C) After 5 to 6 generations (reaching $> 98\%$ exotic inheritance)
Grading-up is considered functionally complete after five or six generations of continuous backcrossing to the improver breed. By this stage, the offspring carry over ninety-eight percent of the genetic material from the purebred sires. The resulting population is then treated as purebred, having effectively replaced the original non-descript genetic background with the desirable traits of the improver breed.

173. (A) Negative correlation between wool quality and meat yield
Breeding programs for dual-purpose sheep often face a challenge due to the negative genetic correlation between wool quality and meat yield. Selecting for extremely fine wool may lead to a reduction in growth rate and carcass weight, and vice versa. Breeders must use balanced selection indices to achieve a compromise that maximizes overall profitability from both wool and mutton production.

174. (C) Sirohi
The Sirohi goat is an important dual-purpose breed native to the semi-arid tracts of Rajasthan. It is highly valued for its rapid growth, good meat quality, and decent milk production. The breed is very hardy and well-adapted to hot, dry climates, making it a popular choice for farmers

throughout western India looking for resilient and productive livestock.

175. (D) Large litter size, high growth, and excellent mothering
The Large White Yorkshire is widely used in swine crossbreeding because of its exceptional reproductive and production characteristics. It is known for having large litter sizes, high growth rates, and excellent mothering ability. By crossing this exotic breed with indigenous pigs, farmers can significantly improve the output and profitability of their herds while maintaining some local environmental resilience.

176. (C) They are the only draught animals in the cold Nubra valley
The conservation of the double-humped camel is critical because it is the only draught animal capable of working in the extreme cold and high-altitude conditions of the Nubra Valley. These animals are uniquely adapted to the freezing temperatures of the region, where other livestock would struggle. They are essential for transport and tourism, representing a vital part of the local economy.

177. (B) Is controlled by genes located on the sex chromosomes (Z or W)
In poultry, sex-linked traits are controlled by genes located on the sex chromosomes, which are designated as Z and W. Unlike mammals, birds are the heterogametic sex in females, carrying both Z and W chromosomes, while males are ZZ. This inheritance pattern allows for unique breeding strategies where certain traits can be used to distinguish between male and female offspring.

178. (D) Auto-sexing of day-old chicks based on feather or color
Commercial poultry breeding utilizes sex-linked traits, such as feather growth rate or plumage color, for the auto-sexing of day-old chicks. This allows hatchery staff to easily and rapidly separate males from females without the need for vent sexing. This efficient process ensures that only the productive female layers are kept, significantly reducing labor and costs in commercial egg operations.

179. (A) Selected superior females
In an Open Nucleus Breeding System, the base population acts as a continuous source of superior genetic material for the nucleus. The highest-performing females are identified in the base herd and moved to the nucleus to produce future sires. This open flow of elite females ensures that the nucleus maintains high genetic diversity and captures the best possible genes from the whole population.

180. (C) Maintains purebred indigenous herds with scientific recording
Gaushalas can become effective centers for in-situ conservation if they transition to scientific management of purebred indigenous herds. By maintaining accurate pedigree and performance records, these institutions can identify superior germplasm and distribute high-merit bulls to surrounding areas. This approach transforms Gaushalas from traditional cattle shelters into active hubs for the genetic improvement and preservation of native cattle breeds.

181. (A) Blood samples or hair follicles
For long-term genetic conservation and DNA banking, blood samples or hair follicles with roots are the most common source materials. These tissues provide high-quality DNA that can be stored and used for future genomic studies, parentage testing, or identifying important genetic markers. Establishing these repositories is essential for preserving a permanent record of the genetic diversity present in indigenous livestock populations.

182. (D) Provide energy, buffer pH, and protect against cold shock
A high-quality semen extender must perform several critical functions to maintain sperm viability. It provides an energy source like glucose, buffers the pH to prevent metabolic acidosis, and includes cryoprotectants to protect against cold shock and freezing damage. These components ensure that the spermatozoa remain motile and fertile throughout the processes of cooling, freezing, storage, and eventual thawing for insemination.

183. (B) Equilibration
Equilibration is the process of gradually cooling semen to about five degrees Celsius and allowing it to sit with the cryoprotectant before freezing. This time allows the cryoprotectant to penetrate the sperm cells and the membranes to stabilize. Proper equilibration is essential for maximizing post-thaw motility and fertility, as it prepares

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the spermatozoa for the extreme stress of deep freezing in liquid nitrogen.

184. (C) Ultra-rapid cooling to form a glass-like state
Vitrification is an ultra-rapid cooling technique for cryopreserving embryos that prevents the formation of damaging ice crystals. By using high concentrations of cryoprotectants and immediate exposure to liquid nitrogen, the fluid inside the embryo transforms directly into a glass-like solid state. This method is often faster and can result in higher survival rates for certain developmental stages compared to traditional slow-freezing.

185. (D) Isotonic, sterile, and supplemented with protein
The medium used for flushing embryos from a donor cow must be isotonic and sterile to maintain the health and viability of the delicate embryos. It is typically supplemented with proteins, such as bovine serum albumin, to provide nutrients and prevent the embryos from sticking to the laboratory equipment. These carefully balanced conditions are essential for successful embryo recovery and subsequent transfer.

186. (A) Oocyte with compact cumulus layers and homogenous cytoplasm
For successful in-vitro fertilization, oocytes are graded based on their morphological quality. A high-quality oocyte suitable for IVF typically has multiple layers of compact cumulus cells and a homogenous, clear cytoplasm. These features indicate that the oocyte is mature and healthy, providing the best chance for successful fertilization and subsequent embryonic development within the laboratory culture system.

187. (B) Linked in close physical proximity to the controlling gene(s)
Identifying a quantitative trait locus means that a specific DNA marker is linked in close physical proximity to the genes that control a particular trait. Because of this linkage, the marker and the gene tend to be inherited together. Breeders can then use the marker as a proxy to select for desirable genetic variations, even without identifying the actual underlying functional mutations.

188. (B) Difficult to measure, sex-limited, or late-expressed
Marker-assisted selection is most beneficial for traits that are difficult or expensive to measure phenotypically. This includes sex-limited traits like milk production, traits expressed late in life like longevity, or characteristics that require slaughter like carcass quality. By selecting animals based on DNA markers early in life, breeders can make faster and more accurate progress for these challenging traits.

189. (A) The sum of the additive effects of all SNPs across the genome
Genomic selection utilizes a statistical model to estimate the additive genetic effects of all single nucleotide polymorphisms across the entire genome. By summing these individual marker effects, breeders can calculate a genomic estimated breeding value for each animal. This comprehensive approach provides a more accurate assessment of genetic merit compared to traditional methods that only use a few markers or pedigree information.

190. (C) I, II, III, IV and V
Advanced reproductive technologies offer diverse applications for livestock improvement. Intracytoplasmic sperm injection bypasses natural fertilization barriers, while embryo splitting can produce identical twins. Ovum pick-up allows for repeated oocyte collection from live donors. Somatic cell nuclear transfer is essential for cloning elite animals. Additionally, in vitro maturation is a critical step in the production of embryos within a laboratory setting.

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191. (D) Aberrant epigenetic reprogramming of the somatic nucleus
A major cause of the low efficiency in somatic cell nuclear transfer is the failure of the somatic nucleus to undergo proper epigenetic reprogramming. When transferred to an oocyte, the donor nucleus must revert to an embryonic state to allow for normal development. Errors in this complex process often lead to abnormal gene expression, resulting in high rates of pregnancy loss and developmental defects.

192. (C) Pronuclear microinjection of DNA into a zygote
One of the classical methods for creating transgenic animals is the pronuclear microinjection of DNA. This technique involves physically injecting

229. (A) It maximizes superior female utility even during gestation
One advantage of Ovum Pick-Up is that it can be performed on cows even during the first trimester of pregnancy. This allows for the continued collection of oocytes from high-merit females without interrupting their natural reproductive cycle. By maximizing the utility of superior individuals throughout their lives, OPU significantly increases the potential for genetic improvement and the production of valuable offspring.

230. (D) Lower pregnancy rates and incidence of large offspring syndrome
A major limitation of in-vitro fertilization in livestock is the lower pregnancy rate and the increased risk of large offspring syndrome. IVF embryos sometimes undergo abnormal development in the laboratory, leading to excessively large calves at birth, which can cause difficult calvings. These challenges mean that IVF requires more intensive management and monitoring compared to standard embryo production through superovulation and flushing.

231. (B) Highly polymorphic and multi-allelic
Microsatellites became preferred markers in early genetic studies because they are highly polymorphic and often carry multiple alleles at a single locus. This high level of variation provides significant power for distinguishing between individuals and populations. Their multi-allelic nature makes them particularly useful for parentage testing and assessing genetic diversity, as they provide more information per locus than bi-allelic markers.

232. (C) Logarithm of Odds, a statistical estimate of linkage
In QTL mapping, the LOD score stands for the Logarithm of Odds. It is a statistical value that indicates the probability that a genetic marker and a trait-controlling gene are linked, compared to the probability that they are unlinked. A higher LOD score provides stronger evidence for the presence of a quantitative trait locus in a specific genomic region, guiding further selection.

233. (D) Milk protein variants like Kappa-casein alleles
Marker-assisted selection has been particularly successful for improving traits controlled by major genes with large effects. A classic example in dairy cattle is selecting for specific milk protein variants, such as Kappa-casein alleles, which are strongly linked to cheese-making quality. By using DNA markers to identify these alleles, breeders can rapidly increase their frequency in the herd to meet specific market demands.

234. (A) Progeny testing of young sires
Genomic selection allows for the estimation of an animal's breeding value at birth using DNA marker information. This bypasses the need for traditional progeny testing, which is time-consuming and expensive. By selecting superior sires much earlier in life, breeders can drastically reduce the generation interval and accelerate the rate of genetic gain for traits like milk yield and reproductive efficiency.

235. (B) Animals of a completely different breed from the reference
The reliability of genomic estimated breeding values decreases significantly when applied to animals from a breed different from the reference population. This is because the statistical relationships between markers and traits are breed-specific and depend on the unique genetic background and linkage patterns of that population. To maintain accuracy, prediction models must be developed or validated using data from the target breed.

236. (B) Mammary gland epithelial cell
Dolly the sheep was the first mammal cloned from an adult somatic cell, representing a landmark achievement in biotechnology. The donor nucleus used for the procedure was taken from a mammary gland epithelial cell of an adult ewe. This breakthrough proved that specialized somatic cells could be reprogrammed to an embryonic state, opening the door for cloning and other advanced reproductive technologies.

237. (A) An endonuclease that cleaves the target DNA
In the CRISPR/Cas9 system, the Cas9 component acts as a molecular pair of scissors. It is an endonuclease enzyme that is guided by RNA to a specific genomic location, where it creates a double-strand break in the DNA. This precise cutting allows for the targeted modification of genes, enabling researchers to deactivate harmful alleles or insert beneficial genetic variations into livestock.

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extent to which the same genes influence both traits. A high correlation indicates that selection for one trait will lead to a predictable and significant correlated response in the other trait.

202. (A) Future performance based on past performance of an individual
Repeatability provides an estimate of how well an individual's past performance predicts its future performance for the same trait. It accounts for both genetic effects and permanent environmental influences that consistently affect the animal throughout its life. A high repeatability value suggests that early measurements are reliable indicators, allowing breeders to make accurate culling or selection decisions after only one or two records.

203. (B) Standardized phenotypic, reproductive, and geographic parameters
Descriptors are standardized sets of parameters used for the systematic evaluation and characterization of animal genetic resources. They include detailed descriptions of phenotypic features, reproductive performance, and the geographic native tract of the breed. Using standardized descriptors ensures that data collected from different regions is comparable, which is essential for breed documentation, registration, and the planning of national conservation.

204. (B) Sikkim and Darjeeling
The Siri cattle breed is an indigenous breed native to the high-altitude regions of Sikkim and the Darjeeling hills. It is uniquely adapted to the steep slopes and cold climate of the eastern Himalayas. Known for its hardiness and draught ability in rugged terrain, the Siri is an essential genetic resource for the livelihoods of mountain communities in these regions.

205. (A) Luit
The Luit buffalo is a swamp-type buffalo breed native to the North-Eastern region of India, particularly Assam. It is characterized by having forty-eight chromosomes, which distinguishes it from the riverine buffaloes that have fifty chromosomes. These buffaloes are well-adapted to swampy environments and are primarily used for draught power and meat, playing a vital role in local agricultural systems.

206. (C) Marwari
The Marwari sheep is an indigenous breed native to the Marwar region of Rajasthan. It is easily recognized by its characteristic black or brown face and is highly valued for producing good quality carpet wool. This hardy breed is well-adapted to the desert environment and migratory management, making it one of the most important sheep breeds in western India.

207. (D) Doom
The Doom pig is an indigenous breed found in the Dooars and valley regions of Assam. It is traditionally reared by the Mising and other local tribes. Characterized by its relatively small body size and early sexual maturity, this breed is well-adapted to local climatic conditions and scavenging systems. It provides a vital source of protein and income for rural communities.

208. (C) Meet demand via improved bulls and scientific rations
The first phase of the National Dairy Plan aimed to increase milk production and improve dairy productivity across India. Key strategies included the production of high genetic merit bulls through organized breeding programs and the promotion of scientific feeding practices through the Ration Balancing Programme. These efforts were designed to meet the growing demand for milk while enhancing the income of smallholder farmers.

209. (B) Recording daughter milk yields across numerous smallholder farms
Implementing field progeny testing in India is challenging due to the decentralized nature of dairy farming. The primary bottleneck is the systematic recording of milk yields from the daughters of test bulls across thousands of smallholder farms. Without reliable performance data, it is impossible to accurately estimate breeding values, which is necessary for identifying and selecting superior sires for genetic improvement.

210. (A) Both A and R are true and R is the correct explanation of A.
Crossbreeding in India is generally recommended for areas with adequate resources because crossbred cattle have higher metabolic and nutritional needs. Compared to indigenous breeds, they are more susceptible to tropical diseases and heat stress. Therefore, successful

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a DNA construct containing the desired gene directly into the male or female pronucleus of a fertilized zygote. Some of the injected DNA may integrate into the host genome, potentially resulting in offspring that carry and express the new transgene in their tissues.

193. (B) Serve as a substitute for imported fine wool
The Bharat Merino sheep was developed to produce fine quality wool that could serve as a substitute for imported fine apparel wool. Created through crossing exotic Merino types with indigenous sheep, this synthetic breed was designed to combine superior wool characteristics with the ability to thrive under Indian climatic conditions, thereby supporting the domestic textile industry and rural sheep farmers.

194. (B) 50%
The Karan Fries cattle breed was developed at the National Dairy Research Institute with a target of fifty percent exotic inheritance. By maintaining this genetic level, the breed achieves high milk production from the Holstein Friesian while retaining the heat tolerance and hardiness of the Tharparkar parentage. This balance is ideal for intensive dairy production in the hot and humid regions of India.

195. (A) Maximizing correlation between index and breeding value
The fundamental goal of calculating a selection index is to maximize the correlation between the index and the true breeding value of the individual. By combining multiple sources of information and weighting traits according to their economic importance, the index provides the most accurate possible estimate of an animal's overall genetic merit, leading to efficient progress across all selected traits simultaneously.

196. (C) The heritability of the trait is zero
The expected response to selection is directly proportional to the heritability of the trait. If a trait has zero heritability, it means that all the observed variation is due to environmental factors and none is due to additive genetic effects. In this case, selecting superior parents will not lead to any genetic change in the offspring, resulting in zero genetic progress.

197. (A) The individual is young or the trait is sex-limited
Pedigree selection is often preferred when the animal being evaluated is too young to have its own performance records or when the trait is sex-limited. It allows breeders to make early selection decisions based on the records of ancestors, which helps in reducing the generation interval. While less accurate than individual or progeny testing, it is a valuable tool for early-stage selection.

198. (D) Alleles at a locus are identical by descent
The inbreeding coefficient measures the probability that two alleles at a specific locus are identical by descent, meaning they both originated from a common ancestor. This probability increases as more closely related individuals are mated. A higher inbreeding coefficient indicates a more homozygous individual, which can lead to the expression of deleterious recessive traits and a reduction in overall fitness and productivity.

199. (B) Greater genetic divergence leads to higher non-additive effects
Crossbreeding exotic breeds with indigenous cattle generally results in higher levels of heterosis because of the greater genetic divergence between these groups. These populations have evolved separately under different environmental pressures, leading to significant differences in their allele frequencies. When crossed, the resulting offspring exhibit high heterozygosity and strong non-additive genetic effects, leading to a substantial boost in fitness and performance.

200. (A) P-1, Q-2, R-3, S-4
Heritability varies across different trait categories in livestock. Reproductive traits usually exhibit low heritability, meaning they are heavily influenced by environmental factors. Production traits like milk yield show moderate heritability, while product quality and morphological traits often have high heritability. Understanding these levels is crucial for choosing the most effective selection methods to achieve genetic progress in a specific breeding program.

201. (D) $\dfrac{\text{Genetic Covariance}(X, Y)}{\sqrt{\text{Gen.Var.}X \times \text{Gen.Var.}\,Y}}$
The genetic correlation between two traits is calculated by dividing their genetic covariance by the square root of the product of their individual genetic variances. This formula quantifies the

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it a powerful tool for developing superior broiler or layer poultry strains.

220. (B) Accumulation of inbreeding and lower female selection intensity
The open nucleus breeding system was developed to address the limitations of closed systems, such as the rapid accumulation of inbreeding and low female selection intensity. By allowing superior females from the large base population to enter the nucleus, the system maintains a broader genetic base and increases the overall selection pressure, leading to more sustainable and rapid genetic progress over time.

221. (C) Bidirectional
In an Open Nucleus Breeding System, the flow of genetic material is bidirectional. Superior females from the base population are moved "upward" into the nucleus to act as dams for future sires. Simultaneously, the best males from the nucleus are moved "downward" into the base population for breeding. This exchange ensures that genetic improvement is shared across the entire structured population.

222. (C) Centers for scientific breeding and superior germplasm distribution
Gaushalas can significantly enhance in-situ conservation efforts if they transition from merely being shelters for old cattle to active centers for scientific breeding. By maintaining purebred indigenous herds and implementing systematic recording, they can identify and multiply superior genetics. Distributing high-merit bulls and semen to local farmers helps in the widespread genetic improvement and preservation of indigenous cattle.

223. (D) Fibroblasts derived from skin or ear cartilage biopsies
Somatic cell banking for animal genetic resource conservation typically involves the cryopreservation of fibroblast cells. These cells are easily obtained through small skin or ear cartilage biopsies. Once stored in liquid nitrogen, these cells serve as a permanent genetic record and can potentially be used to restore the breed through somatic cell nuclear transfer cloning if the live population is lost.

224. (C) Testes during spermatogenesis
Primary sperm abnormalities, such as pyriform heads or coiled tails, originate in the testes during the process of spermatogenesis. These defects often indicate disturbances in the biological environment of the seminiferous tubules. High frequencies of primary abnormalities can significantly reduce the fertility of a bull, making their identification an essential part of regular semen quality evaluation for artificial insemination programs.

225. (B) $15^{\circ}C$ and $5^{\circ}C$
The most critical temperature zone for cold shock in spermatozoa is between fifteen and five degrees Celsius. During this cooling phase, rapid temperature drops can cause irreversible damage to the sperm cell membranes, leading to a significant loss of motility and fertility. Semen extenders and gradual cooling protocols are specifically designed to protect the cells as they pass through this sensitive thermal range.

226. (D) Body of the uterus past the internal cervical os
In bovine artificial insemination, the optimal site for semen deposition is the body of the uterus, just past the internal cervical os. This location ensures that the spermatozoa have a direct path into both uterine horns, maximizing the chances of meeting the egg. Correct placement is a critical skill for inseminators and significantly influences the overall conception rate in dairy herds.

227. (A) Twice daily IM injections in declining doses over 4-5 days
In superovulation protocols, Follicle Stimulating Hormone is typically administered through twice-daily intramuscular injections over a period of four to five days. The dose is usually declined over time to mimic the natural physiological environment. This intensive treatment rescues multiple follicles from atresia, allowing them to mature and ovulate simultaneously, which is necessary for the recovery of multiple embryos.

228. (B) $75\mu m$
During the recovery of embryos in a MOET program, the flush fluid is passed through a specialized micro-filter. The pore size of this filter is typically around seventy-five micrometers. This size allows the fluid to pass through while trapping the much larger embryos. This concentration process makes it easier for technicians to find and evaluate the embryos under a microscope for transfer or freezing.

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crossbreeding programs require a supportive infrastructure including quality feed, efficient healthcare services, and favorable environmental management to ensure the productivity and health of the animals.

211. (A) Selective breeding for traits related to draught power and endurance
For specialized indigenous draught breeds like the Nagori, the most appropriate breeding strategy is selective breeding within the breed. The objective is to enhance their unique strengths, such as draught power, speed, and endurance. Focusing on these traits ensures that the breed remains relevant for traditional agricultural work while preserving the genetic adaptations that make it suitable for its specific environment.

212. (C) Fine wool yield and quality for apparel
Grading-up programs using Rambouillet rams in Rajasthan were primarily aimed at improving the fine wool production of local sheep. By crossing indigenous ewes with purebred exotic rams, breeders sought to increase wool yield and reduce fiber diameter to meet the needs of the apparel industry. This strategy aimed to transform coarse-wool sheep into fine-wool producers while maintaining some local environmental adaptation.

213. (A) Crossbreeding for synthesis
Crossing two indigenous breeds to combine their best traits and then stabilizing the offspring through inter-se mating is known as crossbreeding for synthesis. This method is used to create new synthetic strains that possess a desirable blend of characteristics, such as the growth rate of one breed and the environmental adaptability of another. Once stabilized, these populations are managed as new purebred resources.

214. (D) Jamunapari
The Jamunapari goat is frequently used as an improver breed for increasing milk production in other goat populations. Native to the semi-arid zones of Uttar Pradesh, it is one of the premier dairy goat breeds in India. Grading-up non-descript goats with Jamunapari sires is a common strategy to enhance the genetic potential for milk while maintaining adaptation to similar climates.

215. (B) Pashmina fiber
The Chegu and Changthangi goats are high-altitude breeds predominantly reared for the production of pashmina fiber. These goats produce a soft, warm undercoat that is harvested and processed into high-value textiles. Native to the Himalayan regions, their ability to produce this fine fiber is a specialized adaptation to the extreme cold, making them essential to the local mountain economy.

216. (C) Both maternal and individual heterosis
A three-way crossbreeding system in swine utilizes a crossbred female and a purebred male of a third breed. This strategy maximizes overall productivity by exploiting both maternal heterosis in the crossbred sow and individual heterosis in the market offspring. This combination leads to larger litter sizes, better piglet survival, and improved growth rates compared to purebred or simple two-way cross systems.

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217. (D) In-situ preservation and selective breeding in Ladakh
The conservation of the rare Zanskari pony focuses on in-situ preservation within its native high-altitude habitat in Ladakh. Selective breeding programs aim to maintain the purity of the breed and improve its draught capacity and endurance. These efforts are crucial for preserving a unique genetic resource that is perfectly adapted to the rugged terrain and extreme cold of the Trans-Himalayan region.

218. (A) Dual-purpose breed
The Rhode Island Red is a historically significant poultry breed classified as dual-purpose. It is highly valued for both its egg-laying capacity and its meat quality. RIR birds are hardy, adaptable, and have been widely used in breeding programs to develop specialized strains for commercial and rural production. They are a popular choice for smallholder farmers due to their overall versatility.

219. (B) Combining ability to maximize crossbred performance
Reciprocal recurrent selection is a breeding method specifically designed to improve the combining ability of two different populations or lines. It involves selecting individuals within each line based on the performance of their crossbred offspring. This strategy maximizes the heterosis expressed in the final commercial cross, making

238. (C) High volume commercial egg production
The ILI-80 poultry strain is a high-performance commercial layer developed in India for large-scale egg production. These birds are selected for their high rate of egg laying, efficient feed conversion, and good survivability under commercial management. Developing such specialized strains is essential for meeting the massive urban demand for eggs and supporting the industrial poultry sector through improved genetic efficiency.

239. (C) 4000 kg per lactation
The Frieswal cattle project aimed to develop a stabilized crossbred animal capable of high milk production under Indian conditions. The objective was to achieve a minimum milk yield of four thousand kilograms per lactation. This performance level was targeted to ensure that the breed remained economically viable for commercial dairy farming while maintaining the necessary resilience for the local tropical climate.

240. (C) Poultry have shorter sexual maturity and incubation periods
The generation interval is much shorter in poultry than in cattle because birds reach sexual maturity within months rather than years. Additionally, the incubation period for eggs is only twenty-one days, allowing for a rapid turnaround between generations. These biological factors enable poultry breeders to apply selection much more frequently, leading to faster annual genetic progress for traits like growth and egg laying.

241. (B) Small, isolated populations
Genetic drift refers to the random changes in allele frequencies that occur over generations. This phenomenon is most pronounced in small, isolated populations where chance events can lead to the loss or fixation of alleles. In livestock breeding, genetic drift is a significant concern for rare and endangered breeds, as it can lead to a rapid reduction in genetic diversity and overall fitness.

242. (D) The number of daughters and heritability of the trait
The accuracy of a sire's estimated breeding value in a progeny test depends on the number of daughters evaluated and the heritability of the trait. A larger number of daughters provides more data points, which reduces the influence of environmental variation on the estimate. For traits with higher heritability, the performance of the daughters is a more reliable indicator of the sire's true genetic potential.

243. (C) 0.125
The inbreeding coefficient for the offspring of a half-sibling mating is zero point one two five, or twelve point five percent. This value represents the probability that the offspring will inherit two identical alleles at any given locus from their common grandparent. This level of inbreeding can lead to a noticeable reduction in fitness and productivity, highlighting the importance of managing relationships in breeding.

244. (C) Opposite signs
It is possible for the phenotypic and genetic correlations between two traits to have opposite signs. This occurs when the environmental correlation is strong enough to mask the underlying genetic relationship. For example, two traits might be genetically positively correlated but environmentally negatively correlated. Understanding both values is essential for breeders to accurately predict how selection will influence the overall performance of the animal.

245. (A) Importation of live animals from another country
In a closed breeding herd, the rate of genetic progress is determined solely by internal factors like heritability, selection differential, and generation interval. Since no external genetic material is introduced, the importation of live animals from elsewhere does not directly affect the calculation of progress within that specific closed system. Genetic improvement relies entirely on selecting the best individuals from within the existing population.

246. (D) Telangana
The Poda Thurpu cattle breed is an indigenous draught breed native to the Amrabad forest area of Telangana. It is renowned for its exceptional power and endurance in difficult terrain. The breed is well-adapted to the local dryland ecosystem and is traditionally managed by local communities. Recognition by the NBAGR is an important step toward its organized conservation and systematic genetic improvement.

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300. (D) I, II, III and IV

Marker-assisted selection is a powerful tool for improving livestock by identifying specific DNA markers associated with desirable traits. It is highly effective for monogenic traits and sex-limited characteristics that are difficult to measure. This technology also aids in selecting for complex polygenic traits by identifying major loci. Overall, it enhances the accuracy and speed of genetic improvement across diverse traits in breeding programs.

NODIA

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256. (C) Replacement by mechanized transport reducing functional use
A significant challenge for the conservation of dromedary camels in India is the rapid replacement of animal transport by motorized vehicles. As trucks and tractors become more common in desert regions, the traditional draught and transport utility of camels has declined. This shift has reduced the economic incentive for breeders to maintain large camel populations, threatening the survival of several indigenous breeds.

257. (B) Promoting anti-diabetic therapeutic properties of camel milk
Promoting the unique therapeutic properties of camel milk, particularly its anti-diabetic effects, has emerged as a promising strategy for supporting camel breeders. By developing a high-value market for camel milk products, researchers aim to create new economic incentives for the conservation of indigenous camel breeds. This shift from draught power to dairy production could provide a sustainable future for camel husbandry in Rajasthan.

258. (D) Foraging ability and predator evasion
Poultry strains developed for backyard farming must possess strong foraging abilities and predator evasion behaviors. These birds are typically reared in free-range systems where they must scavenge for much of their food and protect themselves from local predators. Unlike commercial birds kept in confinement, backyard poultry need to be alert, agile, and hardy to survive and produce eggs in rural environments.

259. (A) Can be bred inter-se without maintaining parent lines
A key advantage of using a synthetic breed over continuous crossbreeding is that the synthetic population can be bred inter-se once it is stabilized. This eliminates the need for maintaining separate purebred parent lines to produce each new generation. This makes the system much simpler for farmers to manage while still benefiting from the combination of desirable traits achieved during the initial crossbreeding phase.

260. (C) Some base females exceed average nucleus merit
The genetic gain in an open nucleus breeding system relies on the assumption that some females in the large base population possess higher genetic merit than the average of the nucleus herd. By identifying and moving these superior individuals into the nucleus, the breeder can increase the overall selection intensity. This continuous flow of elite genes from the base ensures that the nucleus remains genetically superior.

261. (A) Ex-situ in-vivo
Ex-situ in-vivo conservation involves the maintenance of a live herd of a breed outside its natural native tract. This could include keeping animals on government farms, research institutions, or in specialized breeding centers. While it preserves the live animals, it differs from in-situ conservation because the population is no longer subject to the same environmental and management pressures of its original habitat.

262. (D) Prevent venereal disease and control bacterial growth
Adding antibiotics to semen extenders is a standard protocol to prevent the transmission of venereal diseases and control bacterial growth during storage. Even with careful collection, semen can contain microbes that could reduce sperm viability or cause infections in the inseminated female. Antibiotics ensure that the extended semen remains safe and sterile, protecting both the genetic material and the health of the herd.

263. (C) 40% to 50%
For bovine semen utilized in artificial insemination, the minimum acceptable post-thaw progressive motility is typically between forty and fifty percent. This threshold ensures that there are enough viable, forward-moving spermatozoa to achieve a high probability of conception. Semen samples that fall below this level are generally discarded, as they are less likely to result in a successful pregnancy under field conditions.

264. (C) Rescue of follicles from atresia to reach pre-ovulatory size
Superovulation in cattle works by using hormones like Follicle Stimulating Hormone to rescue multiple small follicles from their natural process of atresia. In a normal cycle, only one follicle typically reaches pre-ovulatory size and ovulates. Superovulation ensures that many more follicles are allowed to complete their development

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247. (B) Desert production and night grazing behavior
The Banni buffalo, bred by the Maldhari community in Gujarat, is famous for its unique night grazing behavior and adaptation to the desert environment. These buffaloes are highly resilient and can survive on local grasses even during seasonal scarcity. Their ability to graze at night when temperatures are cooler is a specialized physiological adaptation that makes them essential for dairy production in arid regions.

248. (C) Carrying loads in high-altitude mountainous terrains
The Spiti pony is a hardy indigenous breed found in the high-altitude regions of Himachal Pradesh. It is primarily used as a pack animal for carrying heavy loads through steep, rugged mountain terrains. These ponies are perfectly adapted to the thin air and cold climate of the Himalayas, serving as a critical mode of transport for local communities in remote mountain valleys.

249. (D) The elite herd for intensive recording and sire generation
In a structured breeding program, the nucleus is the elite herd where intensive recording and selection take place. This tier is responsible for generating superior sires that are eventually used to improve the genetic merit of the larger base population. Centralizing selection within a nucleus allows for higher accuracy and better control over the genetic improvement process for the entire breeding scheme.

250. (A) Infrastructure, hormone, and synchronization requirements
The widespread adoption of multiple ovulation and embryo transfer in Indian villages is restricted by its high technical and infrastructure requirements. The procedure requires precise hormone treatments, synchronization protocols, and sterile laboratory facilities, which are often unavailable in rural areas. Additionally, the high cost of the technology makes it less accessible for smallholder farmers compared to traditional artificial insemination services.

251. (B) Breakdown in adaptability and heat tolerance
When grading-up non-descript cattle with exotic breeds, it is important to cap the exotic inheritance level to prevent a breakdown in adaptability. Higher levels of exotic genes can make the animals extremely susceptible to heat stress and local diseases. By maintaining a balance between production and resilience, breeders ensure that the crossbred cattle remain healthy and productive within the challenging tropical Indian environment.

252. (B) Rambouillet or Merino rams
To improve the wool quality of indigenous coarse-wool sheep, they are typically crossed with Rambouillet or Merino rams. These exotic breeds possess genes for very fine fiber diameter and high wool density. This crossbreeding strategy aims to produce offspring that yield finer, more valuable wool suitable for the apparel industry while still retaining enough local hardiness to survive under Indian management conditions.

253. (A) Dual-purpose (mutton and wool)
Corriedale sheep are frequently used in crossbreeding programs in India to improve dual-purpose utility. This breed is known for its good mutton characteristics and high-quality wool. By crossing Corriedales with indigenous sheep, breeders aim to enhance both meat and wool production simultaneously. This provides farmers with multiple sources of income while improving the overall genetic potential of their local sheep flocks.

254. (C) Rajasthan
The Sirohi goat is an excellent breed for meat production and is native to the Sirohi district and surrounding semi-arid regions of Rajasthan. It is characterized by its large body size, rapid growth, and hardiness. These goats are well-suited to browsing on local vegetation and can withstand extreme heat, making them a cornerstone of the rural economy throughout western and central India.

255. (D) White coat, long body, and maternal traits
The Landrace pig is a highly valued commercial breed recognized by its white coat, long body, and drooping ears. It is world-renowned for its exceptional maternal traits, including large litter sizes and high milk production. These characteristics make it an ideal choice for crossbreeding programs, where it is often used to improve the reproductive efficiency and growth performance of indigenous pig populations.

NODIA

combine the fine wool quality of the Rambouillet with the hardiness and survival capabilities of the native Malpura. This resulting breed is highly valued for producing superior carpet wool while being well-adapted to the local semi-arid environment.

274. (D) Genetic variance (V_G) and Environmental variance (V_E)
In quantitative genetics, total phenotypic variance is primarily partitioned into genetic variance and environmental variance. Genetic variance is further divided into additive, dominance, and epistatic components. Understanding this breakdown is essential because only the additive genetic portion is predictable and passed on to offspring. This partitioning allows breeders to calculate heritability and estimate the potential for genetic progress through selection.

275. (A) A very small, top proportion of the population is selected
High selection intensity occurs when only a very small, top-performing proportion of the population is chosen to be parents of the next generation. This increases the selection differential, which in turn leads to more rapid genetic progress. However, high intensity must be balanced with the need to maintain genetic diversity and avoid excessive inbreeding, which can occur if the breeding pool is too small.

276. (C) Sires wait for daughter lactation data to prove merit
In traditional progeny testing, the generation interval for males is long because a bull's genetic merit for milk production cannot be directly observed. Instead, breeders must wait for the bull's daughters to mature, be inseminated, and complete at least one full lactation. This process takes several years, meaning that sires are often five or six years old before their true breeding value is proven.

277. (A) Specific crosses yielding better offspring than expected
The term "nick" in animal breeding describes a situation where a specific cross between two individuals or lines results in offspring with much higher performance than predicted based on the parents' average merit. This is often due to favorable non-additive genetic interactions, such as specific combining ability. Identifying these successful "nicking" combinations allows breeders to maximize productivity through targeted and strategic mating plans.

278. (D) Reduced conception rates and calf survivability
A classic sign of inbreeding depression in a dairy herd is a reduction in fitness-related traits. This typically manifests as lower conception rates, increased embryonic loss, and reduced calf survivability and vigor. These traits are heavily influenced by non-additive gene action and are most sensitive to the increased homozygosity caused by inbreeding. Breeders must manage relationship levels to avoid these negative impacts on herd productivity.

279. (B) Maharashtra and Karnataka
The Khillar cattle breed is an indigenous draught breed native to the arid and semi-arid regions of southern Maharashtra and northern Karnataka. It is highly valued for its speed, power, and endurance in heavy agricultural work. These animals are well-adapted to hot climates and sparse grazing, making them essential for farmers in the dryland cultivation areas of the Deccan Plateau.

280. (C) Karnal
The National Bureau of Animal Genetic Resources is headquartered in Karnal, Haryana. This institution is the nodal agency in India for the identification, characterization, and conservation of indigenous livestock and poultry breeds. Its work includes breed registration, maintaining national databases, and coordinating conservation programs across the country to protect India's valuable and diverse animal genetic heritage.

281. (D) Genetic correlation and environmental correlation
Phenotypic correlation is a measure of the observable relationship between two traits. It is a composite value influenced by both the underlying genetic correlation and the environmental correlation between those traits. Understanding this relationship helps breeders predict how the selection for one trait based on its physical appearance will simultaneously influence another trait in the current generation of animals.

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and ovulate simultaneously, providing a larger number of embryos for collection and transfer.

265. (D) Morula to blastocyst stage
Embryos are ideally recovered and transferred at the morula to blastocyst stage, which occurs around six to seven days after fertilization. At this stage, the embryos are relatively hardy and have moved into the uterus, making them easier to collect non-surgically. Transferring embryos at this precise developmental stage ensures the highest possible pregnancy rates and survival after being placed into the recipient cow.

266. (A) Differences in DNA content between X and Y sperm
Sex-sorted semen is produced using flow cytometry to separate X-bearing and Y-bearing spermatozoa based on their DNA content. In cattle, the X-chromosome is significantly larger than the Y-chromosome, meaning X-bearing sperm contain approximately four percent more DNA. Specialized dyes and laser detectors identify this difference, allowing for the collection of a high-purity dose of sperm that will produce offspring of the desired gender.

267. (B) Lower conception rates compared to conventional semen
A major drawback of sex-sorted semen is that it often results in lower conception rates compared to conventional semen. The sorting process involves several stressful steps, including dilution, staining, and high-speed passage through the flow cytometer, which can reduce the overall viability and lifespan of the sperm. Additionally, the concentration of sperm in sorted doses is often lower, making precise timing of insemination even more critical.

268. (B) Abundant, stable, and easily genotyped via chips
Single nucleotide polymorphisms are the preferred markers for genomic selection because they are incredibly abundant across the genome and highly stable over generations. Modern SNP chips allow for the rapid and cost-effective genotyping of thousands of these markers simultaneously. This high-density information provides a detailed genetic map of each animal, enabling the accurate prediction of breeding values for complex and economically important traits.

269. (A) Genotypes and phenotypes are used to estimate SNP effects
The reference population is the foundation of any genomic selection program. In this group, both genotypic and phenotypic data are collected and analyzed to estimate the statistical effects of each marker across the genome. These estimated effects are then used to build prediction models. The accuracy of the whole genomic evaluation system depends on the quality and size of this reference population.

270. (C) Use of a customizable RNA guide for targeting
CRISPR technology is distinguished from older gene editing methods by its use of a customizable guide RNA. This RNA molecule can be easily programmed to target any specific DNA sequence in the genome. This makes the system much simpler, more flexible, and more efficient than earlier technologies like zinc-finger nucleases, which required complex protein engineering for every new genomic target that scientists wanted to modify.

271. (D) Mammary gland
Transgenic animals developed for pharming use tissue-specific promoters to ensure that the human therapeutic protein is expressed exclusively in the mammary gland. This allows the protein to be secreted into the milk, from which it can be easily harvested and purified without harming the animal. This method provides a scalable and efficient way to produce biopharmaceuticals while minimizing any potential side effects on the animal.

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272. (C) Switzerland
The Sunandini crossbred cattle breed was developed in Kerala as part of a bilateral collaboration between the Government of India and the Government of Switzerland. This project, which began in the nineteen-sixties, aimed to improve the productivity of local cattle through systematic crossbreeding with Brown Swiss and other dairy breeds. The project successfully created a sustainable and productive dairy animal for the region.

273. (B) Malpura
The Avikalin synthetic sheep breed was developed at the Central Sheep and Wool Research Institute by crossing exotic Rambouillet rams with indigenous Malpura ewes. The goal was to

291. (A) Allows farms to produce replacement gilts with heterosis
Rotational crossbreeding is highly practical in commercial swine production because it allows farmers to produce their own replacement females while still benefiting from high levels of heterosis. By rotating sires of two or three breeds over successive generations, the herd maintains significant hybrid vigor for both maternal and individual traits without the need to constantly buy expensive replacement animals from outside sources.

292. (C) Heavy draught and transport purposes
The Bikaneri camel is one of the most important camel breeds in India, primarily native to the Bikaner region of Rajasthan. It is renowned for its strength and is predominantly used for heavy draught and transport work in the desert. These hardy animals are well-adapted to long-distance travel across sandy terrain, making them essential for the traditional livelihoods of desert communities.

293. (A) Capitalize on heterosis for growth and efficiency
Synthetic parent lines in broiler production are designed to capitalize on heterosis and the combination of desirable traits from several founder breeds. By crossing these stabilized lines, the commercial offspring exhibit maximized hybrid vigor for growth rate and feed conversion efficiency. This structured breeding system ensures that commercial broilers reach market weight as quickly and economically as possible for the poultry industry.

294. (D) It drastically reduces testing costs and generation intervals
Genomic selection has been highly successful in dairy cattle because it drastically reduces the time and cost associated with traditional progeny testing. By predicting genetic merit from DNA markers at birth, breeders can select superior bulls years earlier. This reduction in the generation interval, combined with high selection accuracy, has led to a major increase in the annual rate of genetic progress.

295. (B) Glycerol
Glycerol is the most widely used cryoprotectant for the deep freezing of bull semen. It is a permeating agent that lower the freezing point of the cytoplasm and helps prevent the formation of lethal ice crystals within the sperm cells. By protecting the cell membranes and stabilizing the internal environment, glycerol ensures that a high proportion of spermatozoa remain viable and fertile after thawing.

296. (B) 10 to 15 million
In standard bovine artificial insemination, a single dose of frozen semen is typically prepared to contain approximately ten to fifteen million progressively motile spermatozoa post-thaw. This concentration is designed to provide enough viable cells to ensure a high probability of fertilization under field conditions. Maintaining this standard is essential for ensuring consistent conception rates across dairy herds utilizing artificial insemination services.

297. (D) Female reproductive tract
Capacitation is the final stage of sperm maturation that is necessary for successful fertilization. This process naturally occurs as the spermatozoa travel through the female reproductive tract, where they are exposed to specific biochemical signals that alter the sperm membrane. This enables the sperm to undergo the acrosome reaction and successfully penetrate the layers of the oocyte to achieve fertilization.

298. (A) Dams to breed Sires and Dams to breed Dams
Embryo transfer technology can significantly increase the selection intensity on the female side of the breeding program. By allowing elite cows to produce dozens of offspring per year through superovulation and transfer, breeders can be much more selective about which females contribute to the next generation of sires and dams. This accelerates genetic improvement by maximizing the impact of the very best females.

299. (B) Cell fusion and simultaneous oocyte activation
During somatic cell nuclear transfer, providing an electrical pulse serves two critical functions. First, the pulse causes the membranes of the donor somatic cell and the enucleated oocyte to fuse, integrating the donor nucleus into the egg. Second, it triggers oocyte activation, mimicking the natural stimulus of fertilization and starting the process of embryonic development. This step is essential for the creation of cloned embryos.

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2018

9. When considering selection against a lethal dominant allele, the allele frequency in the next generation becomes:
(A) 0.5
(B) 1.0
(C) 0.0
(D) Equal to the mutation rate

2012

10. Which equation correctly represents biological fitness (W) for a genotype that produces an average of 4 offspring, assuming the most prolific genotype produces 5 offspring?
(A) $W = \frac{4}{5}$
(B) $W = \frac{5}{4}$
(C) $W = 1 - \frac{4}{5}$
(D) $W = 4 + 5$

2019

11. Which form of selection favors extreme phenotypes over the intermediate phenotype?
(A) Stabilizing selection
(B) Directional selection
(C) Truncation selection
(D) Disruptive selection

2002

12. If the fitness values of genotypes AA, Aa, and aa are $1 - s_1$, 1, and $1 - s_2$ respectively, this represents:
(A) Complete dominance
(B) Overdominance
(C) Incomplete dominance
(D) Underdominance

2024

13. Gametic frequency changes under gametic selection differ from zygotic selection because:
(A) Gametic selection targets specific diploid genotypes during meiosis.
(B) Gametic selection operates exclusively on sex-linked chromosomes.
(C) Gametic selection acts on haploid expressions before fertilization.
(D) Gametic selection bypasses standard zygotic selection coefficients.

2016

14. Estimated Breeding Value (EBV) is defined as:
(A) The phenotypic value of an individual minus the population mean
(B) The sum of additive, dominance, and epistatic effects
(C) The environmental deviation of a selected individual
(D) The transmitting ability of an individual multiplied by two

2018

15. Match the selection concepts in List I with their corresponding definitions in List II and select the correct option.
List I: (Concepts)
P. Phenotypic value
Q. Breeding value
R. Dominance deviation
S. Transmitting ability
List II: (Definitions)
1. Half of the additive genetic value
2. Value of an individual judged by the mean value of its progeny
3. Interaction between alleles at the same locus
4. Observable or measurable characteristic
(A) P-4, Q-2, R-3, S-1
(B) P-4, Q-1, R-3, S-2
(C) P-1, Q-2, R-4, S-3
(D) P-3, Q-1, R-2, S-4

2005

16. An individual's Transmitting Ability (TA) represents the:
(A) Total genetic superiority passed to offspring
(B) Average superiority of its gametes over the population mean
(C) Epistatic interactions passed to the next generation
(D) Phenotypic variance divided by genetic variance

2002

2007

17. The mathematical relationship between an individual's estimated breeding value (EBV), heritability (h^2), and phenotypic deviation ($P - \mu$) from the population mean is:
(A) $\text{EBV} = \frac{h^2}{P - \mu}$
(B) $\text{EBV} = h^2 \times (P - \mu)$
(C) $\text{EBV} = \frac{P - \mu}{h^2}$
(D) $\text{EBV} = h^2 + (P - \mu)$

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CHAPTER 07
Selection & Selection Experiments

2002

1. In a randomly mating population, if the selection coefficient against a recessive genotype is 1, what is the expected change in the frequency of the recessive allele (q) after one generation?

(A) $-\frac{q}{1+q}$

(B) $-\frac{q^2}{1+q}$

(C) $-\frac{q^2}{1+q^2}$

(D) $-\frac{q^2}{1-q^2}$

2005

2. Biological fitness in quantitative genetics is most accurately defined as the:

(A) Relative contribution of an individual's genotype to the next generation

(B) Ability of an individual to express its full phenotypic potential

(C) Survival duration of an organism in a competitive environment

(D) Physical superiority of an individual compared to the herd average

2021

3. If heterozygote advantage (overdominance) is present in a population, selection will eventually lead to:

(A) Fixation of the dominant allele

(B) Fixation of the recessive allele

(C) A stable equilibrium of allele frequencies

(D) Continuous fluctuation of allele frequencies

2004

4. The rate of change of allele frequency under selection is generally slowest when the allele being selected against is:

(A) Dominant and at a high frequency

(B) Dominant and at a low frequency

(C) Recessive and at a high frequency

(D) Recessive and at a low frequency

2022

5. In the context of the fundamental theorem of natural selection, the rate of increase in average fitness is proportional to the:

(A) Phenotypic variance of the population

(B) Environmental variance in fitness

(C) Additive genetic variance in fitness

(D) Dominance variance in fitness

2007

6. Which of the following statements regarding the selection coefficient (s) is INCORRECT?

(A) It quantifies the proportional reduction in gametic contribution of a genotype.

(B) A higher selection coefficient indicates weaker selection pressure.

(C) It ranges from 0 to 1 for deleterious traits.

(D) It is mathematically linked to biological fitness by the equation $W = 1 - s$.

2014

7. The following question consists of two statements, one labeled Assertion (A) and the other labeled Reason (R). Select the correct answer using the codes given below.

Assertion (A): In complete selection against a recessive allele, the allele is eliminated from the population in a single generation.

Reason (R): Complete selection prevents all recessive homozygotes from reproducing.

(A) Both A and R are true and R is the correct explanation of A.

(B) Both A and R are true but R is not the correct explanation of A.

(C) A is true but R is false.

(D) A is false but R is true.

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2013

8. The change in genotypic frequencies due to partial selection against a dominant allele primarily depends on:

(A) The selection coefficient and initial allele frequency

(B) The frequency of the recessive allele only

(C) The degree of dominance and initial allele frequency

(D) The mutation rate of the recessive allele

282. (A) Family selection or progeny testing
For traits with low heritability, individual phenotypic selection is generally ineffective because the environment masks much of the genetic potential. In these cases, family selection or progeny testing are more effective strategies. By using the average performance of relatives or daughters, breeders can more accurately estimate an individual's true breeding value, leading to more consistent and predictable genetic improvement over time.

283. (B) Lustrous carpet wool in migratory systems
The Gaddi sheep is a hardy breed native to the hilly regions of Himachal Pradesh and Uttarakhand. It is well-adapted to migratory management systems, moving between alpine pastures and lower valleys. Gaddi sheep are renowned for producing high volumes of lustrous carpet wool, which is a major source of income for nomadic pastoralist communities in the western Himalayan region.

284. (B) Bhadawari
The Bhadawari buffalo is characterized by its relatively lighter body and a peculiar copper-colored coat. Native to the Uttar Pradesh and Madhya Pradesh border regions, it is famous for its exceptional ability to produce milk with a very high fat content. This breed is highly resilient and thrives under traditional low-input management systems, making it a valuable genetic resource for rural farmers.

285. (A) Marginalized rearing with little capital for infrastructure
A major bottleneck for systematic swine breeding in India is that the sector is dominated by marginalized communities with very little capital for infrastructure. Pigs are often reared in traditional scavenging or semi-scavenging systems with minimal investment in housing or feed. This lack of organized management and recording makes it difficult to implement scientific selection programs or utilize advanced genetic improvement technologies.

286. (C) Exceptional prolificacy with large litter sizes
The Ghungroo pig is a highly valued indigenous breed from the Dooars region of West Bengal, primarily recognized for its exceptional prolificacy. These pigs regularly produce large litter sizes, often exceeding ten to twelve piglets per farrowing. Conserving this breed is a priority because its high reproductive capacity and adaptability make it a critical genetic resource for enhancing pork production in smallholder systems.

287. (D) All India Coordinated Research Projects (AICRP)
The All India Coordinated Research Projects are the primary frameworks for coordinating livestock improvement research across the country. These projects involve multiple research centers and state agricultural universities working together to evaluate breeding strategies and management practices for different species. This collaborative approach ensures that research is relevant to diverse agro-climatic zones and facilitates the systematic improvement of India's animal genetic resources.

288. (C) Genomic selection combined with MOET
To rapidly multiply superior genetics and overcome the shortage of progeny-tested bulls, breeders are increasingly using genomic selection combined with multiple ovulation and embryo transfer. Genomic selection allows for the early identification of elite animals, while MOET enables these superior females to produce many more offspring than through natural reproduction. This combination significantly accelerates the rate of genetic gain for indigenous livestock breeds.

289. (B) Top-crossing
The term "top-crossing" is sometimes used as a synonym for grading-up, especially when referring to the continuous use of purebred sires from a superior breed on a non-descript or common population. This strategy aims to rapidly increase the frequency of desirable alleles in the herd. Over several generations, the population's genetic makeup is transformed to resemble that of the superior sire breed.

290. (D) They exploit maternal heterosis while maintaining high individual merit
Three-way crosses are often preferred in rural poultry or swine breeding because they exploit both individual and maternal heterosis. By using a crossbred female as a dam, the system benefits from improved litter size, chick survival, and maternal care. Mating her to a third purebred sire ensures that the market offspring also exhibit high growth rates and feed efficiency, maximizing overall productivity.

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2024

18. Why is dominance deviation generally ignored when estimating breeding values in a random-mating livestock population?
(A) It cannot be passed predictably from parent to offspring
(B) It contributes only to maternal effects
(C) It is always zero in quantitative traits
(D) It is perfectly correlated with environmental variance

2002

19. If a bull's EBV for milk yield is +400 kg, the expected average phenotypic deviation of his large number of daughters from the population mean, assuming dams are average, is:
(A) +100 kg
(B) +200 kg
(C) +400 kg
(D) +800 kg

2002

20. The reliability or accuracy of an Estimated Breeding Value (EBV) increases with:
(A) Decreased heritability estimates of the specific trait
(B) Increased environmental variance within the population
(C) Reduced generation interval among breeding animals
(D) Increased amount of performance information utilized

2024

21. Which component of the phenotypic value is defined as the difference between the genotypic value and the breeding value?
(A) Additive genetic variance
(B) General environmental effect
(C) Non-additive genetic deviation
(D) Special environmental effect

2012

22. Consider the following statements regarding transmitting ability (TA):
I. TA is exactly equal to the expected breeding value of the progeny.
II. TA equals half the breeding value of the parent.
III. Progeny difference is synonymous with transmitting ability.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I, II and III

2003

23. In animal breeding, the Most Probable Producing Ability (MPPA) is utilized primarily to estimate:
(A) Sire evaluation for single-record traits
(B) The mutation rate of a quantitative trait
(C) The genetic correlation between two distinct traits
(D) Future performance of an individual for repeated traits

2023

24. A cow has a milk yield deviation of +500 kg from the herd average. If the heritability of milk yield is 0.3, her EBV based on this single record is:
(A) +150 kg
(B) +300 kg
(C) +75 kg
(D) +500 kg

2008

25. Phenotypic value can be partitioned into:
(A) Additive and non-additive values only
(B) Breeding value and dominance deviation only
(C) Genotypic value and environmental effect
(D) Permanent and temporary environmental effects only

2007

26. Which of the following does NOT improve the estimation of a sire's breeding value?
(A) Evaluating performance within one restricted environment
(B) Including phenotypic records from available full-sibs
(C) Utilizing information from half-sib progeny records
(D) Adjusting records for all known non-genetic factors

2024

27. The selection differential (S) is defined mathematically as:
(A) Phenotypic standard deviation adjusted by heritability
(B) Average offspring performance minus parental average
(C) Difference in breeding values between males and females
(D) Difference between selected group mean and population mean

2012

28. Standardized selection intensity (i) is calculated by:

NODIA

(A) Multiplying selection differential by heritability
(B) Dividing selection differential by phenotypic standard deviation
(C) Dividing selection differential by additive genetic variance
(D) Multiplying truncation point by the population mean

2003

29. In truncation selection, assuming a normal distribution, the standardized selection intensity (i) equals:

(A) $\frac{z}{p}$

(B) $\frac{p}{z}$

(C) $1 - \frac{z}{p}$

(D) $z \times p$

2009

30. Which factor leads to a reduction in expected selection intensity in small, finite populations?
(A) Increased mutation rate within the specific group
(B) Heterosis resulting from crossing distinct lines
(C) Linkage disequilibrium among neighboring loci
(D) Order statistics from finite population samples

2021

31. The following question consists of two statements, one labeled Assertion (A) and the other labeled Reason (R). Select the correct answer using the codes given below.
Assertion (A): As the proportion of animals selected for breeding increases, the selection intensity decreases.
Reason (R): Selecting a larger proportion includes animals whose phenotypic values are closer to the population mean.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2018

32. If the mean body weight of a base flock is 1.5 kg, and the selected breeders have a mean weight of 1.8 kg, what is the selection differential?
(A) 0.3 kg
(B) 1.5 kg
(C) 1.8 kg
(D) 3.3 kg

2018

33. The maximum standardized selection intensity achievable depends strictly on:
(A) Heritability of the trait
(B) The proportion of individuals selected
(C) Generation interval
(D) The breeding value of the top individual

2001

34. Which of the following scenarios maximizes the selection differential?
(A) Selecting 10% of the population
(B) Selecting 50% of the population
(C) Selecting 90% of the population
(D) Selecting individuals randomly

2018

35. For a trait with a phenotypic variance of 100, a selection intensity (i) of 1.5 yields a selection differential (S) of:
(A) 15
(B) 150
(C) 1.5
(D) 100

2025

36. What is the consequence of applying truncation selection on a non-normally distributed quantitative trait?
(A) The standard formula predicts intensity without error.
(B) Selection intensity becomes mathematically undefined.
(C) Heritability levels drop to zero almost immediately.
(D) The formula may incorrectly predict actual intensity.

2008

37. Which term describes the difference between the mean phenotypic value of selected individuals and the mean of their generation?
(A) Selection response
(B) Genetic slippage
(C) Selection differential
(D) Realized heritability

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2015

38. The standardized selection intensity for males is typically higher than for females in livestock species primarily because:
(A) Males have higher heritability for growth traits.
(B) A smaller proportion of males is required for reproduction.
(C) Males display greater phenotypic variance.
(D) Male traits are less affected by environmental variance.

2008

39. An unbiased estimation of the selection differential in a generation must account for:
(A) The inbreeding coefficient of the base population
(B) The non-additive genetic interactions
(C) The generation interval only
(D) The number of offspring each selected parent successfully produces

2021

40. Generation interval in an animal breeding program is defined as:
(A) The average age of parents when their selected offspring are born
(B) The lifespan of the longest-living breeding animal
(C) The time taken for an animal to reach sexual maturity
(D) The time gap between sequential pregnancies of a female

2015

41. The annual genetic progress (ΔG_{year}) is inversely proportional to:
(A) Accuracy of selection
(B) Selection intensity
(C) Generation interval
(D) Genetic standard deviation

2024

42. Choose the correct sequence of steps for calculating the average generation interval in a multi-pathway breeding scheme.
I. Determine the average age of sires to breed sons
II. Calculate the average age across all four parental pathways
III. Determine the average ages for dams to breed sons, sires to breed daughters, and dams to breed daughters
IV. Sum the age values of all four pathways and divide by four (assuming equal genetic contribution)
(A) I, III, IV, II
(B) III, I, IV, II
(C) I, III, II, IV
(D) II, I, III, IV

2014

43. Which parental pathway typically has the longest generation interval in traditional dairy cattle breeding?
(A) Sires to breed daughters (SD)
(B) Dams to breed sons (DS)
(C) Dams to breed daughters (DD)
(D) Sires to breed sons (SS)

2024

44. To maximize the rate of genetic change per year, a breeder should aim to:
(A) Minimize generation interval and selection accuracy
(B) Minimize generation interval while optimizing selection accuracy
(C) Maximize selection accuracy and generation interval
(D) Maximize generation interval and selection intensity

2017

45. In a closed herd, the average age of sires when calves are born is 4 years, and the average age of dams is 6 years. What is the approximate generation interval of the herd?
(A) 2 years
(B) 4 years
(C) 5 years
(D) 10 years

NODIA

2013

46. The generation interval for the "sires to breed sons" pathway in dairy cattle can be significantly reduced by implementing:
(A) Progeny testing
(B) Extended lactation cycles
(C) Repeated phenotypic measurements
(D) Genomic selection

2012

47. A primary disadvantage of relying exclusively on progeny testing is that it:
(A) Substantially increases the generation interval
(B) Lowers the accuracy of selection
(C) Decreases the selection intensity
(D) Masks the additive genetic variance

2023

48. Genetic response per year is calculated using the formula $\Delta G = \frac{(i_m + i_f)\, r_{TI}\, \sigma_A}{L_m + L_f}$. Here, L_m and L_f represent:
(A) Lethal alleles in males and females
(B) Generation intervals for males and females
(C) Longevity of males and females
(D) Selection limits in males and females

2011

49. Which species typically exhibits the shortest natural generation interval, allowing for rapid selection response?
(A) Cattle
(B) Poultry
(C) Swine
(D) Sheep

2025

50. Consider the following statements regarding generation interval:
I. Generation interval is identical across all livestock species.
II. Lowering the generation interval always reduces the accuracy of conventional selection.
III. Embryo transfer generally decreases the maternal generation interval.
IV. AI (Artificial Insemination) with young sires decreases the paternal generation interval.
Which of the above statements is/are incorrect?
(A) I and II
(B) I and III
(C) II and IV
(D) III and IV

2006

51. The introduction of multiple ovulation and embryo transfer (MOET) primarily impacts genetic gain by:
(A) Increasing selection intensity for the male pathway exclusively
(B) Eliminating non-additive genetic variance through inbreeding
(C) Decreasing generation intervals and increasing female intensity
(D) Increasing heritability of lowly heritable fertility traits

2023

52. If decreasing the generation interval severely reduces the accuracy of selection, the overall genetic gain per year will likely:
(A) Always increase due to the higher rate of generation turnover
(B) Always decrease toward zero due to extreme losses in accuracy
(C) Remain essentially the same regardless of accuracy changes
(D) Depend on the net balance between time and accuracy levels

2021

53. Individual (mass) selection is based solely on:
(A) The performance of the individual's full-sibs
(B) The average performance of the individual's parents
(C) The phenotypic performance of the individual itself
(D) The genomic estimated breeding value

2002

54. Mass selection is most highly effective for traits possessing:
(A) Low heritability
(B) High heritability
(C) Strong sex-limitation
(D) High dominance variance

2004

55. The accuracy of individual selection is mathematically equal to:
(A) The heritability (h^2)
(B) The repeatability
(C) The selection differential
(D) The square root of heritability (h)

2004

56. Pedigree selection relies on performance records from:
(A) Direct ancestors and collateral relatives in previous generations
(B) Phenotypic performance of direct offspring in the next generation
(C) The individual's own performance for the target selection trait
(D) Unrelated individuals within the same herd or management group

2012

57. Pedigree selection is particularly valuable early in an animal's life because:
(A) It provides higher accuracy than progeny testing
(B) It relies on traits with high heritability
(C) It allows for early selection before the animal expresses its own phenotype
(D) Ancestors' records perfectly predict dominance deviation

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2010

58. The maximum theoretical accuracy of evaluating an individual strictly based on the performance record of one of its parents is:
(A) 0.25
(B) 0.50
(C) 0.707
(D) 1.00

2017

59. Which of the following is a major limitation of individual (mass) selection?
(A) It is too complex computationally for practical use.
(B) It requires extensive multi-generation record keeping.
(C) It excessively increases the generation interval.
(D) It cannot be used for sex-limited traits or traits measured post-mortem.

2006

60. When evaluating an animal based on both parents' phenotypic records (assuming parents are unrelated and unselected), the accuracy of this pedigree selection is:
(A) $0.5h$
(B) $\sqrt{0.5h^2}$
(C) h
(D) $0.5h^2$

2021

61. Match the selection type in List I with its ideal application scenario in List II and select the correct option.
List I: (Selection Type)
P. Mass Selection
Q. Pedigree Selection
R. Progeny Testing
S. Within-Family Selection
List II: (Application)
1. Evaluation of sires for sex-limited traits like milk yield
2. Selection when there is a large common environmental effect among families
3. Early culling of animals before their own phenotype is expressed
4. Selection for a highly heritable growth trait in beef cattle
(A) P-4, Q-3, R-1, S-2
(B) P-3, Q-4, R-2, S-1
(C) P-1, Q-2, R-4, S-3
(D) P-2, Q-1, R-3, S-4

2006

62. In pedigree selection, records of an individual's grand-dam provide less information than records of its dam because:
(A) The grand-dam exhibits a significantly lower heritability.
(B) Phenotypic variance diminishes across subsequent generations.
(C) Environmental variance grows exponentially across generations.
(D) The additive relationship is 0.25 rather than 0.5 for the dam.

2024

63. Under which condition does adding pedigree information to an individual's own performance record provide the greatest relative increase in selection accuracy?
(A) When heritability of the trait is extremely low
(B) When heritability of the trait is extremely high
(C) When the generation interval is very short
(D) When the trait is highly influenced by dominance deviation

2016

64. A breeder uses mass selection for body weight in poultry. The primary risk of intense mass selection over many generations in a closed flock is:
(A) Lengthening of the generation interval
(B) Rapid accumulation of inbreeding
(C) Immediate fixation of lethal recessives
(D) An increase in additive genetic variance

2013

65. The correlation between an individual's breeding value and the phenotypic value of its half-sib is:
(A) $0.5h$
(B) $0.25h$
(C) $0.5h^2$
(D) $0.25h^2$

2010

66. Family selection evaluates individuals based on the:
(A) Mean phenotypic value of their family
(B) Best performing individual within the family
(C) Average of their ancestors' performance
(D) Deviation of their performance from the family mean

2010

67. Within-family selection is defined as selecting individuals based on:

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(A) Lower heritability of traits
(B) Smaller herd sizes and weaker systematic recording structures
(C) Shorter natural generation intervals
(D) Complete lack of AI techniques

2013

87. If a trait has a heritability of 0.25, what is the value of "a" in the accuracy equation $r_{TI} = \sqrt{\frac{n}{n+a}}$ for half-sib progeny?
(A) 3
(B) 4
(C) 15
(D) 16

2012

88. A dairy sire is evaluated using 15 daughters for a trait where $a = 15$. The expected accuracy of this progeny test is:
(A) 0.25
(B) 0.50
(C) 0.71
(D) 0.85

2006

89. Progeny testing is less attractive for traits that are:
(A) Traits that are expressed exclusively in one sex
(B) Traits measured only after the animal's slaughter
(C) Traits with high heritability measurable at an early age
(D) Traits characterized by having extremely low heritabilities

2011

90. To maximize genetic gain per unit of time in a progeny testing scheme, a breeder must find the optimum balance between:
(A) Number of sires tested and number of progeny per sire
(B) Milk yield and fat percentage
(C) Inbreeding depression and heterosis
(D) Progeny testing and crossbreeding

2022

91. The "Contemporary Comparison" method used in sire evaluation fundamentally relies on the principles of:
(A) Principles of individual selection based on ancestors
(B) Mass selection strategies within high-performing herds
(C) Within-family selection methods for non-sex-limited traits
(D) Progeny testing against contemporaries in similar herds

2013

92. Multi-trait selection aims to improve more than one economic trait simultaneously. Which of the following is NOT a standard method of multi-trait selection?
(A) Tandem selection
(B) Contemporary comparison
(C) Independent culling levels
(D) Selection index

2001

93. In tandem selection, the breeder selects for:
(A) All desired traits simultaneously using a weighted score
(B) Two traits using established minimum thresholds for both
(C) One trait at a time, moving to the next once a target is reached
(D) A single trait for the entire lifespan of the breeding program

2024

94. Tandem selection is least effective when:
(A) The traits have a high positive genetic correlation
(B) The traits are completely genetically independent
(C) The heritability of the primary trait is extremely high
(D) The traits have a strong negative (antagonistic) genetic correlation

2023

95. Independent Culling Levels (ICL) involve:
(A) Selecting sequentially, improving one trait per generation
(B) Developing an economic index to score animals
(C) Culling based on environmental deviations only
(D) Setting minimum standards for every individual trait

2018

96. Select the correct sequence of multi-trait selection methods ordered from theoretically least efficient to most efficient for overall aggregate genetic gain:
I. Selection Index
II. Tandem Selection
III. Independent Culling Levels
(A) III, II, I

NODIA

rational to separate genetic from environmental superiority?
(A) Mass selection
(B) Between-family selection
(C) Within-family selection
(D) Progeny testing

2004

78. A key disadvantage of extensive reliance on between-family selection is:
(A) Rapid increases in the population's generation interval
(B) Complete loss of non-additive genetic variance components
(C) Absolute inability to measure slaughter-based trait data
(D) High rate of inbreeding due to selection of whole families

2015

79. Progeny testing is fundamentally designed to estimate an individual's:
(A) Breeding value by evaluating offspring phenotypic means
(B) Genotypic value by measuring its own phenotype repeatedly
(C) Environmental deviation by rearing offspring in different climates
(D) Non-additive genetic merit within the selected group

2012

80. The primary justification for implementing progeny testing in dairy cattle breeding is that milk production is:
(A) A highly heritable trait
(B) A sex-limited trait
(C) Measurable in both sexes
(D) Exclusively determined by dominance deviation

2016

81. The accuracy of progeny testing ($r_{\{TI\}}$) for a sire evaluated on n half-sib progeny is mathematically given by:
(A) $\frac{n}{n+a}$
(B) $\sqrt{\frac{n}{n+a}}$
(C) $\sqrt{\frac{n+a}{n}}$
(D) $\frac{n-1}{n}$

2008

82. In the formula for progeny testing accuracy, $r_{TI} = \sqrt{\frac{n}{n+a}}$, the term "$a$" represents:
(A) $\frac{4-h^2}{h^2}$
(B) $\frac{1-h^2}{h^2}$
(C) $\frac{h^2}{4-h^2}$
(D) $\frac{4}{h^2}$

2001

83. As the number of progeny (n) increases toward infinity, the accuracy of progeny testing approaches:
(A) 0.50
(B) 0.75
(C) 1.00
(D) h^2

2021

84. In the optimization formulation for progeny testing, the optimum progeny group size for a sire is determined by balancing:
(A) Heritability and dominance variance
(B) Male and female generation intervals
(C) Direct and maternal genetic effects
(D) Selection intensity and selection accuracy within limited testing facilities

2017

85. Consider the following statements about progeny testing:
I. It significantly increases the generation interval compared to mass selection.
II. It is highly inaccurate for low heritability traits.
III. It facilitates the evaluation of sex-limited traits.
IV. It requires extensive record-keeping and robust identification systems.
V. It measures the exact dominance deviation of the sire.
Which of the above statements are correct?
(A) I, II, III and IV
(B) I, III and IV
(C) II, III, IV and V
(D) I, IV and V

2025

86. Which of the following limits the widespread use of progeny testing in sheep and goats compared to dairy cattle?

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R. G
S. a
List II: (Definitions)
1. Vector of unknown index weighting factors
2. Vector of relative economic values
3. Matrix of phenotypic variances and covariances
4. Matrix of genetic variances and covariances
(A) P-4, Q-2, R-3, S-1
(B) P-3, Q-1, R-4, S-2
(C) P-1, Q-4, R-2, S-3
(D) P-3, Q-2, R-4, S-1

2015

108. To solve for the index weights (b) in the Smith-Hazel equation $Pb = Ga$, one must compute:
(A) $b = G^{\{-1\}}Pa$
(B) $b = P^{\{-1\}}Ga$
(C) $b = PGa$
(D) $b = \left(PG\right)^{\{-1\}}a$

2004

109. The economic value (a_i) of a trait in the Smith-Hazel index represents the:
(A) Change in profit per unit increase in phenotypic standard deviation
(B) Total economic cost of measuring the specific trait in the population
(C) Expected profit increase per unit improvement in the breeding value
(D) Final market price of the animal at the time of commercial sale

2008

110. Which of the following is essential for the construction of a robust Smith-Hazel selection index?
(A) Use of only completely uncorrelated traits
(B) Setting the environmental variance to zero
(C) Having an infinite population size
(D) Accurate estimates of genetic and phenotypic parameters

2002

111. The accuracy of a selection index ($r_{\{IH\}}$) is determined by the formula:
(A) $\frac{\sigma_I}{\sigma_H}$
(B) $\frac{\sigma_H}{\sigma_I}$
(C) $\sigma_I \times \sigma_H$
(D) $\frac{\sigma_I^2}{\sigma_H}$

2006

112. If inaccurate genetic correlation parameters are used in constructing a Smith-Hazel index, the primary consequence is:
(A) Immediate negative genetic gain for all traits
(B) Suboptimal index weights leading to reduced genetic progress
(C) Complete mathematical failure of matrix inversion
(D) Conversion of the index into Independent Culling Levels

2001

113. A restricted selection index is utilized when the breeder desires to:
(A) Maximize aggregate genetic gain without bounds
(B) Hold the genetic change in one or more specific traits to zero
(C) Limit the number of phenotypic traits measured
(D) Restrict breeding to only a single sire line

2024

114. The variance of the selection index (σ_I^2) is equal to:
(A) $bâ€™Pb$
(B) $bâ€™Gaâ€™$
(C) $aâ€™Ga$
(D) $bâ€™Pa$

NODIA

2022

115. In a multi-trait index, if Trait A has a high positive economic value but a strong negative genetic correlation with Trait B (which also has a positive economic value), the index weight (b) for Trait A will likely be:
(A) Remain exactly equal to its stated economic value
(B) Increase higher than its value to provide compensation
(C) Be lowered to prevent degradation of the correlated trait
(D) Become zero regardless of its primary economic importance

2009

116. The base point or mean value of a calculated selection index score in a population is typically set to:
(A) 100
(B) The phenotypic mean of the primary trait
(C) The sum of the economic weights
(D) The heritability of the aggregate genotype

(B) II, III, I
(C) I, III, II
(D) II, I, III

2021

97. A major drawback of the Independent Culling Levels method is that:
(A) Requiring complex calculations of the aggregate genotype
(B) Culling superior animals for missing one specific threshold
(C) Limiting the selection to a maximum of only two traits
(D) Completely ignoring genetic correlations between traits

2007

98. The selection index method allows an animal's superiority in one trait to compensate for inferiority in another. This concept is termed:
(A) Aggregate balancing (or compensation)
(B) Genetic antagonism
(C) Compensatory mating
(D) Phenotypic substitution

2004

99. The theoretical superiority of the selection index over independent culling levels increases as:
(A) The number of traits under selection decreases
(B) The heritability of all traits approaches zero
(C) The number of traits under selection increases
(D) The economic weights of traits become exactly equal

2023

100. If two traits are favorably correlated, implementing Independent Culling Levels is:
(A) Less intense than tandem selection
(B) Completely impossible
(C) More efficient than if they were uncorrelated
(D) More efficient than the Selection Index

2016

101. Which multi-trait selection method requires the estimation of genetic and phenotypic variances and covariances, as well as relative economic values?
(A) Tandem selection
(B) Independent culling levels
(C) Selection index
(D) Progeny testing

2008

102. When an economic weighting shifts dramatically in the market, which selection method requires a complete recalculation of selection parameters?
(A) Tandem selection
(B) Selection index
(C) Individual mass selection
(D) Within-family selection

2002

103. The primary reason tandem selection is rarely used in modern commercial livestock breeding is:
(A) Requiring complex mathematical matrix inversion techniques
(B) Being impossible to apply to sex-limited performance traits
(C) Inherently causing sudden occurrences of lethal mutations
(D) Requiring too many generations to achieve multi-trait goals

2019

104. In Independent Culling Levels, what happens to the overall selection intensity for Trait A if a second trait, Trait B, is added to the culling criteria?
(A) It decreases
(B) It increases
(C) It remains constant
(D) It becomes exactly 1.0

2004

105. The Smith-Hazel selection index aims to maximize the correlation between the index score (I) and the:
(A) Individual's phenotypic value
(B) Environmental variance
(C) Aggregate breeding value (aggregate genotype, H)
(D) Maternal genetic effect

2017

106. In the formulation of the Smith-Hazel index, the aggregate genotype (H) is defined as:
(A) $H = \Sigma(a_i \times G_i)$
(B) $H = \Sigma(P_i \times G_i)$
(C) $H = \Sigma(h_i^2 \times P_i)$
(D) $H = \Sigma(a_i \times P_i)$

2005

107. Match the matrix terms used in the Smith-Hazel index equations in List I with their definitions in List II and select the correct option.
List I: (Matrix Terms)
P. P
Q. b

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(A) The average phenotypic value of the family
(B) The superiority of their sire's family over other sire families
(C) The deviation of their own performance from the mean of their family
(D) Their ability to mate successfully within the family

2015

68. Family selection is more efficient than individual selection when:
(A) Environmental effects common to the family are very large
(B) The heritability of the trait is very high
(C) Phenotypic variation within families is near zero
(D) The heritability is low and common environmental effects are minimal

2007

69. Within-family selection is advantageous and superior to mass selection particularly when:
(A) Traits have extremely high heritabilities
(B) Families are reared in identical, highly controlled environments
(C) There is a large common environmental variance shared by family members
(D) The genetic correlation among family members is zero

2002

70. The expected accuracy of family selection depends on the heritability of the trait, the number of individuals per family (n), and the:
(A) Additive relationship between the families
(B) Intraclass correlation among family members (t)
(C) Standard deviation of the mutation rate
(D) Difference between dominance and epistatic variance

2011

71. Sib selection is primarily used for traits that are:
(A) Easily measured on the live animal
(B) Governed strictly by maternal effects
(C) Highly heritable and uninfluenced by environment
(D) Expressed only in one sex or require slaughter for measurement

2007

72. The following question consists of two statements, one labeled Assertion (A) and the other labeled Reason (R). Select the correct answer using the codes given below.
Assertion (A): Within-family selection restricts the rate of inbreeding compared to mass selection.
Reason (R): Within-family selection ensures a more equal genetic contribution from all families to the next generation.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

NODIA

2019

73. If full-sib families are used, the additive genetic relationship among family members is:
(A) 0.25
(B) 0.50
(C) 0.75
(D) 1.00

2016

74. In which selection scheme is the individual's own phenotypic value completely ignored in favor of its relatives' performance?
(A) Sib selection
(B) Mass selection
(C) Family selection
(D) Within-family selection

2011

75. The phenotypic variance of family means (V_f) is defined in relation to total phenotypic variance (V_P), family size (n), and intraclass correlation (t) as:
(A) $V_f = \dfrac{V_P \times [1-(n-1)\,t]}{n}$
(B) $V_f = \dfrac{V_P}{n}$
(C) $V_f = V_P \times t$
(D) $V_f = \dfrac{V_P \times [1+(n-1)\,t]}{n}$

2015

76. Combined selection is best described as:
(A) Selecting for multiple traits simultaneously
(B) Using an optimally weighted index of individual performance and family mean
(C) Combining pedigree and progeny test results
(D) Crossing two different breeds and selecting the hybrids

2018

77. For traits with a high environmental variance common to the litter (e.g., pre-weaning growth in pigs), which selection method is most biologically

2008

117. Which component is NOT explicitly required to define the aggregate genotype (H)?
(A) True breeding values of the traits
(B) Relative economic weights
(C) Phenotypic variances
(D) Traits of economic importance

2016

118. The following question consists of two statements, one labeled Assertion (A) and the other labeled Reason (R). Select the correct answer using the codes given below.
Assertion (A): Simple daughter average is an unbiased method of sire evaluation.
Reason (R): It assumes all sires are mated to a random sample of dams with equal genetic merit.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2016

119. The Equal Parent Index (EPI) estimates the sire's index (I) based on daughter average (D) and dam average (M) as:
(A) $I = D - M$
(B) $\frac{D+M}{2}$
(C) $2M - D$
(D) $I = 2D - M$

2025

120. A fundamental flaw of the Equal Parent Index (EPI) is that it assumes:
(A) Perfect inheritance without any regression to the population mean
(B) Heritability of the target trait is essentially equal to zero
(C) Sires contribute no genetic material to their female offspring
(D) Maternal effects completely dictate the phenotypic performance

2015

121. The Contemporary Comparison method evaluates a sire by comparing the performance of his daughters to:
(A) The milk production performance of their own dams
(B) The milk production average of the entire national herd
(C) The performance of daughters of other sires in the same herd
(D) The lifetime production performance of the grand-dams

2002

122. In the context of the Contemporary Comparison method, "contemporaries" refers to animals that:
(A) Are managed under uniform environmental conditions (same herd, season, and year)
(B) Share the same sire
(C) Are born in different geographic regions in the same year
(D) Have the same genetic merit

2001

123. The formula for genetic evaluation using Contemporary Comparison often involves a weighting factor W based on the number of daughters (n_1) and contemporaries (n_2). W is proportional to:
(A) $\frac{n_1 + n_2}{n_1 \times n_2}$
(B) $\frac{n_1}{n_2}$
(C) $n_1 + n_2$
(D) $\frac{n_1 \times n_2}{n_1 + n_2}$

2017

124. The concept of "regression to the population mean" is incorporated into sire evaluation to account for:
(A) The chronological age of the sire at the time of evaluation
(B) Incomplete heritability and the specific number of daughters
(C) Significant changes in environmental conditions over decades
(D) Observed dominance deviations within the progeny group

2014

125. The Herdmate Comparison expands on Contemporary Comparison by:
(A) Comparing only the first-lactation heifer records
(B) Ignoring the herd's specific geographical location
(C) Including records from older animals producing in the same herd
(D) Eliminating the need to record the sire's identity

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(C) Generation interval
(D) Selection intensity

2017

167. Which phenomenon can cause the realized heritability estimate to artificially approach zero over many generations?
(A) High initial genetic variance
(B) Complete elimination of environmental variance
(C) Increased mutation rate
(D) A selection plateau being reached

2007

168. An advantage of estimating realized heritability via divergent selection rather than unidirectional selection is:
(A) Eliminating the need for a contemporaneous control population
(B) Doubling the effective selection intensity in a single line
(C) Preventing any form of inbreeding within the selected lines
(D) Guaranteeing that the selection response remains symmetric

2015

169. What does the "selection differential" represent in the context of realized heritability?
(A) The expected genetic superiority of the progeny group
(B) The environmental noise present over one generation
(C) The phenotypic superiority of animals retained for breeding
(D) The heritability calculated from available sibling data

2010

170. Multi-stage selection optimizes selection response primarily by:
(A) Reducing recording costs by culling inferior animals early
(B) Increasing the generation interval to improve overall accuracy
(C) Selecting exclusively based on the final adult performance trait
(D) Relying solely on the available genomic and molecular data

2017

171. A potential risk of intense first-stage culling in multi-stage selection is:
(A) Over-inflation of genetic variance
(B) Decreasing the generation interval excessively
(C) Eliminating environmental variance
(D) Suboptimal genetic gain for the primary trait measured at the final stage

2015

172. Marker-Assisted Selection (MAS) combines phenotypic data with molecular marker information to optimize response. MAS is most advantageous for traits that are:
(A) Highly heritable and easily measured on young individuals
(B) Low in heritability, sex-limited, or measured late in life
(C) Exclusively controlled by the environment
(D) Perfectly correlated with phenotypic mass

NODIA

2002

173. The following question consists of two statements, one labeled Assertion (A) and the other labeled Reason (R). Select the correct answer using the codes given below.
Assertion (A): Optimizing the age structure of a breeding herd maximizes annual genetic progress.
Reason (R): Keeping only very young parents minimizes the generation interval but may reduce the average selection accuracy compared to a herd with proven older sires.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2011

174. In a breeding program, optimizing age structure means finding the ideal proportion of individuals in each age class to balance:
(A) Meat quality and wool production
(B) Dominance and epistasis
(C) Inbreeding and mutation rate
(D) Selection intensity, accuracy, and generation interval

2022

175. The efficiency of Marker-Assisted Selection (MAS) over traditional phenotypic selection is greatest when the proportion of additive genetic variance explained by the markers (p) is:
(A) Large
(B) Zero
(C) Very small
(D) Exactly equal to heritability

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(D) Identity matrix

2022

137. Which method directly accommodates non-random mating, selection bias, and overlapping generations in genetic evaluation?
(A) Contemporary Comparison
(B) Simple Daughter Average
(C) BLUP (Animal Model)
(D) Equal Parent Index

2022

138. The inclusion of the inverse of the additive genetic relationship matrix (A^{-1}) in the mixed model equations serves to:
(A) Tying together information from all relatives for the estimation
(B) Eliminating the requirement to know the trait's heritability
(C) Converting all random effects into fixed effect parameters
(D) Removing the direct influence of the sire's genetic merit

2001

139. Fixed effects in a BLUP evaluation model for dairy cattle typically include:
(A) Sire breeding values
(B) Dam breeding values
(C) Mendelian sampling
(D) Herd-year-season (HYS) effects

2014

140. Match the mathematical components of the Animal Model in List I with their descriptions in List II and select the correct option.
List I: (Mathematical Component)
P. y
Q. b
R. Z
S. e
List II: (Description)
1. Incidence matrix for random effects
2. Vector of fixed effects
3. Vector of residual random errors
4. Vector of phenotypic observations
(A) P-4, Q-2, R-1, S-3
(B) P-3, Q-1, R-4, S-2
(C) P-4, Q-1, R-2, S-3
(D) P-2, Q-3, R-1, S-4

2001

141. The Least Squares method for sire evaluation is considered suboptimal compared to BLUP because:
(A) Requiring the inversion of excessively large mathematical matrices
(B) Being unable to calculate significant environmental trends over time
(C) Treating sire effects as fixed and ignoring genetic distributions
(D) Utilizing only dam records for the estimation of breeding values

2013

142. BLUP estimates environmental (fixed) effects and genetic (random) effects:
(A) Sequentially, calculating fixed effects first
(B) Completely independently using different datasets
(C) By assuming random effects are zero
(D) Simultaneously, adjusting each for the other

2008

143. Which of the following is required a priori (in advance) to perform a BLUP evaluation using the Animal Model?
(A) The ratio of residual variance to genetic variance (e.g., $\frac{1-h^2}{h^2}$)
(B) True breeding values of the base population
(C) The exact environmental deviation of each animal
(D) Future performance records of progeny

NODIA

2011

144. The prediction of expected genetic response per generation (R) relies on the breeder's equation:
(A) $R = i \times h^2 \times \sigma_P$
(B) $R = i \times h^2 \times \sigma_A$
(C) $R = S \times h$
(D) $R = i \times \sigma_P$

2019

145. If the selection differential for yearling weight is 20 kg and the heritability is 0.4, the predicted genetic response per generation is:
(A) 5 kg
(B) 8 kg
(C) 10 kg
(D) 20 kg

2005

146. In a closed herd, the male selection differential is 30 units and the female selection differential is 10 units. If heritability is 0.5, the expected response per generation is:
(A) 20 units
(B) 15 units
(C) 10 units
(D) 5 units

selection and BLUP animal models

2010

204. How does the BLUP animal model account for the Bulmer effect?
(A) By ignoring the relationship matrix during the estimation
(B) By utilizing the pedigree and relationship matrix in BLUP
(C) By explicitly assuming variance increases over time periods
(D) It cannot account for the Bulmer effect mathematically

2015

205. The negative linkage disequilibrium generated by truncation selection means that an individual with a highly favorable allele at one locus is statistically:
(A) More likely to have favorable alleles at other loci
(B) Guaranteed to be homozygous at all loci
(C) Less likely to have favorable alleles at other loci compared to a random combination
(D) Immune to environmental effects

2005

206. Choose the correct sequence of events describing the Bulmer effect under continuous selection:
I. Truncation selection favors specific combinations of alleles, creating negative linkage disequilibrium
II. Additive genetic variance stabilizes at a new, lower asymptotic level
III. A base population undergoes intense directional selection
IV. The additive genetic variance available for the next generation is reduced
(A) III, I, IV, II
(B) I, III, II, IV
(C) III, IV, I, II
(D) IV, I, II, III

2025

207. If the Bulmer effect is ignored in the theoretical design of a long-term selection program, the breeder will:
(A) Overestimate the genetic gain
(B) Accurately predict genetic gain
(C) Underestimate the genetic gain
(D) Prevent genetic slippage

2005

208. Recombination during meiosis counteracts the Bulmer effect by:
(A) Introducing new mutations
(B) Halving the chromosome number
(C) Increasing the selection intensity
(D) Breaking down the selection-induced linkage disequilibrium

2025

209. The primary purpose of maintaining a control population in a selection experiment is to:
(A) Provide a source of replacement animals for the selected line
(B) Distinguish genetic trends from environmental trends over time
(C) Increase the overall selection intensity across the program
(D) Maximize the rate of inbreeding within the elite breeding group

2017

210. An ideal randombred control population should:
(A) Maintain a large effective size to minimize drift and inbreeding
(B) Be subjected to mild directional selection for the target trait
(C) Have a completely different genetic base than the selected line
(D) Consist of only one sire and multiple dams for the entire herd

2001

211. Which mating design is specifically utilized to estimate environmental trends without requiring a completely separate, unselected control line?
(A) Positive assortative mating
(B) Brother-sister mating
(C) Repeat-mating design
(D) Rotational crossbreeding

2006

212. In a repeat-mating design, environmental trend is estimated by comparing the performance of:
(A) Parents and their offspring measured in the same calendar year
(B) Unrelated individuals measured in completely different environments
(C) Full-sibs reared in different herds with varying management levels
(D) Progeny from same parents born and reared in consecutive years

2007

213. To minimize genetic drift in a control population, breeders often use a mating scheme where:
(A) Only the top 5% of males are allowed to mate in the population
(B) Full-sibs are preferentially mated to maintain genetic identity

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differential to the generation interval
(B) The regression of offspring phenotype on parent phenotype
(C) The ratio of the realized selection response to the realized selection differential
(D) The additive genetic variance divided by phenotypic variance

2008

158. If a selection experiment yields a cumulative response of +15 units over 5 generations, and the cumulative selection differential is +50 units, the realized heritability is:
(A) 0.15
(B) 0.30
(C) 0.50
(D) 0.65

2001

159. The most statistically robust method to estimate realized heritability from multiple generations of selection is:
(A) Linear regression of cumulative response on selection differential
(B) Dividing the final generation's mean by the base generation mean
(C) Averaging the selection intensity values over all generations
(D) The regression of the generation number on phenotypic means

2003

160. Why might realized heritability differ significantly from the base population's estimated heritability (calculated via sib correlations)?
(A) Realized heritability includes only environmental effects.
(B) Realized heritability is purely theoretical in nature.
(C) Realized heritability assumes there is no genetic variance.
(D) Shifts in gene frequencies or environmental trends alter variance.

2013

161. A divergent selection experiment involves:
(A) Selecting two distinct traits simultaneously
(B) Selecting one line for high values and another line for low values of the same trait
(C) Crossing two divergent breeds to observe heterosis
(D) Selecting one trait and observing the correlated response in another

2004

162. Consider the following statements regarding realized heritability:
I. It requires the presence of an unselected control population to adjust for environmental trends.
II. It is estimated prospectively before selection begins.
III. It can be asymmetric in up-versus-down selection lines.
IV. It utilizes the cumulative selection differential.
Which of the above statement(s) is/are incorrect?
(A) I and II
(B) II only
(C) III and IV
(D) I and IV

2014

163. Asymmetrical response in a divergent selection experiment (where realized heritability differs between high and low lines) is primarily caused by:
(A) Directional dominance
(B) Balanced polymorphism
(C) Absence of maternal effects
(D) Constant allele frequencies

2014

164. To accurately calculate realized response per generation, deviations must be measured against:
(A) The original base population mean without any adjustment
(B) The selected parents belonging to the current generation
(C) The theoretical maximum phenotype achievable in the species
(D) An unselected control population reared contemporaneously

NODIA

2003

165. If the selection response in generation 3 is 6 units and the cumulative selection differential is 24 units, the estimated realized heritability up to generation 3 is:
(A) 0.15
(B) 0.25
(C) 0.35
(D) 0.50

2018

166. In a plot of cumulative genetic response (Y-axis) against cumulative selection differential (X-axis), the slope of the fitted line represents:
(A) The genetic correlation
(B) Realized heritability

2004

126. A limitation of both Contemporary Comparison and early Herdmate Comparison methods was that they:
(A) Evaluating only those traits with heritabilities above 0.5
(B) Requiring animal populations to be completely inbred
(C) Being too mathematically complex for computers of that era
(D) Assuming that the genetic merit of herdmate sires was average

2012

127. If a sire's daughters average 4000 kg milk, and their dams average 3800 kg, what is the sire's Equal Parent Index (EPI)?
(A) 4200 kg
(B) 4000 kg
(C) 3800 kg
(D) 4100 kg

2022

128. Why did the simple daughter average method frequently over- or under-estimate a sire's true breeding value?
(A) Perfectly accounting for environmental differences across herds
(B) Confounding sire merit with management and environmental levels
(C) Including all maternal effects inherited from the dam's side
(D) Utilizing genomic testing data incorrectly during the process

2001

129. Consider the following statements concerning the limitations of the Herdmate Comparison method:
I. It does not account for the genetic trend (improvement over time).
II. It assumes environmental effects are genetically inherited.
III. It assumes all herdmates have sires of equal genetic merit.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I, II and III

2001

130. The Modified Contemporary Comparison (MCC) improved upon earlier methods primarily by:
(A) Grouping sires by genetic merit to account for genetic trend
(B) Removing the regression to the mean factor
(C) Ignoring partial lactations
(D) Using the Equal Parent Index alongside it

2024

131. BLUP stands for:
(A) Basic Linear Unbiased Predictor
(B) Balanced Linear Uniform Prediction
(C) Best Linear Unbiased Prediction
(D) Broad Linear Unbiased Parameter

2023

132. In the context of BLUP, the term "Best" implies that the prediction mathematically:
(A) Maximizes the phenotypic variance
(B) Maximizes the generation interval
(C) Uses the most number of traits
(D) Minimizes the prediction error variance

2017

133. BLUP is "Unbiased" because:
(A) Completely removing all sources of genetic variance
(B) Yielding identical breeding values for all relatives
(C) Producing a predictor equal to the true breeding value
(D) Treating all environmental factors as being identical

2005

134. A major mathematical advantage of the Animal Model in BLUP is its use of the:
(A) Phenotypic correlation matrix
(B) Numerator relationship matrix (A-matrix)
(C) Equal parent index
(D) Tandem selection framework

2016

135. In the generalized mixed model equation used in BLUP is $y = Xb + Zu + e$. The term "u" represents:
(A) Fixed environmental effects
(B) The vector of observable phenotypes
(C) The vector of random residual errors
(D) The vector of random genetic effects (breeding values)

2006

136. In the BLUP mixed model equation $y = Xb + Zu + e$, the matrix X represents the:
(A) Incidence matrix relating observations to fixed effects
(B) Incidence matrix relating observations to random effects
(C) Inverse of the relationship matrix

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2011

176. Genomic Selection optimizes selection response over classical progeny testing primarily by:
(A) Increasing the dominance variance
(B) Drastically reducing the generation interval via early prediction of breeding values
(C) Eliminating the need to ever record phenotypes
(D) Selecting purely on mitochondrial DNA

2004

177. When allocating selection intensity across multiple stages (e.g., weaning weight then yearling weight), the overall selection intensity is:
(A) The sum of the selection intensities at each stage
(B) A function of the independent culling proportions and genetic correlations between the stages
(C) Determined only by the final stage
(D) Always 1.0

2016

178. What limits the theoretical maximum genetic response achieved by highly intense truncation selection?
(A) Finite population size leading to rapid inbreeding and loss of genetic variance
(B) Exhaustion of environmental variance
(C) The decrease of the generation interval
(D) The increase in multi-stage accuracy

2018

179. In optimizing a dairy cattle breeding scheme, replacing widespread progeny testing entirely with genomic selection yields:
(A) Higher reliability per young sire but longer generation interval
(B) Higher environmental variance
(C) Slightly lower initial reliability per young sire but a massively reduced generation interval
(D) Complete eradication of genetic defects

2013

180. To optimize selection response, the breeder must maximize the correlation between:
(A) The phenotypic value and environmental effects
(B) The generation interval and selection intensity
(C) Dominance variance and epistatic variance
(D) The selection criterion and the true breeding value

NODIA

2003

181. In an optimized two-stage selection process, trait 1 (measured early) is used for initial culling, and trait 2 (the primary goal) is measured later. Trait 1 must be:
(A) Uncorrelated with Trait 2
(B) Negatively correlated with Trait 2
(C) Positively genetically correlated with Trait 2
(D) A discrete Mendelian trait

2023

182. A closed nucleus breeding system aims to optimize selection response by:
(A) Dispersing elite animals to commercial herds randomly
(B) Concentrating intense selection in a small elite herd
(C) Ignoring multi-stage selection entirely in the program
(D) Crossbreeding with indigenous non-descript animal lines

2006

183. A selection plateau occurs when:
(A) The population continues to respond linearly to selection pressure.
(B) The selection differential becomes mathematically undefined.
(C) Realized heritability abruptly equals 1.0.
(D) The population ceases to respond to continued selection pressure.

2010

184. Match the causes of selection plateaus in List I with their descriptions in List II and select the correct option.
List I: (Causes of Selection Plateaus)
P. Exhaustion of additive variance
Q. Overdominance
R. Negative genetic correlation
S. Inbreeding depression
List II: (Descriptions)
1. Favorable alleles are fixed, leaving no selectable genetic variation.
2. Heterozygotes are favored, preventing the fixation of either allele.
3. General decline in fitness and vigor due to increased homozygosity.
4. Improvement in the selected trait causes a detrimental decline in a linked fitness trait.
(A) P-1, Q-2, R-4, S-3
(B) P-4, Q-3, R-1, S-2
(C) P-1, Q-3, R-4, S-2
(D) P-2, Q-1, R-3, S-4

2021

185. "Genetic slippage" is best described as:
(A) The immediate increase in performance upon relaxation of selection
(B) A decline in the mean phenotypic value when selection pressure is relaxed after a plateau
(C) The sudden appearance of a lethal mutation
(D) The increase of additive genetic variance in a small population

2021

186. Which genetic architecture is a primary theoretical cause of genetic slippage following the cessation of selection?
(A) Extensive epistatic interactions favoring specific combinations
(B) Complete fixation of dominant alleles within the population
(C) A perfectly normal distribution of all alleles in the herd
(D) High additive variance present throughout the selection process

2019

187. A selection plateau caused by negative genetic correlations between the selected trait and fitness components means that:
(A) Artificial selection intensity must be increased infinitely
(B) Heritability has reached 1.0
(C) The trait is no longer influenced by genetics
(D) Natural selection opposes artificial selection

2017

188. Which strategy is most commonly used to break a selection plateau caused by the exhaustion of additive genetic variance?
(A) Increasing selection intensity within the plateaued line
(B) Crossing the line with an unrelated population or mutation
(C) Reducing the generation interval of the breeding animals
(D) Relaxing selection completely for several generations

2009

189. If a plateau is caused by overdominance at multiple loci, relaxing selection will cause the phenotypic mean to:
(A) Continue increasing
(B) Remain exactly at the plateau
(C) Decline due to the loss of forced heterozygote advantage
(D) Drop to zero instantly

2025

190. Selection limits in finite populations are largely dictated by:
(A) The phenotypic standard deviation of the base population
(B) The specific sequence of nucleotides in the markers
(C) The environmental variance during the first generation
(D) The initial frequency of favorable alleles and effective population size (N_e)

2003

191. Natural selection can stall artificial selection progress because:
(A) Extreme phenotypes selected by humans often possess lower natural reproductive fitness.
(B) Natural selection always favors higher body weights.
(C) Natural selection completely eliminates dominance.
(D) Artificial selection genes are easily mutated by nature.

2009

192. Reverse selection after reaching a plateau usually:
(A) Yields no response because all variance is effectively gone
(B) Causes complete sterility within the selected breeding lines
(C) Triggers an immediate increase in the selection differential
(D) Produces a rapid response if natural selection was an factor

2014

193. The ultimate limit to selection in an idealized population without new mutations is reached when:
(A) Inbreeding reaches exactly 0.5.
(B) All favorable alleles are either fixed or lost due to drift.
(C) Environmental variance equals genetic variance.
(D) Selection intensity equals zero.

2014

194. If selection for increased egg production in poultry results in a plateau despite remaining additive genetic variance for egg number, the most likely cause is:
(A) A strong negative genetic correlation with essential fitness
(B) The fixation of all alleles across the entire poultry genome

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(C) Positive epistasis occurring within the egg production traits
(D) Over-nutrition of the flock resulting in physiological limits

2025

195. Consider the following statements regarding genetic slippage:
I. It occurs only during active, intense selection.
II. It is characterized by a regression towards the original population mean upon relaxation of selection.
III. It can be caused by the breakdown of favorable epistatic combinations.
IV. It indicates that the population had reached fixation for all traits.
V. It demonstrates the tension between artificial and natural selection.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) II, III and V
(C) I, III and IV
(D) III, IV and V

2001

196. The "Bulmer effect" describes the phenomenon where directional truncation selection:
(A) Increases the mutation rate of all linked genetic loci
(B) Increases phenotypic variance within the select population
(C) Causes immediate and complete inbreeding across the herd
(D) Decreases genetic variance through linkage disequilibrium

2025

197. The reduction in genetic variance caused by the Bulmer effect is due primarily to:
(A) The physical loss of alleles from the population
(B) The sudden increase in environmental variance
(C) Negative linkage disequilibrium generated among trait-enhancing alleles
(D) Positive assortative mating

2007

198. Does the Bulmer effect permanently eliminate alleles from the population?
(A) Yes, by selectively eliminating homozygotes from the group
(B) No, it changes covariance between loci via linkage balance
(C) Yes, it acts exactly like genetic drift in small populations
(D) No, it actually increases the frequency of deleterious genes

2001

199. When directional selection is relaxed after a few generations, the genetic variance reduced by the Bulmer effect will:
(A) Remain permanently reduced throughout the subsequent history
(B) Drop to exactly zero following the cessation of selection
(C) Double its original base value within a single generation
(D) Gradually recover over a few generations as linkage breaks

2016

200. Because of the Bulmer effect, the actual selection response in the second generation of a breeding program will typically be:
(A) Lower than predicted by the base population heritability
(B) Higher than predicted by the base population heritability
(C) Exactly equal to the first generation's response
(D) Completely unpredictable

NODIA

2005

201. The magnitude of the variance reduction caused by the Bulmer effect depends on:
(A) Only the effective population size
(B) The number of chromosomes in the species
(C) The selection intensity and the trait's heritability
(D) Only the environmental variance

2016

202. Under continuous truncation selection, the additive genetic variance eventually reaches an equilibrium called the:
(A) Asymptotic variance
(B) Selection plateau
(C) Gametic phase balance
(D) Epistatic limit

2014

203. The Bulmer effect is particularly pronounced and important to account for in:
(A) Random mating populations with no selection
(B) Crossbreeding systems utilizing heterosis
(C) Conservation programs of endangered species
(D) Elite breeding schemes utilizing intense

2022

147. Annual genetic response is calculated as the generation response divided by the:
(A) Heritability
(B) Selection intensity
(C) Average generation interval of both sexes
(D) Genetic standard deviation

2010

148. Which factor does NOT influence the predicted rate of genetic response to selection?
(A) Additive genetic variance within the population
(B) Accuracy of the specific selection method used
(C) Generation interval between parents and offspring
(D) Dominance deviation present in a strictly additive model

2016

149. The expected response from indirect selection on Trait X to improve Trait Y relies heavily on the:
(A) Phenotypic variance of Trait X only
(B) Environmental correlation between the traits
(C) Genetic correlation between Trait X and Trait Y
(D) Generation interval of Trait Y

2013

150. A negative predicted genetic response in a trait of economic importance despite selection for a different positive trait implies:
(A) The selection intensity is too high.
(B) The two traits have an antagonistic (negative) genetic correlation.
(C) Heritability is equal to 1.0.
(D) Environmental variance has completely masked the genotype.

2001

151. Choose the correct sequence of parameters required to accurately predict annual genetic gain in a four-pathway selection program:
I. Calculate the sum of generation intervals ($L_{\{SS\}} + L_{\{SD\}} + L_{\{DS\}} + L_{\{DD\}}$)
II. Determine selection intensities and accuracy for each pathway
III. Divide the total multi-pathway genetic gain by the sum of the generation intervals
IV. Sum the genetic superiority $(i \times r \times \sigma_A)$ contributed by each of the four pathways
(A) IV, II, I, III
(B) II, I, IV, III
(C) I, II, III, IV
(D) II, IV, I, III

2011

152. Under multi-pathway selection (e.g., dairy cattle), which pathway generally contributes the largest portion to the total predicted genetic superiority?
(A) Sires to breed sons
(B) Dams to breed daughters
(C) Dams to breed sons
(D) Sires to breed daughters

2002

153. When a population is subjected to truncation selection, the predicted genetic response for the next generation assumes that:
(A) All genetic variance in the population is non-additive
(B) The selection differential is effectively equal to zero
(C) The trait follows an infinitesimal model with normal distribution
(D) The base population is completely inbred across all loci

2023

154. Correlated response to selection (CR_Y) in Trait Y when selection is applied to Trait X is predicted by:
(A) $i_X \times h_X \times h_Y \times r_G \times \sigma_{PY}$
(B) $i_X \times h_X \times r_G \times \sigma_{PX}$
(C) $i_X \times h_Y \times r_G \times \sigma_{AX}$
(D) $i_X \times h_X \times h_Y \times \sigma_{PY}$

2017

155. If the accuracy of selection ($r_{\{TI\}}$) equals 1.0, the predicted genetic response simplifies to:
(A) $i \times \sigma_P$
(B) $i \times h^2$
(C) $S \times \sigma_A$
(D) $i \times \sigma_A$

2008

156. In predicting genetic response, the "Bulmer effect" must often be accounted for because it:
(A) Significantly increases the phenotypic standard deviation
(B) Reduces additive genetic variance via linkage disequilibrium
(C) Dramatically changes the economic weights of selected traits
(D) Renders BLUP evaluations as being mathematically biased

2011

157. Realized heritability is estimated retrospectively from a selection experiment by calculating:
(A) The ratio of the cumulative selection

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(C) Every sire leaves one son and every dam leaves one daughter
(D) Generations are turned over as rapidly as possible in the line

2011

214. If the selected line's mean phenotypic value increases by 10 units, and the control line's mean increases by 4 units due to better nutrition, the estimated actual genetic response is:
(A) 14 units
(B) 10 units
(C) 6 units
(D) 4 units

2011

215. A control population's base allele frequencies should ideally:
(A) Be fixed at 1.0 for all dominant alleles
(B) Lack any additive genetic variance
(C) Differ completely from the selected line to provide contrast
(D) Be identical to the base population from which the selected line is derived

2021

216. Cryopreservation of semen or embryos is increasingly used to establish controls because it:
(A) Completely halting genetic drift and mutation in the samples
(B) Increasing the mutation rate artificially for research purposes
(C) Forces mutations to revert to wild-type states over time
(D) Shortens the generation interval of the breeding population

2009

217. Consider the following statements regarding control populations:
I. They must be maintained in the same environment as the selected line.
II. They must undergo the same truncation selection as the experimental line.
III. They are essential for accurately estimating realized heritability.
Which of the above statements are correct?
(A) I and II
(B) II and III
(C) I and III
(D) I, II and III

2006

218. When estimating environmental variance, a randombred control population assumes that:
(A) Its genetic mean remains constant over time
(B) Its genetic mean changes exactly parallel to the selected line.
(C) It has no environmental variance.
(D) Genetic drift will push it towards higher productivity.

2015

219. The "Gowe mating system" (or similar cyclical pedigree designs) used in poultry control populations is designed specifically to:
(A) Maximize inbreeding levels within the poultry population
(B) Select for multiple traits simultaneously in the same bird
(C) Facilitate natural selection under commercial farm conditions
(D) Minimize inbreeding while maintaining stable genetic variance

2017

220. If a control population suffers from significant undetected genetic drift, the calculated genetic response of the selected line will be:
(A) Mathematically perfect
(B) Biased (over- or under-estimated)
(C) Completely unaffected
(D) Reduced to zero

2008

221. A major challenge in maintaining live animal control populations over many generations, compared to using frozen semen, is:
(A) Live animals cannot reproduce naturally in a control setting
(B) Live animals do not respond to the local farm environment
(C) The accumulative cost and accumulation of inbreeding or drift
(D) They inherently develop hybrid vigor within the control lines

2002

222. Classic selection experiments in mice primarily focused on selecting for:
(A) Coat color mutations
(B) Tail length and visual acuity
(C) Resistance to induced tumors
(D) 6-week body weight

2021

223. In classic two-way selection experiments for mouse body weight, the asymmetrical response observed was partially attributed to:
(A) Maternal effects providing superior pre-weaning environments
(B) Complete dominance of small body weight

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2001

282. Tocher's method of clustering starts by grouping two populations that have:
(A) The minimum D^2 value
(B) The maximum D^2 value
(C) An average D^2 value
(D) A D^2 value of zero only

2006

283. In evaluating divergence among cattle breeds, the D^2 statistic is robust because it:
(A) Focuses solely on milk yield in the distance calculation
(B) Requires only simple addition of the metric trait values
(C) Eliminates the need to measure any traits in the population
(D) Standardizes measurement scales for different types of traits

2003

284. If two populations have identical means for all measured traits, their Mahalanobis D^2 value will be:
(A) 1.0
(B) Zero
(C) Infinite
(D) Undefined

2009

285. Mahalanobis distance is considered a generalized form of:
(A) Nei's genetic distance
(B) Wright's F-statistics
(C) Euclidean distance
(D) Manhattan distance

2019

286. Which statistical software procedure is most directly aligned with utilizing Mahalanobis distance to separate predefined groups?
(A) Linear Regression
(B) Chi-Square Goodness of Fit
(C) Student's t-test
(D) Canonical Discriminant Analysis

2005

287. Wright's Fixation Index ($F_{\{ST\}}$) is a measure of:
(A) Population differentiation due to structure and divergence
(B) Morphological distance between two specific breeding animals
(C) Inbreeding level of a single individual within the population
(D) The heritability of a molecular marker used in the study

2008

288. An $F_{\{ST\}}$ value of 0 indicates:
(A) Complete genetic isolation between subpopulations (fixation of different alleles)
(B) No genetic differentiation; subpopulations share identical allele frequencies
(C) The population is completely inbred
(D) A high rate of mutation

2015

289. Nei's Standard Genetic Distance (D) estimates the:
(A) Average number of codon substitutions per locus between groups
(B) Physical distance in base pairs between two linked genes
(C) Morphological divergence based on the pooled covariance data
(D) Number of chromosomes in a species of agricultural interest

NODIA

2001

2004

290. Nei's genetic identity (I) and genetic distance (D) are mathematically related by:
(A) $D = -\ln(I)$
(B) $D = 1 - I$
(C) $D = I^2$
(D) $D = \exp(I)$

2016

291. If two populations have identical allele frequencies at all loci, Nei's genetic identity (I) equals:
(A) 0
(B) 0.5
(C) 1.0
(D) Infinity

2011

292. Microsatellite markers have been historically preferred for breed characterization and calculating $F_{\{ST\}}$ because they are:
(A) Highly conserved with no variation
(B) Located strictly on mitochondrial DNA
(C) Dominant markers
(D) Highly polymorphic and codominantly inherited

2024

293. The calculation of $F_{\{ST\}}$ relies on comparing:
(A) Phenotypic mean of subpopulation A compared to subpopulation B
(B) The mutation rates of different markers used in the study
(C) Heterozygosity within groups compared to the total population

2007

232. In a classic selection experiment for pupal weight in Tribolium, crossing the plateaued line with an unselected control line resulted in renewed response. This demonstrated that the plateau was primarily due to:
(A) Exhaustion of additive genetic variance in the selected line
(B) Overdominance occurring within the specific loci of interest
(C) Negative genetic correlation between growth and fitness traits
(D) Environmental constraints limiting the growth of the beetle

2021

233. The concept of "realized herizability" was practically cemented through the analysis of data from:
(A) Wild animal population tracking
(B) Short-term divergent selection experiments in lab models like mice and Drosophila
(C) Single-generation progeny tests
(D) Cloning experiments

2002

234. Selection experiments in mice for litter size revealed that maternal performance is:
(A) Highly genetically correlated with litter size in a complex way
(B) Irrelevant to the survival of the offspring during weaning
(C) Dependent solely on single-gene Mendelian inheritance traits
(D) Inversely related to the number of litters produced per female

2025

235. The Major Histocompatibility Complex (MHC) in animals plays a crucial role in genetic resistance to disease because it:
(A) Encodes for massive muscle growth in the skeletal structure
(B) Prevents the entry of pathogens through the external skin
(C) Regulates the body's internal temperature and metabolism
(D) Determines the specificity of immune response to antigens

2016

236. The MHC in poultry is known as the:
(A) BoLA complex
(B) B-complex
(C) SLA complex
(D) OLA complex

2023

237. Breeding for mastitis resistance in dairy cattle is challenging because mastitis resistance generally has:
(A) A heritability that is effectively equal to 1.0 in the herd
(B) A highly favorable genetic correlation with overall milk yield
(C) An antagonistic genetic correlation with overall milk yield
(D) No genetic basis whatsoever within the dairy cattle population

2009

238. Which trait is most commonly used as an indirect indicator trait for selection against mastitis in dairy cattle?
(A) Udder depth and physical structure measurements
(B) Milk fat percentage recorded during the lactation
(C) Calving ease and birth weight of the dairy calves
(D) Somatic Cell Score or Somatic Cell Count in milk

2012

239. Marek's disease in poultry is caused by a herpesvirus. Genetic resistance to Marek's disease has been strongly linked to specific alleles in the:
(A) MHC B-complex
(B) Z chromosome
(C) W chromosome
(D) Mitochondrial genome

2006

240. The heritability of disease resistance traits in livestock is generally:
(A) Exceptionally high (>0.8)
(B) Low to moderate (<0.3)
(C) High (0.5 - 0.7)
(D) Exactly zero

2003

241. Selecting for disease resistance rather than relying solely on vaccines or antibiotics is advantageous because:
(A) Pathogens cannot mutate against host genetic resistance
(B) It offers a permanent and cumulative population improvement
(C) It works instantaneously within a single breeding generation
(D) It is mathematically simpler than selecting for growth rates

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2019

242. Consider the following statements concerning genetic resistance:

I. Somatic cell count is positively genetically correlated with clinical mastitis.

II. The BoLA complex in cattle is orthologous to the human HLA complex.

III. Selecting exclusively for milk yield tends to increase susceptibility to mastitis.

IV. Disease resistance traits are typically highly heritable.

V. Resistance to Marek's disease is unlinked to the poultry B-complex.

Which of the above statements are correct?

(A) I, II and III
(B) II, III and V
(C) I, III and IV
(D) III, IV and V

2015

243. In cattle, the Major Histocompatibility Complex is referred to as:

(A) DLA
(B) SLA
(C) BoLA (Bovine Leukocyte Antigen)
(D) ELA

2018

244. A major barrier to direct selection for clinical disease resistance (like counting sick animals) is:

(A) It requires completely eliminating all additive variance
(B) All animals get sick regardless of their genetic merit
(C) Clinical disease exhibits codominance in its inheritance
(D) Binary data nature and incomplete exposure to the pathogen

2023

245. Genomic selection is particularly highly beneficial for improving disease resistance because:

(A) Resistance traits being usually limited to only one sex
(B) Pathogens being unable to infect any genotyped animals
(C) Avoiding intentional exposure of candidates to pathogens
(D) Disease resistance traits having a perfect heritability

2005

246. In sheep, which set of codons in the Prion Protein (PrP) gene is most commonly analyzed to determine genetic susceptibility to scrapie?

(A) 136, 154, and 171
(B) 12, 18, and 24
(C) 101, 112, and 123
(D) 210, 220, and 230

2003

247. To incorporate mastitis resistance into a dairy breeding objective without sacrificing too much milk yield, a breeder should use:

(A) Tandem selection for milk yield followed by mastitis resistance
(B) Independent culling levels for somatic cell counts exclusively
(C) Single-trait mass selection for total milk yield per lactation
(D) A multi-trait index with weighted values for yield and SCS

2010

248. In purpose-based breeding of dairy cattle, the genetic correlation between total milk yield and milk fat percentage is generally:

(A) Negative (antagonistic)
(B) Strongly positive
(C) Perfectly zero
(D) Dependent on the coat color

2014

249. Selection primarily for lean carcass yield in meat animals (like pigs) tends to:

(A) Increase the total amount of backfat in the meat carcasses
(B) Decrease feed efficiency during the finishing growth phase
(C) Increase susceptibility to stress if specific genes are ignored
(D) Decrease the overall body weight of the animal at processing

2019

250. The primary antagonistic relationship in purpose-based breeding of layer poultry is between:

(A) Egg production (number) and egg weight
(B) Egg weight and eggshell thickness
(C) Plumage color and feed intake
(D) Body temperature and egg production

NODIA

2008

251. Breeding strategies for draught (draft) purpose cattle traditionally emphasize:

(A) High milk production across multiple lactations
(B) Extreme dairy character and angular skeletal structure
(C) Maintaining a small and manageable skeletal body size
(D) Heavy musculature, strong feet/legs, and

endurance levels

2010

252. If a dairy breeder desires to increase total milk fat yield (kg) rather than fat percentage, they must:
(A) Select exclusively for the fat percentage in the milk
(B) Select for total yield as it drives total component mass
(C) Select against protein percentage to favor fat production
(D) Significantly decrease the herd's overall feed intake

2016

253. In meat-producing birds (broilers), intense selection for rapid juvenile growth rate has resulted in a correlated detrimental effect on:
(A) Feed conversion ratios within the growing population
(B) Pectoral muscle mass at the time of broiler processing
(C) Skeletal integrity and cardiovascular capacity in birds
(D) Plumage development and feather coverage over the body

2022

254. Selecting for improved eggshell quality (thickness/strength) is crucial in aging layer flocks to:
(A) Increase the yolk cholesterol content within the eggs
(B) Increase the total number of eggs laid per hen per year
(C) Change the shell color according to market preferences
(D) Reduce the incidence of downgraded and broken eggs produced

2005

255. Dual-purpose cattle breeds (e.g., Sahiwal, Haryana) are bred to balance:
(A) Milk production and draught capability
(B) Wool and meat production
(C) Meat and egg production
(D) Fine fiber and milk components

2015

256. A significant risk of exclusively pursuing terminal sire traits (growth and carcass) in a mammalian meat breed is:
(A) An increase in the generation interval of the herd
(B) A decline in maternal traits like fertility and milk
(C) The total loss of male fertility in breeding sires
(D) Complete loss of genetic drift within the population

2011

257. In genetic evaluation for meat traits, ultrasound is routinely used on live animals primarily to measure:
(A) Bone density and skeletal structure of the live animal
(B) Backfat thickness and loin eye area in meat-producing birds
(C) Heart rate and lung capacity of the animal under stress
(D) Blood flow to the brain and vital organs during growth

2003

258. To mitigate the antagonistic relationship between egg number and egg size, commercial poultry breeders heavily utilize:
(A) Using specialized male and female lines for commercial hybrids
(B) Tandem selection over the course of fifty breeding years
(C) Within-family selection methods applied to purebred lines
(D) Selection based exclusively on the sire's own phenotype

2004

259. Draught power in cattle is positively genetically correlated with:
(A) High milk letdown speed in dairy-purpose breeds
(B) Small and fine bone structure across the skeleton
(C) Body size, bone structure, and muscularity levels
(D) High somatic cell counts in the milk produced by cows

2017

260. A shift in the dairy market from fluid milk pricing to cheese-yield pricing requires the selection index to heavily weight:
(A) Fluid volume
(B) Lactose percentage
(C) Somatic cell count alone
(D) Protein and fat yield

2007

261. Feed Conversion Ratio (FCR) is mathematically calculated as:

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in the mouse population
(C) Higher mutation rates occurring within the low-weight line
(D) Inability to measure smaller mice with sufficient accuracy

2007

224. The Illinois long-term selection experiment is famous for its extensive duration, though it involves:
(A) Mice selected for litter size
(B) Corn (maize) selected for high and low oil/protein content
(C) Tribolium selected for pupal weight
(D) Poultry selected for egg weight

2004

225. Tribolium castaneum (flour beetle) is widely used as a laboratory model for livestock quantitative genetics because:
(A) It possesses a massive body size relative to other insects
(B) It has a short generation interval and high reproductive rate
(C) Its genetics are entirely identical to mammalian genetics
(D) It lacks environmental variance under laboratory conditions

2013

226. Classical experiments using Tribolium (flour beetle) investigated the efficiency of:
(A) Efficiency of recurrent selection and individual selection
(B) Selecting for resistance to specific mammalian virus types
(C) The inheritance of feather color within the insect population
(D) Horn development within the pupal stage of the flour beetle

2004

227. The Virginia body weight lines of chickens are a landmark model demonstrating:
(A) Complete genetic fixation within five generations of selection
(B) The inheritance of the blue eggshell trait in poultry lines
(C) Extreme phenotypic divergence from bidirectional selection
(D) Total resistance to avian influenza in high-growth populations

2012

228. In long-term selection experiments (e.g., beyond 50 generations), continued genetic response despite the expected exhaustion of initial additive variance is often attributed to:
(A) Continuous crossbreeding with unrelated poultry populations
(B) Intense natural selection favoring the high-growth phenotypes
(C) Complete absence of environmental effects in the laboratory
(D) New mutations contributing to quantitative genetic variance

2013

229. A significant finding from the long-term selection for high body weight in poultry lines was the correlated detrimental effect on:
(A) Feather coloration and plumage patterns in high-growth birds
(B) Appetite levels and feed consumption behavior in the flocks
(C) Reproductive traits such as egg production and fertility levels
(D) Bone calcification and skeletal mineral density in the legs

2013

230. Laboratory animal selection experiments validated the quantitative genetic theory that selection limits are highly dependent on:
(A) The exact starting temperature of the laboratory environment
(B) The effective population size of the selected animal lines
(C) The color and material of the rearing cages in the facility
(D) The use of individual versus mass selection only in the trial

2010

231. Consider the following statements concerning landmark selection experiments:
I. Classic mouse experiments demonstrated maternal effects confounding direct genetic response.
II. Tribolium experiments provided empirical validation of selection index theory.
III. Long-term poultry selection for growth improved reproductive fitness simultaneously.
IV. Divergent selection lines often exhibit asymmetrical responses.
Which of the above statement(s) is/are incorrect?
(A) I and II
(B) III only
(C) II and IV
(D) I and IV

NODIA

2024

272. If a pig has an actual feed intake of 2.5 kg/day and an expected feed intake of 2.8 kg/day, its RFI is:
(A) -0.3 kg/day
(B) +0.3 kg/day
(C) 1.12 kg/day
(D) 5.3 kg/day

2011

273. Because FCR is a ratio trait, directly selecting on it can cause complex statistical issues such as:
(A) Immediate fixation of lethal alleles within the population
(B) Asymmetric changes in the numerator and denominator traits
(C) Complete loss of environmental variance across the herds
(D) Perfect normal distribution of the trait across generations

2008

274. Mahalanobis D^2 statistic is utilized in quantitative genetics primarily to estimate:
(A) Genetic divergence between populations based on multiple traits
(B) Inbreeding depression occurring within a closed breeding line
(C) The selection differential achieved in a single generation
(D) The mutation rate of single genes governing the metric traits

2021

275. Unlike simple Euclidean distance, Mahalanobis distance accounts for:
(A) Only one trait at a time during the distance calculation
(B) Molecular markers exclusively for the distance estimation
(C) Phenotypic correlation between variables via covariance data
(D) Dominance variance perfectly within the distance model used

2008

276. The mathematical calculation of Mahalanobis D^2 requires the inversion of the:
(A) Additive relationship matrix
(B) Matrix of economic weights
(C) Identity matrix
(D) Pooled within-group variance-covariance matrix

2015

277. The D^2 statistic between two populations A and B is calculated using the vector of mean differences (d) and the inverse of the covariance matrix (S^{-1}) as:
(A) $dâ€™Sd$
(B) $dâ€™ + S^{-1}$
(C) $D^2 = dâ€™S^{-1}d$
(D) $\frac{S}{d}$

2017

278. Once D^2 values are computed for a set of breeds, they are often grouped into distinct clusters using:
(A) BLUP Animal Model
(B) Tocher's optimization method
(C) Robertson's optimal progeny size
(D) The Smith-Hazel index

2011

279. In livestock conservation, a large Mahalanobis D^2 value between two native breeds suggests:
(A) They are identical and one can be discarded from the herd
(B) They recently have been crossbred extensively in the field
(C) They share the exact same environment and management levels
(D) They have high divergence and distinct phenotypic features

2011

280. A limitation of using Mahalanobis D^2 based on morphometric traits for genetic distance is that:
(A) Morphological traits being influenced by environmental factors
(B) Requiring the use of molecular DNA sequencing techniques
(C) Being unable to handle more than two traits simultaneously
(D) Completely ignoring the genetic correlation between traits

2012

281. The transformation of correlated variables into uncorrelated orthogonal variables before clustering is related to:
(A) Independent Culling Levels
(B) Progeny Testing
(C) Principal Component Analysis (PCA)
(D) Mass Selection

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(A) Total weight gain / Total feed consumed
(B) Average daily gain / Body weight
(C) Total feed consumed / Total weight gain
(D) Total feed consumed - Total weight gain

2023

262. A lower Feed Conversion Ratio (FCR) value indicates:
(A) Poorer feed efficiency
(B) Higher feed efficiency
(C) The animal is losing weight
(D) Zero additive variance

2018

263. Residual Feed Intake (RFI) is defined as the difference between:
(A) Total feed consumed and total feed excreted by the animal
(B) FCR and Feed Efficiency values calculated for the period
(C) Maximum feed capacity and actual intake of the individual
(D) Actual feed intake and expected intake based on growth data

2006

264. An animal with a negative RFI value is:
(A) Efficient, consuming less feed than expected for its size and growth
(B) Highly inefficient, consuming more than expected
(C) Losing weight
(D) Genetically defective

2002

265. The primary theoretical advantage of selecting for RFI over FCR is that RFI is:
(A) Being much easier and cheaper to measure on the commercial farm
(B) Being dependent solely on the environmental conditions present
(C) Being independent of production traits used in the calculation
(D) Being mathematically identical to the total feed intake recorded

2015

266. Which trait requires expensive, specialized individual feed intake recording equipment (e.g., GrowSafe systems) to accurately measure on a large scale?
(A) Residual Feed Intake
(B) Average daily gain
(C) Backfat thickness
(D) Mature body weight

2021

267. The heritability of Residual Feed Intake (RFI) in beef cattle and pigs is generally considered to be:
(A) Zero
(B) Low (< 0.10)
(C) Extremely high (> 0.90)
(D) Moderate (0.20 to 0.40)

2024

268. Selecting animals with favorable (negative) RFI generally results in:
(A) Significant increase in mature body weight of the animal
(B) Reduced overall feed intake with no change in growth rates
(C) Decreased average daily gain throughout the testing phase
(D) Increased methane emissions per unit of beef produced by sires

NODIA

2018

269. The expected feed intake in the RFI calculation is typically modeled using a multiple linear regression involving:
(A) Coat color and horn length of the individual animal
(B) Milk yield and somatic cell count recorded in females
(C) Metabolic body weight and average daily gain of the animal
(D) Backfat thickness only at the time of the intake recording

2018

270. In poultry, selection for improved FCR over the past several decades has been indirectly driven largely by:
(A) Selection for increased feed consumption
(B) Selection for smaller body size
(C) Natural selection
(D) Selection for rapid early growth rate

2017

271. Genetic variation in RFI is biologically attributed to differences in:
(A) Differences in digestibility, metabolic rate, and activity
(B) The physical capacity of the rumen in ruminant animals
(C) The color and consistency of the feed provided to animals
(D) The size and structural integrity of the animal's hooves

(D) The physical sizes of the populations being studied for distance

2024

294. The specific formula for $F_{\{ST\}}$ based on heterozygosity is:

(A) $\frac{H_S - H_T}{H_S}$

(B) $\frac{H_T - H_S}{H_T}$

(C) $\frac{H_T}{H_S}$

(D) $1 - \frac{H_T}{H_S}$

2002

295. Single Nucleotide Polymorphisms (SNPs) are now widely used for genetic distance studies. A key characteristic of SNPs compared to microsatellites is that SNPs are generally:

(A) Multi-allelic (e.g., 10-15 alleles per locus)
(B) Unusable for $F_{\{ST\}}$ calculations
(C) Only found in coding regions
(D) Biallelic

2023

296. In conservation genetics, identifying breeds with high pairwise $F_{\{ST\}}$ values and high unique allele frequencies is important for:

(A) Prioritizing them for conservation to maintain global diversity
(B) Culling them from the registry to simplify genetic management
(C) Crossbreeding them until they are genotypically identical
(D) Increasing the inbreeding coefficient to 1.0 for all animals

2003

297. $F_{\{IS\}}$, another of Wright's F-statistics, specifically measures:

(A) Divergence between distinct species in the animal kingdom
(B) The total mutation rate of the population across all loci
(C) Inbreeding of individuals relative to their own subpopulation
(D) The geographic distance between various animal herds in a region

2010

298. Phylogenetic trees (e.g., UPGMA or Neighbor-Joining) are constructed from molecular data by using a matrix of:

(A) Pairwise genetic distances between all targeted populations
(B) Phenotypic correlations calculated for the metric traits
(C) Breeding values estimated for individuals in the groups
(D) Selection differentials achieved across the breeding history

2001

299. If $H_T = 0.50$ and $H_S = 0.40$, the calculated $F_{\{ST\}}$ for the population is:

(A) 0.10
(B) 0.20
(C) 0.80
(D) 1.25

2012

300. Genetic bottlenecks and the founder effect in a closed breed typically result in:

(A) An increase in allelic richness
(B) A loss of rare alleles and increased genetic drift, altering genetic distance
(C) A decrease in $F_{\{ST\}}$ relative to other breeds
(D) Perfect Hardy-Weinberg equilibrium

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ANSWERS

1. (B) $-\frac{q^2}{1+q}$
In a randomly mating population, complete selection against the recessive homozygote removes individuals with the recessive genotype from the breeding pool. The new allele frequency is calculated as the initial frequency divided by the sum of one and that frequency. The resulting mathematical change reflects a reduction defined by the square of the initial frequency relative to its incremented value.

2. (A) Relative contribution of an individual's genotype to the next generation
Biological fitness serves as a fundamental metric for reproductive success within quantitative genetics. It quantifies the proportional genetic contribution an individual provides to the subsequent generation relative to other genotypes. This measure integrates both survival and fertility, determining how effectively specific alleles proliferate over time under various natural or artificial selection pressures within a specific population or breeding environment.

3. (C) A stable equilibrium of allele frequencies
Overdominance occurs when the heterozygous genotype exhibits higher biological fitness than both homozygous forms. This selective advantage prevents either allele from reaching fixation or being completely eliminated from the population. Consequently, selection maintains a stable genetic polymorphism through balancing selection. This results in an equilibrium state where allele frequencies remain constant over generations, preserving genetic diversity within the breeding herd.

4. (D) Recessive and at a low frequency
The effectiveness of selection depends heavily on the visibility of alleles in the phenotype. When a deleterious recessive allele is at a very low frequency, most copies are hidden within phenotypically normal heterozygous carriers. Selection cannot act upon these carriers, making the rate of change extremely slow. As the frequency decreases, the probability of forming affected homozygotes diminishes significantly.

5. (C) Additive genetic variance in fitness
Fisher's fundamental theorem of natural selection states that the rate of increase in the mean fitness of a population is equal to the additive genetic variance in fitness at that time. This principle emphasizes that only the additive portion of genetic variation, which determines breeding values, directly contributes to the predictable response to selection and subsequent improvement in population fitness.

6. (B) A higher selection coefficient indicates weaker selection pressure.
The selection coefficient quantifies the intensity of selection against a specific genotype by measuring the proportional reduction in its gametic contribution. It ranges from zero, indicating no selection, to one, representing complete lethality or sterility. Therefore, a higher coefficient signifies stronger selection pressure, reflecting a greater disadvantage for the genotype in contributing to the genetic composition of the next generation.

7. (D) A is false but R is true.
Complete selection against recessive genotypes prevents homozygotes from reproducing, effectively removing those individuals from the gene pool. However, the recessive allele persists within the population because it remains carried by heterozygous individuals who are not selected against. Therefore, a single generation of selection cannot eliminate the allele entirely, as it stays hidden within the carriers of the population.

8. (A) The selection coefficient and initial allele frequency
When selection acts against a dominant allele, both the homozygous dominant and heterozygous genotypes are disadvantaged. The change in genotypic frequencies is primarily determined by the intensity of selection, represented by the selection coefficient, and the starting frequency of the allele. Because the dominant allele is expressed in both genotypes, selection is generally more efficient at reducing its frequency quickly.

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9. (C) 0.0
A lethal dominant allele is expressed in every individual that carries even a single copy of the gene. If selection against this genotype is complete, meaning all carriers fail to reproduce or survive to breeding age, the allele cannot be transmitted to the next generation. Consequently, the frequency of a lethal dominant allele drops to zero immediately after selection occurs.

10. (A) $W = \frac{4}{5}$
Biological fitness is often expressed as relative fitness, which compares the reproductive success of a genotype to the most successful genotype in the population. It is calculated by dividing the average number of offspring produced by a specific genotype by the maximum average number produced by any genotype. This scaling ensures that the highest fitness value in the group equals one.

11. (D) Disruptive selection
Disruptive selection favors individuals at both extremes of the phenotypic distribution while selecting against those with intermediate values. This process can lead to a bimodal distribution within the population and is often associated with diversifying environments. Over time, this form of selection may contribute to the development of distinct subpopulations or even speciation by promoting divergent phenotypic traits and behaviors.

12. (B) Overdominance
Overdominance is a genetic condition where the fitness of the heterozygote exceeds the fitness of both homozygous genotypes. In the provided scenario, the heterozygote has a fitness value of one, while both homozygotes are reduced by selection coefficients. This pattern creates a stable equilibrium, as selection favors the maintenance of both alleles in the population to maximize the frequency of heterozygotes.

13. (C) Gametic selection acts on haploid expressions before fertilization.
Gametic selection occurs when the fitness of individuals is determined during the haploid stage of the life cycle. This process targets the success of gametes, such as sperm or pollen, based on their own genetic composition before the formation of a diploid zygote. This differs from zygotic selection, which operates on the phenotypes expressed by diploid individuals throughout their life stages.

14. (D) The transmitting ability of an individual multiplied by two
Estimated Breeding Value represents the genetic merit of an individual as a parent. It is defined as twice the transmitting ability because an individual passes only a random half of its genes to its offspring. Therefore, the total additive genetic superiority of an animal is twice the average superiority it transmits through its gametes to the next generation of progeny.

15. (A) P-4, Q-2, R-3, S-1
Phenotypic value refers to measurable performance, while breeding value reflects an individual's worth through its offspring's mean. Dominance deviation represents non-additive interactions between alleles at a single locus. Transmitting ability constitutes exactly half of the additive genetic value passed to progeny. These concepts collectively define how genetic and environmental components partition to form the observable characteristics of breeding animals in populations.

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16. (B) Average superiority of its gametes over the population mean
Transmitting ability represents the expected average deviation of an individual's progeny from the population mean, assuming they are mated to average individuals. It reflects the value of the specific sample of genes the parent passes to its offspring. Because each parent contributes exactly half of the offspring's genetic material, the transmitting ability is equivalent to half of the animal's breeding value.

17. (B) EBV $= h^2 \times (P - \mu)$
The estimated breeding value of an animal is determined by the proportion of its phenotypic superiority that is expected to be passed to its offspring. This is calculated by multiplying the animal's phenotypic deviation from the population mean by the heritability of the trait. Heritability acts as a regression coefficient, predicting the genetic merit based on the observed phenotypic performance.

18. (A) It cannot be passed predictably from parent to offspring
Dominance deviation results from the specific interaction between two alleles at a locus

within a diploid individual. During meiosis, these allele pairs are separated, and only single alleles are passed to the offspring. The effect of the interaction is not transmitted; instead, new interactions are formed in the progeny. Consequently, dominance effects are non-additive and do not contribute to breeding values.

19. (B) +200 kg
An individual's transmitting ability is defined as half of its estimated breeding value. When an elite sire with a specific breeding value is mated to average dams, the expected phenotypic deviation of the daughters represents the sire's transmitting ability. Since the breeding value is four hundred kilograms, the sire transmits half of this genetic superiority, resulting in a two hundred kilogram deviation.

20. (D) Increased amount of performance information utilized
The accuracy of an estimated breeding value reflects the correlation between the estimate and the true breeding value. This reliability improves as more relevant data are incorporated into the evaluation. Information from the individual's own records, its ancestors, and particularly its progeny reduces the prediction error. Consequently, larger datasets allow for more precise identification of genetically superior animals for selection purposes.

21. (C) Non-additive genetic deviation
Genotypic value is composed of additive effects and non-additive deviations, which include dominance and epistatic interactions. The breeding value specifically represents the sum of the additive effects of the genes. Therefore, the difference between the total genotypic value and the breeding value is defined as the non-additive genetic deviation. These effects are unique to the individual and are not inherited predictably.

22. (B) II and III
Transmitting ability, also known as progeny difference, is a measure of the genetic merit an individual passes to its offspring. It is mathematically defined as exactly one-half of the individual's breeding value. While it predicts the expected average performance of the progeny, it is not identical to the progeny's own breeding value, which also depends on the other parent's genetic contribution.

23. (D) Future performance of an individual for repeated traits
The Most Probable Producing Ability is used for traits that are measured multiple times during an animal's life, such as milk yield or litter size. It combines the animal's genetic merit with its permanent environmental effects. By utilizing repeatability and the animal's previous records, it provides an estimate of the individual's expected performance in subsequent production cycles within the same environment.

24. (A) +150 kg
To calculate the estimated breeding value from a single phenotypic record, the individual's deviation from the population mean is multiplied by the heritability of the trait. In this instance, a five hundred kilogram deviation multiplied by a heritability of zero point three results in an estimated breeding value of one hundred and fifty kilograms. This value represents the expected genetic superiority.

25. (C) Genotypic value and environmental effect
The phenotypic value of an individual is the result of the combined influence of its genetic makeup and the environment in which it was raised. This relationship is fundamentally expressed as the sum of the genotypic value and the environmental deviation. While the genotypic value can be further partitioned into additive and non-additive components, the primary division remains between genetic and non-genetic factors.

26. (A) Evaluating performance within one restricted environment
Improving the estimation of breeding values requires minimizing environmental noise and maximizing genetic information. While using records from relatives and adjusting for non-genetic factors enhances accuracy, restricting evaluations to a single environment limits the ability to account for environmental variation across different herds. Broad data collection across diverse environments provides a more robust and accurate prediction of an individual's true genetic merit.

27. (D) Difference between selected group mean and population mean
The selection differential is a measure of the phenotypic superiority of the individuals chosen to be parents of the next generation. It is

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calculated by subtracting the average phenotypic value of the entire population from the average phenotypic value of the selected group. This value represents the amount of phenotypic change intended through selection before considering the heritability of the specific trait.

28. (B) Dividing selection differential by phenotypic standard deviation
Standardized selection intensity expresses the selection differential in terms of phenotypic standard deviation units. This standardization allows for the comparison of selection pressure across different traits and populations regardless of their original units of measurement. It is calculated by dividing the observed selection differential by the phenotypic standard deviation, reflecting the intensity of the culling process applied by the breeder.

29. (A) $\frac{z}{p}$
In truncation selection applied to a normally distributed trait, the standardized selection intensity is determined by the properties of the normal curve. It is defined as the height of the normal ordinate at the truncation point divided by the proportion of the population that is selected. This ratio provides a mathematical way to estimate selection pressure based on the culling threshold used.

30. (D) Order statistics from finite population samples
In small populations, the actual selection intensity may be lower than predicted by standard normal distribution formulas. This reduction occurs because the selection of the best individuals is limited by the finite sample size, which may not contain individuals at the extreme tails of the theoretical distribution. Order statistics are used to adjust for these sampling effects in finite breeding groups.

31. (A) Both A and R are true and R is the correct explanation of A.
Selection intensity represents the average superiority of selected individuals. When a larger proportion of the population is kept for breeding, the truncation point moves closer to the population mean. This inclusion of less superior animals reduces the average phenotypic difference between the selected group and the original population. Consequently, as the selection proportion increases, the resulting selection intensity inevitably decreases.

32. (A) 0.3 kg
The selection differential is the difference between the mean of the selected individuals and the mean of the population from which they were chosen. In this flock, subtracting the base population mean of one point five kilograms from the selected breeders' mean of one point eight kilograms results in a selection differential of zero point three kilograms. This represents the phenotypic superiority.

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33. (B) The proportion of individuals selected
The standardized selection intensity is fundamentally determined by the fraction of the population that is retained for breeding purposes. Under the assumption of a normal distribution, the intensity is a direct mathematical function of this proportion. As the proportion selected becomes smaller and more exclusive, the selection intensity increases, reflecting the greater phenotypic superiority of the highly elite group of animals.

34. (A) Selecting 10% of the population
Selecting a smaller percentage of the population increases the selection differential because only the most extreme and superior individuals are chosen as parents. A ten percent selection rate is more restrictive than fifty or ninety percent, resulting in a mean value for the selected group that is further from the population average. This maximizes the phenotypic superiority of the breeding candidates.

35. (A) 15
The selection differential is calculated by multiplying the standardized selection intensity by the phenotypic standard deviation. In this case, the phenotypic variance is one hundred, meaning the phenotypic standard deviation is ten. Multiplying the selection intensity of one point five by the standard deviation of ten yields a selection differential of fifteen units. This reflects the average superiority of the selected group.

36. (D) The formula may incorrectly predict actual intensity.
The standard formula for selection intensity relies on the assumption that the trait follows a normal distribution. If the distribution is skewed or non-

55. (D) The square root of herizability (h)
The accuracy of selection is defined as the correlation between the individual's true breeding value and the information used for selection. In mass selection, where only the individual's own phenotype is used, this accuracy is equal to the square root of the heritability. This mathematical relationship shows that the reliability of individual selection increases directly with the trait's heritability level.

56. (A) Direct ancestors and collateral relatives in previous generations
Pedigree selection involves choosing breeding individuals based on the performance records of their relatives, particularly their parents, grandparents, and other ancestors. This method utilizes the genetic relationships defined in the pedigree to estimate the breeding value of a young animal before it has expressed its own phenotype. It is a valuable tool for early selection decisions in a breeding program.

57. (C) It allows for early selection before the animal expresses its own phenotype
A major advantage of pedigree selection is its ability to provide genetic evaluations early in an animal's life. By using information from parents and ancestors, breeders can identify potentially superior animals for retention or further testing long before the animals themselves reach maturity or produce their first records. this helps in reducing the generation interval and managing rearing costs effectively.

58. (B) 0.50
The maximum accuracy of pedigree selection using information from a single parent is limited by the genetic relationship. Because an offspring shares only half of its genes with each parent, the parent's record can only explain a portion of the offspring's genetic merit. Even if the parent's breeding value is known perfectly, the correlation with the offspring's breeding value cannot exceed zero point five.

59. (D) It cannot be used for sex-limited traits or traits measured post-mortem.
Mass selection relies entirely on measuring the trait on the individual being selected. This makes it impossible to apply to traits that are expressed only in one sex, such as milk production or egg laying, when selecting males. Similarly, it cannot be used for traits that require the animal to be slaughtered, such as carcass quality, as the animal must remain alive to reproduce.

60. (B) $\sqrt{0.5h^2}$
When both parents have phenotypic records, the accuracy of the resulting pedigree selection increases compared to using only one parent. The accuracy is calculated as the square root of half the heritability, assuming the parents are unrelated and unselected. This combined information provides a more reliable estimate of the genes the individual likely inherited, although it still excludes the effects of Mendelian sampling.

61. (A) P-4, Q-3, R-1, S-2
Mass selection is ideal for highly heritable traits like growth, where individual performance accurately reflects genetic merit. Pedigree selection allows for early culling before an animal expresses its own phenotype. Progeny testing is essential for sex-limited traits like milk yield to evaluate sires. Within-family selection is used when large common environmental effects might bias evaluations between different families in the herd.

62. (D) The additive relationship is 0.25 rather than 0.5 for the dam.
In pedigree selection, the value of information from relatives depends on their genetic relationship to the individual. An individual shares half of its genes with its dam but only one-quarter with its grand-dam. Because the genetic linkage is weaker, the grand-dam's phenotypic record is a less accurate predictor of the individual's breeding value, providing less information for selection decisions.

63. (A) When heritability of the trait is extremely low
For traits with low heritability, an individual's own phenotype is a poor indicator of its genetic merit due to high environmental noise. In such cases, incorporating information from relatives through pedigree selection significantly increases the accuracy of the estimated breeding value. As heritability increases, the individual's own performance becomes a better predictor, reducing the relative importance of additional pedigree information.

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46. (D) Genomic selection
Genomic selection allows for the estimation of breeding values using DNA markers early in an animal's life, even before phenotypic records are available. By using genomic information, young sires can be selected to produce the next generation of sons without waiting for lengthy progeny tests. This significantly reduces the generation interval, particularly in the "sires to breed sons" pathway of dairy cattle.

47. (A) Substantially increases the generation interval
While progeny testing provides high accuracy for sex-limited and lowly heritable traits, its primary drawback is the time required to obtain offspring records. In species like cattle, this process takes several years, as daughters must mature and complete a lactation. This significant delay increases the generation interval, which can slow down the annual rate of genetic progress in the breeding program.

48. (B) Generation intervals for males and females
In the annual genetic response formula, the terms in the denominator represent the time components of the breeding cycle. Specifically, these variables denote the average generation intervals for the male and female pathways. The total annual gain is the sum of the genetic superiorities from both parents divided by the sum of their respective generation intervals, reflecting progress per unit of time.

49. (B) Poultry
Poultry species exhibit the shortest natural generation interval among common livestock, as they reach sexual maturity quickly and have high reproductive rates. This biological characteristic allows breeders to complete selection cycles in approximately one year. Frequent generation turnover enables faster accumulation of genetic gain over time compared to large ruminants like cattle, which have much longer maturity and gestation periods.

50. (A) I and II
Generation intervals vary significantly between species due to differences in biological maturity and reproductive rates. While traditional selection often requires waiting for phenotypic records, which increases accuracy at the expense of time, new technologies can reduce intervals without always sacrificing accuracy. For example, genomic selection maintains high accuracy while allowing for much younger parents, effectively decoupling the traditional time-accuracy trade-off.

51. (C) Decreasing generation intervals and increasing female intensity
Multiple ovulation and embryo transfer (MOET) allows superior cows to produce many more offspring than possible through natural service. This increases the selection intensity on the female side by allowing a smaller proportion of females to provide replacements. Additionally, by using these technologies on younger animals, breeders can reduce the generation interval, thereby accelerating the overall annual rate of genetic gain.

52. (D) Depend on the net balance between time and accuracy levels
The annual genetic gain is determined by the ratio of genetic gain per generation to the generation interval. If reducing the interval causes a sharp drop in selection accuracy, the gain per generation may decrease more than the time savings can compensate for. Breeders must find the optimal point where the increase in generation turnover outweighs any potential losses in prediction reliability.

53. (C) The phenotypic performance of the individual itself
Individual selection, commonly known as mass selection, is a breeding strategy where animals are chosen based solely on their own observed phenotypic value. In this method, no information from ancestors, siblings, or progeny is utilized. Animals that exceed a certain performance threshold for the target trait are selected to become the parents of the next generation, regardless of their family background.

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54. (B) High heritability
Mass selection is most effective for traits where the individual's phenotype is a strong predictor of its genotype. This occurs when heritability is high, meaning a large proportion of the phenotypic variation is due to additive genetic effects. For such traits, selecting the best-performing individuals leads to significant and predictable genetic improvement in the subsequent generation without requiring complex pedigree records.

Tandem selection, independent culling levels, and selection indexes are the standard approaches for this purpose. Contemporary comparison, however, is a method used for sire evaluation of a single trait, such as milk yield, and is not a strategy for balancing multiple traits in a breeding objective.

93. (C) One trait at a time, moving to the next once a target is reached
Tandem selection is a multi-trait strategy where selection pressure is applied to only one trait for several generations until a desired level of improvement is achieved. Once the target for the first trait is met, the breeder shifts focus to a second trait. This sequential approach is easy to implement but ignores the genetic correlations between the traits under selection.

94. (D) The traits have a strong negative (antagonistic) genetic correlation
Tandem selection is least effective when traits are negatively correlated. In this scenario, selecting for improvement in the first trait will cause a genetic decline in the second trait due to their antagonistic relationship. When the breeder eventually switches to select for the second trait, the progress made in the first trait will be lost, making it difficult to improve both traits simultaneously.

95. (D) Setting minimum standards for every individual trait
Independent culling levels involve establishing minimum performance thresholds for each trait included in the breeding objective. An individual must meet or exceed the standards for all traits simultaneously to be selected for breeding. If an animal fails to meet the requirement for even a single trait, it is culled, regardless of how exceptional its performance may be in other areas.

96. (B) II, III, I
Tandem selection is generally the least efficient method because it ignores correlations and loses progress when switching traits. Independent culling levels are more efficient as they select for multiple traits at once but can still cull superior animals. The selection index is theoretically the most efficient method because it uses economic weights and genetic parameters to maximize the overall genetic gain.

97. (B) Culling superior animals for missing one specific threshold
A major limitation of independent culling levels is its lack of flexibility. Because an animal must meet all thresholds, a candidate with outstanding genetic merit in several traits will be culled if it falls slightly below the minimum standard for just one trait. This rigid approach can lead to the loss of highly valuable individuals that could have contributed significantly to the population's overall progress.

98. (A) Aggregate balancing (or compensation)
The selection index method allows for compensation between traits, where an animal's exceptional performance in one trait can offset a slightly lower performance in another. This is achieved by combining all traits into a single numerical score based on their economic importance and genetic relationships. This flexibility ensures that the individuals with the highest overall economic merit are selected for breeding.

99. (C) The number of traits under selection increases
The theoretical advantage of the selection index over other methods, such as independent culling levels, becomes more pronounced as the number of traits in the breeding objective increases. This is because the index can more effectively manage the complex genetic and phenotypic correlations between many traits, ensuring that selection pressure is optimally distributed to achieve the maximum possible total genetic gain.

100. (C) More efficient than if they were uncorrelated
When traits are favorably correlated, selection for one trait naturally leads to improvement in the other. In this case, independent culling levels become more efficient because individuals that meet the threshold for one trait are more likely to meet it for the other. This synergy reduces the number of superior animals culled and increases the overall selection intensity compared to selecting for uncorrelated traits.

101. (C) Selection index
The selection index method is the most mathematically rigorous approach to multi-trait selection. It requires detailed information about the population, including genetic and phenotypic variances for all traits, the genetic and phenotypic correlations between them, and

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64. (B) Rapid accumulation of inbreeding
Intense mass selection often leads to the selection of closely related individuals who share superior phenotypes. In small or closed populations, this increases the probability of mating related animals, leading to a rapid accumulation of inbreeding. High levels of inbreeding can result in inbreeding depression, which negatively affects fitness traits and may eventually reduce the overall genetic variance available for selection.

65. (B) $0.25h$
The correlation between an individual's breeding value and the phenotypic record of its half-sib is used to estimate genetic merit in sib selection. This correlation is calculated as the additive relationship between half-sibs, which is zero point two five, multiplied by the square root of the heritability. This relationship reflects how much of the sibling's performance is due to shared genes.

66. (A) Mean phenotypic value of their family
Family selection is a method where whole families are selected or culled based on their average phenotypic performance. Instead of focusing on individual records, the breeder uses the family mean as the selection criterion. All members of the chosen families are typically kept for breeding, while members of inferior families are rejected, regardless of their individual performance within the family.

67. (C) The deviation of their own performance from the mean of their family
Within-family selection focuses on the relative performance of individuals compared to their own family average. By selecting the best individuals from each family, this method effectively ignores differences between family means. This approach is particularly useful for removing the influence of environmental factors that are shared by all members of a family but differ between different families in the population.

68. (D) The heritability is low and common environmental effects are minimal
Family selection becomes more efficient than individual selection when heritability is low. In such cases, the family mean provides a more accurate estimate of the family's breeding value by averaging out individual environmental deviations. This efficiency is maximized when there are no common environmental effects that would otherwise cause family members to appear more similar for non-genetic reasons.

69. (C) There is a large common environmental variance shared by family members
Within-family selection is highly advantageous when members of the same family share a common environment, such as a single litter or a shared pen. These common effects can make families appear genetically superior or inferior when they are not. By selecting based on deviations from the family mean, the common environmental influence is subtracted, allowing for a more accurate comparison of genetic merit.

70. (B) Intraclass correlation among family members (t)
The accuracy of family selection is influenced by the number of individuals in each family and the intraclass correlation. This correlation measures the phenotypic resemblance between family members and includes both genetic and common environmental effects. A high intraclass correlation relative to the herizability suggests large common environmental influences, which can reduce the effectiveness of between-family selection compared to other methods.

71. (D) Expressed only in one sex or require slaughter for measurement
Sig selection is a valuable strategy for traits that cannot be measured on the breeding candidates themselves. This includes sex-limited traits, such as egg production in poultry or milk yield in dairy cattle, and carcass traits that require the animal to be slaughtered. By using the performance of siblings, breeders can estimate the genetic merit of the live breeding candidates.

72. (A) Both A and R are true and R is the correct explanation of A.
Within-family selection ensures that every family contributes a more equal number of individuals to the next generation because the best animals are chosen from every group. This prevents a single superior family from dominating the breeding pool, as can happen in mass selection. By maintaining a wider representation of families, the rate of inbreeding is significantly reduced, preserving more genetic diversity.

73. (B) 0.50
Full-sibs share both parents and, on average, inherit fifty percent of the same genes. This means

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their additive genetic relationship is zero point five. This high level of genetic similarity makes full-sib information very valuable for estimating breeding values, although it also increases the risk of common environmental effects, such as maternal influences, that must be accounted for during selection.

74. (A) Sib selection
In sib selection, the individual's own performance is not used, often because the trait is impossible to measure on the candidate while keeping it alive for breeding. Instead, the selection decision is based entirely on the performance records of its siblings. This allows for genetic improvement in traits like meat quality or sex-limited production where the candidate's own phenotype is unavailable.

75. (D) $V_f = \dfrac{V_P \times [1 + (n-1)\,t]}{n}$
The phenotypic variance of family means is calculated using the total phenotypic variance, the family size, and the intraclass correlation. This formula shows that the variance of the means is smaller than the individual variance but increases as family members become more similar to each other. Accurate estimation of this variance is necessary to predict the response to between-family selection.

76. (B) Using an optimally weighted index of individual performance and family mean
Combined selection integrates information from both the individual's own phenotype and its family mean to estimate breeding value. By applying optimal weights to these sources of information based on heritability and family size, this method maximizes selection accuracy. It is theoretically the most efficient selection method for a single trait because it utilizes all available phenotypic information within a generation.

77. (C) Within-family selection
For traits heavily influenced by a common environment, such as the maternal environment in a pig litter, between-family differences often reflect environmental rather than genetic superiority. Within-family selection is most biologically rational here because it evaluates animals against their own littermates. This process automatically adjusts for the shared environment, allowing the breeder to identify individuals with superior additive genetic potential for growth.

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78. (D) High rate of inbreeding due to selection of whole families
A significant disadvantage of between-family selection is the rapid increase in inbreeding. Since entire families are selected or rejected together, the individuals chosen for breeding are highly related. This reduces the effective population size and increases the probability of mating close relatives in the next generation, which can lead to inbreeding depression and a loss of genetic variation over time.

79. (A) Breeding value by evaluating offspring phenotypic means
Progeny testing is a selection method designed to estimate an individual's breeding value by measuring the performance of its offspring. By averaging the phenotypes of many progeny, the environmental effects and non-additive genetic deviations tend to cancel out. This provides a very accurate assessment of the additive genetic merit that the parent actually transmits to the next generation of the population.

80. (B) A sex-limited trait
Milk production is a sex-limited trait expressed only in females. Consequently, the breeding value of a sire cannot be measured directly through his own performance. Progeny testing is essential in dairy cattle because it allows the sire's genetic merit for milk yield to be evaluated based on the production records of his daughters, ensuring that superior males are identified.

81. (B) $\sqrt{\dfrac{n}{n+a}}$
The accuracy of progeny testing represents the correlation between the individual's true breeding value and its progeny average. This accuracy is calculated as the square root of the ratio of the number of progeny to the sum of the progeny number and a constant related to heritability. As the number of progeny increases, the accuracy of the estimate improves significantly.

82. (A) $\dfrac{4 - h^2}{h^2}$
In the progeny testing accuracy formula, the term "a" is a constant that depends on the heritability of the trait and the relationship between the progeny. For half-sib progeny, it is defined as the quantity four minus heritability divided by the heritability. This value determines how many progeny are needed to achieve a specific level of accuracy in the breeding evaluation.

83. (C) 1.00
As the number of progeny used in a progeny test increases toward infinity, the average performance of the offspring becomes a perfect predictor of the parent's transmitting ability. In this theoretical limit, environmental effects and Mendelian sampling are completely averaged out. Therefore, the correlation between the progeny average and the parent's true breeding value, which represents the accuracy, approaches one.

84. (D) Selection intensity and selection accuracy within limited testing facilities
In a breeding program with limited resources, there is a trade-off between testing many sires with few progeny or fewer sires with many progeny. Testing more sires increases selection intensity, while more progeny per sire increases selection accuracy. The optimum progeny group size is reached when these two factors are balanced to maximize the overall genetic gain per generation.

85. (B) I, III and IV
Progeny testing is a powerful but time-consuming tool. It significantly increases the generation interval because of the time required for offspring to grow and produce records. However, it is essential for sex-limited traits and provides high accuracy when many progeny are used. Successful implementation requires extensive and accurate record-keeping systems to track animal performance and pedigree relationships across generations.

86. (B) Smaller herd sizes and weaker systematic recording structures
Progeny testing requires a large number of offspring and robust data collection systems to be effective. In sheep and goat production, smaller individual flock sizes and less developed national recording infrastructures make it difficult to implement large-scale progeny testing programs. Compared to the highly organized dairy industry, these structural limitations hinder the widespread use of systematic progeny-based evaluations in smaller ruminants.

87. (C) 15
The constant "a" in the progeny testing accuracy formula for half-sibs is calculated as four minus heritability divided by heritability. For a trait with a heritability of zero point two five, the calculation is four minus zero point two five, which is three point seven five, divided by zero point two five. This results in a value of fifteen for the constant.

88. (C) 0.71
Accuracy is calculated as the square root of the number of progeny divided by the sum of the progeny number and the constant "a". With fifteen daughters and an "a" value of fifteen, the accuracy is the square root of fifteen divided by thirty, which equals the square root of zero point five. This results in an accuracy of approximately zero point seven one.

89. (C) Traits with high heritability measurable at an early age
Progeny testing is least attractive for traits that have high heritability and can be measured early in the candidate's life. For such traits, mass selection provides high accuracy and a much shorter generation interval, leading to faster annual genetic gain. The extra time and expense required for progeny testing are not justified when the individual's own phenotype is a reliable genetic indicator.

90. (A) Number of sires tested and number of progeny per sire
To maximize genetic gain, a breeder must optimize the use of testing space. Testing more sires increases the selection intensity but reduces the number of progeny per sire and thus the accuracy. Conversely, more progeny per sire improve accuracy but reduce intensity. The optimum balance between these two factors depends on the trait's heritability and the total number of test slots available.

91. (D) Progeny testing against contemporaries in similar herds
The Contemporary Comparison method is a sire evaluation technique that compares the performance of a sire's daughters with the performance of other cows in the same herd, year, and season. By comparing daughters to their contemporaries, the method adjusts for environmental differences between herds. This ensures that the sire's genetic merit is estimated based on how his offspring perform relative to their peers.

92. (B) Contemporary comparison
Multi-trait selection involves methods designed to improve several economic traits at once.

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normal, the relationship between the proportion selected and the resulting mean superiority may deviate from theoretical expectations. This discrepancy leads to inaccurate predictions of selection intensity and, subsequently, the expected genetic response if the underlying distribution is not considered.

37. (C) Selection differential
The selection differential quantifies the phenotypic superiority of the individuals selected to be parents. It is defined as the difference between the average phenotypic value of the selected group and the average phenotypic value of the entire generation from which they originated. This value is a critical component in the breeder's equation used to predict the genetic response to selection.

38. (B) A smaller proportion of males is required for reproduction.
In livestock breeding, a single male can often be mated to many females, especially with technologies like artificial insemination. This allows breeders to select a much smaller, more elite proportion of the available males compared to females. Because a smaller selection proportion results in a higher selection intensity, the selection pressure applied through the male pathway is typically much greater.

39. (D) The number of offspring each selected parent successfully produces
An unbiased estimate of the selection differential must account for the actual genetic contribution of the selected parents to the next generation. If superior animals produce more offspring than others within the selected group, the effective selection differential is weighted by their reproductive success. This ensures that the differential accurately reflects the phenotypic superiority that is actually transmitted to the subsequent progeny.

40. (A) The average age of parents when their selected offspring are born
The generation interval is a critical measure of time in a breeding program. it is defined as the average age of the parents at the birth of the offspring that are eventually selected to replace them in the breeding population. Shorter generation intervals allow for a more rapid turnover of generations, which can increase the annual rate of genetic progress.

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41. (C) Generation interval
Annual genetic progress is calculated by dividing the total genetic gain achieved per generation by the length of the generation interval. Therefore, as the generation interval increases, the genetic gain is spread over a longer period, reducing the progress made each year. Maximizing annual progress requires a balance between achieving high gain per generation and minimizing the time between generations.

42. (A) I, III, IV, II
In a multi-pathway selection scheme, the average generation interval is determined by first calculating the specific ages of parents across four distinct pathways. These include sires and dams producing both sons and daughters. Once the average ages for these pathways are determined, their values are summed and divided by four to establish the overall generation interval for the entire breeding program.

43. (D) Sires to breed sons (SS)
In traditional progeny testing programs for dairy cattle, the "sires to breed sons" pathway typically has the longest generation interval. This is because a sire must be extensively progeny tested before he is considered elite enough to produce future sires. This evaluation process, which involves waiting for his daughters to complete lactations, significantly delays the birth of his selected male offspring.

44. (B) Minimize generation interval while optimizing selection accuracy
To maximize the annual rate of genetic change, breeders must reduce the generation interval while maintaining or improving selection accuracy. Reducing the time between generations allows for more frequent selection opportunities. However, if the generation interval is shortened too much, it may limit the amount of information available for evaluation, potentially decreasing accuracy and the total genetic gain per generation.

45. (C) 5 years
The generation interval for a herd is calculated as the average age of the parents when their offspring are born. In this closed herd, the average age of the sires is four years and the average age of the dams is six years. The mean of these two values, four plus six divided by two, results in a generation interval of five years.

the relative economic value of each trait. This data is used to calculate index weights that maximize the correlation between the index and the aggregate genotype.

102. (B) Selection index
The selection index is highly sensitive to changes in the economic importance of traits. If market conditions shift and the relative value of one trait increases significantly, the weights assigned to all traits in the index must be recalculated to remain optimal. This ensures that the breeding program continues to focus on the traits that contribute most to the overall profitability.

103. (D) Requiring too many generations to achieve multi-trait goals
Tandem selection is rarely used in commercial breeding because it is an inefficient use of time. By focusing on only one trait at a time, it takes many generations to achieve significant improvement in multiple traits. Modern breeding programs require simultaneous progress in many areas to remain competitive, making multi-trait methods like selection indexes much more practical and effective for achieving long-term goals.

104. (A) It decreases
In independent culling levels, adding more traits to the selection criteria inevitably reduces the selection intensity for each individual trait. This happens because a larger proportion of the population is culled for failing to meet the additional standards. To maintain the same number of breeding replacements, the breeder must lower the standards for each trait, thereby reducing the average superiority of selected animals.

105. (C) Aggregate breeding value (aggregate genotype, H)
The Smith-Hazel selection index is designed to maximize the correlation between the index score, which is based on phenotypic measurements, and the aggregate breeding value of the individual. The aggregate genotype represents the total genetic merit of the animal, where the breeding value of each trait is weighted by its relative economic importance to the overall breeding objective.

106. (A) $H = \Sigma(a_i \times G_i)$
The aggregate genotype is a mathematical representation of the total economic genetic merit of an individual. It is calculated as the sum of the true breeding values of the traits in the breeding objective, with each breeding value multiplied by its respective relative economic weight. This value serves as the target that the selection index aims to predict as accurately as possible.

107. (B) P-3, Q-1, R-4, S-2
In the Smith-Hazel index, the matrix P contains the phenotypic variances and covariances of the measured traits. The vector b represents the unknown weighting factors to be solved. The matrix G includes the genetic variances and covariances between the phenotypic traits and the traits in the breeding objective. Finally, the vector a contains the relative economic values for the traits.

108. (B) $b = P^{\{-1\}}Ga$
To find the optimal index weights that maximize the accuracy of the selection index, the Smith-Hazel equations must be solved. This involves multiplying the inverse of the phenotypic variance-covariance matrix by the product of the genetic variance-covariance matrix and the vector of economic weights. This mathematical operation provides the weights that should be applied to the phenotypic records.

109. (C) Expected profit increase per unit improvement in the breeding value
The relative economic value of a trait in a selection index represents the expected change in total profit resulting from a one-unit genetic improvement in that trait, while holding all other traits constant. These values ensure that the breeding program prioritizes traits that have the greatest impact on the financial success and sustainability of the livestock production system.

110. (D) Accurate estimates of genetic and phenotypic parameters
The construction of an effective selection index depends entirely on the quality of the parameters used in the calculation. Accurate estimates of heritabilities, genetic correlations, and phenotypic correlations are essential. If these parameters are poorly estimated or outdated, the resulting index weights will be suboptimal, leading to reduced genetic progress

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sires evaluated in later years or against superior contemporaries were not fairly compared to sires from earlier periods.

130. (A) Grouping sires by genetic merit to account for genetic trend
The Modified Contemporary Comparison introduced a grouping system to account for the fact that sires from different generations have different average genetic merits. By grouping sires based on their pedigree information, the method could better estimate the genetic trend and provide more accurate comparisons between bulls of different ages. This improvement led to more reliable breeding values for the dairy industry.

131. (C) Best Linear Unbiased Prediction
BLUP is a sophisticated statistical method used to estimate breeding values in animal populations. It is widely considered the gold standard for genetic evaluation because it simultaneously accounts for fixed environmental effects and random genetic effects. By utilizing all available pedigree and performance information, it provides the most accurate and reliable predictions of an individual's genetic merit for various traits of economic importance.

132. (D) Minimizes the prediction error variance
In the context of BLUP, the term "Best" refers to the property that the method provides the most accurate possible predictions. Specifically, it mathematically minimizes the variance of the error between the true breeding value and the predicted value. This ensure that the estimated breeding values are as close to the animal's actual genetic merit as possible, given the data available for the analysis.

133. (C) Producing a predictor equal to the true breeding value
BLUP is "unbiased" because the expected value of the predicted breeding values is equal to the true breeding values of the individuals. This means that, on average, the method does not systematically over- or under-estimate the genetic merit of any group of animals. This property is crucial for making fair comparisons between individuals from different herds, years, or management systems across the whole population.

134. (B) Numerator relationship matrix (A-matrix)
The Animal Model in BLUP utilizes the numerator relationship matrix, which contains all known pedigree links between all animals in the population. This matrix allows the model to incorporate information from every relative of an individual, including ancestors, siblings, and offspring. By accounting for these relationships, the model more effectively separates genetic from environmental effects, leading to more accurate breeding value estimates.

135. (D) The vector of random genetic effects (breeding values)
In the standard mixed model equation used for BLUP, the term "u" represents the vector of random effects that the model aims to predict. In an animal breeding context, these are typically the additive genetic effects, or breeding values, for each individual in the analysis. The model estimates these values while simultaneously adjusting for fixed environmental effects that also influence the observed phenotypic records.

136. (A) Incidence matrix relating observations to fixed effects
In the BLUP mixed model equation, the matrix "X" is an incidence matrix that connects each phenotypic observation to its corresponding fixed effects, such as herd, year, and season. This matrix ensures that the model correctly assigns the environmental influences to the appropriate records. By accurately modeling these fixed effects, BLUP can more effectively isolate the underlying genetic variation from non-genetic sources of noise.

137. (C) BLUP (Animal Model)
The BLUP Animal Model is superior to earlier methods because it can handle complex data structures common in livestock populations. It automatically accounts for non-random mating, selection bias, and overlapping generations by using the complete pedigree and the relationship matrix. This flexibility makes it the most robust method for genetic evaluation in modern breeding programs, providing accurate results even in highly selected populations.

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138. (A) Tying together information from all relatives for the estimation
The inverse of the additive genetic relationship matrix is a critical component of the mixed model equations in BLUP. It incorporates all

and the low heritability of most production traits. It ignores the biological reality of regression to the population mean, which occurs because phenotypes are not perfect indicators of genotypes. This leads to overestimation of the genetic merit of superior sires and dams.

121. (C) The performance of daughters of other sires in the same herd
The Contemporary Comparison method evaluates a sire's genetic merit by comparing his daughters' performance to the performance of other cows, known as contemporaries, that were raised in the same herd at the same time. This approach helps to remove the confounding effects of different management and environmental levels between herds, providing a more accurate estimate of the sire's true genetic superiority.

122. (A) Are managed under uniform environmental conditions (same herd, season, and year)
In livestock evaluation, contemporaries are animals that are likely to have experienced the same environmental and management conditions. This typically means they are of similar age and are raised in the same herd during the same season and year. By comparing animals within these contemporary groups, breeders can more effectively isolate genetic differences from the surrounding environmental variation that affects performance.

123. (D) $\frac{n_1 \times n_2}{n_1 + n_2}$
In the Contemporary Comparison method, the weighting factor "W" is used to account for the number of daughters and the number of contemporaries in each herd. It is calculated as the product of the two group sizes divided by their sum. This factor ensures that herds with more information contribute more to the sire's overall evaluation, increasing the reliability of the final breeding value.

124. (B) Incomplete herizability and the specific number of daughters
Regression to the population mean is a statistical concept used to adjust sire evaluations based on the amount of information available. If a sire has only a few daughters, their average is a less reliable estimate of his true merit. The evaluation is regressed toward the mean to avoid overestimating his genetic value, with the amount of regression decreasing as more daughter records are added.

125. (C) Including records from older animals producing in the same herd
The Herdmate Comparison method improved upon Contemporary Comparison by including records from all other cows in the herd, not just those of the same age. By comparing a sire's daughters to a larger group of herdmates, the method increases the amount of information available for the evaluation. This provides a more stable and potentially more accurate estimate of the sire's relative genetic performance.

126. (D) Assuming that the genetic merit of herdmate sires was average
A significant limitation of early evaluation methods was the assumption that all herdmates were sired by bulls of average genetic merit. In reality, some herds use better sires than others, creating a genetic trend over time. If a sire's daughters were compared to herdmates with superior genetics, the sire would appear worse than his true value. This bias was eventually addressed by more advanced models.

127. (A) 4200 kg
Using the Equal Parent Index formula, the sire's index is calculated as twice the daughter average minus the dam average. In this case, two multiplied by four thousand kilograms is eight thousand kilograms. Subtracting the dam average of three thousand eight hundred kilograms results in a sire index of four thousand two hundred kilograms. This represents the sire's estimated genetic contribution to the daughters.

128. (B) Confounding sire merit with management and environmental levels
The simple daughter average often misrepresents a sire's true genetic quality because it does not separate genetic merit from the environment. A sire whose daughters are in a high-producing herd with excellent nutrition will have a high average, even if he is genetically mediocre. Without adjusting for these environmental differences, the daughter average provides a biased and unreliable estimate of the sire's breeding value.

129. (B) I and III
The Herdmate Comparison method had two major flaws. It did not account for the genetic improvement occurring in the population over time, known as the genetic trend. Additionally, it assumed that the sires of all herdmates were of equal genetic merit. These issues meant that

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182. (B) Concentrating intense selection in a small elite herd
A closed nucleus system is designed to maximize genetic progress by concentrating the most elite animals and the most intense selection pressure within a single, highly managed herd. This nucleus herd produces superior sires and dams that are then used to spread genetic improvement to the rest of the population. By focusing resources on a small group, breeders can achieve higher accuracy and intensity than possible in a larger population.

183. (D) The population ceases to respond to continued selection pressure.
A selection plateau is a point in a breeding program where the mean phenotypic value of the population no longer increases, despite continued selection pressure and a positive selection differential. This indicates that the genetic response has stalled. Plateaus can be temporary or permanent and are caused by various factors, including the exhaustion of genetic variance, reaching biological limits, or opposing forces like natural selection within the population.

184. (A) P-1, Q-2, R-4, S-3
Selection plateaus have multiple genetic causes. The exhaustion of additive variance occurs when all favorable alleles are fixed. Overdominance maintains alleles at equilibrium, preventing further progress. Negative genetic correlations can cause a decline in fitness traits, which opposes the selected improvement. Inbreeding depression reduces the overall vigor and performance of the population as homozygosity increases due to selection of related individuals.

185. (B) A decline in the mean phenotypic value when selection pressure is relaxed after a plateau
Genetic slippage is the phenomenon where the progress made during selection is partially lost once the selection pressure is removed. This typically occurs after a population has reached a plateau. The decline suggests that the high performance achieved was maintained by selection against opposing forces, such as natural selection or deleterious epistatic interactions, which pull the population mean back toward a more biologically stable state.

186. (A) Extensive epistatic interactions favoring specific combinations
A primary cause of genetic slippage is the presence of favorable epistatic interactions that were held together by intense selection. These specific combinations of alleles at different loci provide a phenotypic boost but are easily broken apart by recombination during meiosis. Once selection is relaxed, the recombination process continues without the counteracting selection pressure, leading to a decline in the average phenotypic performance of the subsequent generations.

187. (D) Natural selection opposes artificial selection
When a selected trait becomes negatively correlated with reproductive fitness, artificial selection for higher performance is eventually balanced by natural selection for survival. This results in a plateau where any further genetic gain in the selected trait is offset by a decrease in the number of offspring produced. In this state, the population mean remains stable because the net selective force on the trait becomes zero.

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188. (B) Crossing the line with an unrelated population or mutation
If a selection plateau is caused by the exhaustion of additive genetic variance, the most effective way to resume progress is to introduce new genetic variation. This can be achieved by crossing the plateaued line with another unrelated population or by waiting for new mutations to occur. These new alleles provide fresh material for selection to act upon, potentially allowing the population to move beyond its previous limit.

189. (C) Decline due to the loss of forced heterozygote advantage
When a plateau is maintained by overdominance, the selection pressure is required to keep the heterozygote frequency at its maximum. If selection is relaxed, the population will return to a random-mating equilibrium, which will inevitably contain a higher proportion of the less fit homozygous genotypes. This change in genotypic frequencies leads to a decline in the overall phenotypic mean of the population from the previously held plateau level.

190. (D) The initial frequency of favorable alleles and effective population size (N_e)
The total amount of genetic progress possible in a closed population is fundamentally limited by its initial genetic makeup and its size.

pedigree information into the analysis, allowing the performance of relatives to influence an individual's breeding value estimate. This connectivity increases the amount of information available for every animal, leading to higher accuracy and better predictions, especially for individuals with few records.

139. (D) Herd-year-season (HYS) effects
Fixed effects in a BLUP model are factors that are expected to have a consistent and measurable impact on performance across the population. In dairy cattle, these commonly include herd, year, and season effects, as well as the age of the cow at calving. By including these as fixed effects, the model adjusts the phenotypic records to account for environmental differences between different management groups.

140. (A) P-4, Q-2, R-1, S-3
In the Animal Model, "y" is the vector containing all phenotypic observations. "b" represents the vector of fixed effects to be estimated, while "Z" is the incidence matrix that relates these phenotypic records to the random genetic effects. "e" is the vector of residual random errors, which accounts for the variation in performance that cannot be explained by either the fixed or genetic effects.

141. (C) Treating sire effects as fixed and ignoring genetic distributions
The Least Squares method is less effective than BLUP because it treats sire effects as fixed parameters rather than random variables with an underlying genetic distribution. This approach fails to account for the genetic relationships between sires and doesn't utilize information from other relatives. Consequently, Least Squares is more susceptible to errors and provides less accurate estimates of genetic merit compared to mixed model methods.

142. (D) Simultaneously, adjusting each for the other
A key feature of BLUP is that it solves for fixed environmental effects and random genetic effects at the same time using a set of mixed model equations. This simultaneous estimation ensures that the genetic effects are adjusted for environmental differences, and the environmental effects are adjusted for the genetic merit of the animals. This reciprocal adjustment leads to the most accurate and unbiased results for both components.

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143. (A) The ratio of residual variance to genetic variance (e.g., $\frac{1-h^2}{h^2}$)
To perform a BLUP evaluation, the model requires prior knowledge of the variance components of the trait, specifically the ratio of the residual variance to the additive genetic variance. This ratio, which is related to the heritability, determines how much weight is given to the phenotypic records versus the information from relatives in the relationship matrix. Accurate variance estimates are essential for optimal predictions.

144. (A) $R = i \times h^2 \times \sigma_P$
The predicted genetic response per generation, also known as the breeder's equation, is calculated by multiplying the selection intensity, the heritability of the trait, and the phenotypic standard deviation. This formula predicts the expected change in the population mean after one round of selection. It highlights the importance of applying high selection pressure and working with highly heritable traits to achieve rapid progress.

145. (B) 8 kg
The expected genetic response is the product of the selection differential and the heritability. For yearling weight with a selection differential of twenty kilograms and a heritability of zero point four, the response is twenty multiplied by zero point four, which equals eight kilograms. This value represents the average genetic improvement expected in the offspring of the selected parents compared to the previous generation.

146. (C) 10 units
The total selection differential is the average of the male and female selection differentials. In this herd, thirty plus ten divided by two equals twenty units. To find the expected response per generation, this average differential of twenty is multiplied by the heritability of zero point five. The resulting genetic response is ten units, reflecting the progress achieved through both parental pathways combined.

147. (C) Average generation interval of both sexes
To calculate the annual rate of genetic progress, the total response achieved per generation must be divided by the average generation interval of the parents. This calculation accounts for the time required to complete one selection cycle.

By minimizing the generation interval, breeders can increase the number of selection cycles over time, leading to a faster annual rate of genetic improvement in the population.

148. (D) Dominance deviation present in a strictly additive model
The predicted genetic response to selection in a standard additive model depends on the selection intensity, accuracy, and the amount of additive genetic variance. Dominance deviations are non-additive and are not predictably passed from parents to offspring. Therefore, they do not contribute to the response predicted by the breeder's equation, which focuses solely on the additive genetic component that determines an animal's breeding value.

149. (C) Genetic correlation between Trait X and Trait Y
Indirect selection occurs when a breeder selects for one trait to improve another. The effectiveness of this strategy depends on the genetic correlation between the two traits. If the traits are strongly and positively correlated genetically, selection for the first trait will lead to a significant and favorable response in the second. This approach is useful when the target trait is difficult or expensive to measure.

150. (B) The two traits have an antagonistic (negative) genetic correlation.
A negative genetic response in an important trait, despite selection for improvement in another area, indicates a genetic antagonism. This happens when the alleles that improve the selected trait tend to have a detrimental effect on the other trait. Breeders must be aware of these negative correlations to avoid inadvertently degrading important performance or fitness characteristics while pursuing specific breeding goals for other traits.

151. (D) II, IV, I, III
Predicting annual genetic gain in a four-pathway program involves first determining the selection parameters for each pathway. Next, the genetic superiority contributed by each of the four paths is summed. The average generation interval is then calculated by summing the intervals for all pathways. Finally, the total genetic superiority is divided by the sum of the generation intervals to arrive at the predicted annual rate of progress.

152. (A) Sires to breed sons
In large-scale breeding programs like dairy cattle, the "sires to breed sons" pathway typically contributes the most to the total genetic gain. This is due to the extremely high selection intensity possible for sires, combined with the high accuracy of progeny testing. Because only a few elite bulls are chosen to produce the next generation of sires, their genetic influence on the entire population is immense.

153. (C) The trait follows an infinitesimal model with normal distribution
The standard prediction of genetic response assumes the infinitesimal model, where the trait is controlled by a very large number of genes, each with a small effect. This model implies that the trait is normally distributed and that the heritability and genetic variance remain relatively constant over a few generations of selection. This provides a simplified mathematical framework for estimating the progress expected from truncation selection in a population.

154. (A) $i_X \times h_X \times h_Y \times r_G \times \sigma_{PY}$
The correlated response in one trait due to selection on another is predicted by a formula that includes several factors. These are the selection intensity applied to the first trait, the square root of heritability for both traits, their genetic correlation, and the phenotypic standard deviation of the second trait. This calculation allows breeders to estimate the side effects of their selection decisions on other important characteristics.

155. (D) $i \times \sigma_A$
If selection accuracy is perfect, meaning the estimated breeding value is exactly equal to the true breeding value, the prediction equation simplifies. The expected genetic response is then the product of the selection intensity and the additive genetic standard deviation. This theoretical scenario represents the maximum possible response to selection, where environmental noise is completely eliminated from the decision-making process within the breeding program.

156. (B) Reduces additive genetic variance via linkage disequilibrium
The Bulmer effect is a phenomenon where intense truncation selection reduces the additive genetic variance in the next generation. This

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reduction is caused by the creation of negative linkage disequilibrium between alleles at different loci. This effect must be accounted for because it causes the actual selection response to be lower than predicted by the base population parameters, especially in the early generations of a program.

157. (C) The ratio of the realized selection response to the realized selection differential
Realized heritability is an empirical estimate of heritability derived from the results of a selection experiment. It is calculated by dividing the observed genetic response to selection by the actual selection differential applied over several generations. This value provides a retrospective measure of how effectively the selection process translated phenotypic superiority into genetic improvement within the specific population and environment of the experiment.

158. (B) 0.30
To calculate realized heritability, the cumulative selection response is divided by the cumulative selection differential. In this experiment, dividing fifteen units of response by fifty units of selection differential results in a realized heritability of zero point three. this value indicates that thirty percent of the phenotypic superiority of the parents was successfully transmitted to the offspring as genetic improvement over five generations.

159. (A) Linear regression of cumulative response on selection differential
The most robust way to estimate realized heritability is by performing a linear regression where the cumulative selection response is plotted against the cumulative selection differential. The slope of this regression line provides the estimate of herizability. This method is preferred because it utilizes all available data points across generations, making it less sensitive to random fluctuations or environmental changes during the course of the experiment.

160. (D) Shifts in gene frequencies or environmental trends alter variance.
Realized heritability can differ from initial estimates because selection changes the population over time. As selection proceeds, gene frequencies shift, and intense selection can create linkage disequilibrium, which reduces the genetic variance. Additionally, long-term environmental trends can mask or exaggerate the genetic response. Therefore, realized heritability reflects the actual progress achieved under the specific conditions of the experiment, which may evolve from the starting point.

161. (B) Selecting one line for high values and another line for low values of the same trait
A divergent selection experiment involves creating two separate lines from a single base population and selecting one line for high performance and the other for low performance for the same trait. This design is powerful for studying genetic variation because it creates two groups with extreme phenotypic differences. It also allows for the estimation of realized heritability without necessarily requiring a separate unselected control group.

162. (B) II only
Realized heritability is a retrospective measure, meaning it is calculated after a selection experiment has been conducted, not before it begins. It relies on observed data such as cumulative response and selection differentials. While it often requires control populations to adjust for environmental changes, it is particularly useful for detecting asymmetries in response and providing a practical measure of the effectiveness of long-term selection strategies.

163. (A) Directional dominance
Asymmetrical response in divergent selection occurs when the high and low lines respond at different rates. This can be caused by directional dominance, where alleles for one direction are consistently dominant over those for the other. Other factors include differences in selection intensity, changes in genetic variance as allele frequencies approach fixation, and maternal effects that may favor one direction of selection over the other.

164. (D) An unselected control population reared contemporaneously
To accurately measure the genetic response to selection, it is essential to adjust for any environmental trends that might occur over time. This is done by maintaining an unselected control population in the same environment as the selected lines. The actual genetic response is calculated as the difference between the selected and control lines, ensuring that changes

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in performance are due to genetics rather than nutrition or management.

165. (B) 0.25
The realized heritability is calculated by dividing the cumulative response by the cumulative selection differential. In this scenario, dividing the six units of response by the twenty-four units of selection differential yields a realized heritability of zero point two five. This means that one-quarter of the total selection pressure applied over the three generations resulted in a permanent genetic change in the population mean.

166. (B) Realized heritability
When cumulative genetic response is plotted against the cumulative selection differential, the slope of the resulting line represents the realized heritability. A steeper slope indicates a higher heritability, meaning that a larger proportion of the selection pressure resulted in genetic progress. This graphical method provides a clear visual and statistical summary of the efficiency of selection over the entire course of a breeding experiment.

167. (D) A selection plateau being reached
A selection plateau occurs when the population no longer responds to selection pressure, causing the realized heritability to drop toward zero. This can happen for several reasons, such as the exhaustion of additive genetic variance, reaching a physiological limit, or the opposition of natural selection. At this point, even with a high selection differential, no further genetic progress is made, indicating that the selection limit has been reached.

168. (A) Eliminating the need for a contemporaneous control population
One advantage of divergent selection is that the difference between the high and low lines serves as the measure of response, which can often eliminate the need for a separate control group. Any environmental changes are assumed to affect both lines equally, so the divergence between them is primarily due to genetic differences. This doubles the phenotypic range and provides a robust estimate of heritability.

169. (C) The phenotypic superiority of animals retained for breeding
In the context of realized heritability, the selection differential is the measure of the phenotypic superiority of the individuals that were actually chosen to be parents. It is calculated by comparing the mean of the selected parents to the mean of their entire generation. This value represents the total potential for change that was applied through the selection process in each generation of the experiment.

170. (A) Reducing recording costs by culling inferior animals early
Multi-stage selection is a practical strategy where animals are evaluated and culled in several sequential steps. By removing obviously inferior animals at an early stage based on simple or inexpensive traits, the breeder can focus resources on the remaining candidates for more detailed and costly measurements later. This optimizes the efficiency of the breeding program by reducing overall recording and management costs.

171. (D) Suboptimal genetic gain for the primary trait measured at the final stage
A risk of very intense culling in the early stages of a multi-stage program is that some animals with low genetic merit for the final trait might be culled for poor early performance. If the correlation between early and late traits is not perfect, this initial selection can reduce the total potential for improvement in the primary goal, leading to a suboptimal overall genetic gain.

172. (B) Low in heritability, sex-limited, or measured late in life
Marker-assisted selection is most valuable for traits where traditional phenotypic selection is difficult or inefficient. This includes traits with low heritability, where phenotypic records are poor indicators of genetic merit, and sex-limited traits that cannot be measured in both sexes. It is also highly effective for traits measured late in life or after slaughter, as markers allow for selection much earlier in the animal's life.

173. (B) Both A and R are true but R is not the correct explanation of A.
Optimizing age structure is essential for maximizing genetic gain, as it balances the need for young parents to shorten the generation interval with the need for older, more proven

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individuals to increase selection accuracy. While very young parents speed up generation turnover, they often have less performance information available. The ideal structure finds the best compromise to achieve the highest possible annual rate of progress.

174. (D) Selection intensity, accuracy, and generation interval
In animal breeding, optimizing the age structure of a herd involves finding the ideal balance between three critical factors. These are the intensity of selection, the accuracy of the genetic evaluations, and the length of the generation interval. By adjusting the proportions of different age groups, breeders can maximize the annual genetic gain, ensuring that the most superior animals are used efficiently over time.

175. (A) Large
Marker-assisted selection is most efficient when a significant portion of the total additive genetic variance is explained by the molecular markers used. When markers capture a large part of the genetic influence on a trait, they provide a very reliable estimate of the animal's breeding value. This high correlation between markers and the true genetic merit allows for more effective and accurate selection compared to using phenotypes alone.

176. (B) Drastically reducing the generation interval via early prediction of breeding values
Genomic selection has revolutionized animal breeding by allowing for the estimation of breeding values using DNA markers at birth. This eliminates the need to wait for phenotypic records, which can take several years in species like cattle. By selecting parents as soon as they are genotyped, breeders can drastically shorten the generation interval, leading to a much faster annual rate of genetic improvement across the entire population.

177. (B) A function of the independent culling proportions and genetic correlations between the stages
The overall selection intensity in a multi-stage program is not a simple sum but a complex function of the culling thresholds at each stage. It also depends on the genetic and phenotypic correlations between the traits measured at different times. Calculating the total intensity requires accounting for how much selection pressure is applied at each step and how those decisions affect the genetic variation remaining for the final selection.

178. (A) Finite population size leading to rapid inbreeding and loss of genetic variance
Theoretical limits to genetic response are largely set by the effective population size. In finite populations, very intense selection can lead to a rapid increase in inbreeding and the accidental loss of favorable alleles due to genetic drift. This process reduces the available genetic variance over time, eventually causing the population to reach a selection limit or plateau where no further genetic improvement can be achieved.

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179. (C) Slightly lower initial reliability per young sire but a massively reduced generation interval
Replacing progeny testing with genomic selection involves a trade-off. While the reliability of a young sire's genomic evaluation may be lower than a full progeny test with many daughters, the generation interval is greatly reduced. Because sires can be used as parents much earlier, the increase in generation turnover more than compensates for the slightly lower accuracy, resulting in a higher total annual genetic gain for the population.

180. (D) The selection criterion and the true breeding value
The goal of any optimized selection program is to maximize the correlation between the information used to make selection decisions, known as the selection criterion, and the true breeding value of the individuals. A higher correlation means the selection process is more accurate, leading to a greater genetic response. This accuracy is a fundamental component of the breeder's equation and is the focus of most advanced breeding technologies.

181. (C) Positively genetically correlated with Trait 2
For a two-stage selection process to be effective, the trait measured in the first stage must have a strong positive genetic correlation with the primary trait of interest in the second stage. This ensures that the animals culled early for poor performance would also likely have been inferior for the final goal. Without this correlation, early culling would be random with respect to the ultimate breeding objective, reducing the efficiency of the program.

and potentially incorrect selection decisions within the breeding population.

111. (A) $\frac{\sigma_I}{\sigma_H}$
The accuracy of a selection index is defined as the correlation between the index score and the true aggregate genotype. Mathematically, this is calculated as the ratio of the standard deviation of the index to the standard deviation of the aggregate genotype. A higher accuracy indicates that the index is a more reliable predictor of an individual's overall genetic economic merit.

112. (B) Suboptimal index weights leading to reduced genetic progress
Using incorrect genetic correlation parameters when building a selection index will result in weighting factors that do not truly maximize the overall genetic gain. While the index will still work, it will not be as efficient as it could have been with accurate data. This leads to a slower rate of progress toward the breeding goals and a loss of potential economic improvement.

113. (B) Hold the genetic change in one or more specific traits to zero
A restricted selection index is a specialized tool used when a breeder wants to improve some traits while ensuring that another trait remains unchanged. This is often necessary when a trait is already at an optimal level or when further change would be undesirable. By adding constraints to the index equations, the weights are adjusted to prevent any genetic progress in the restricted trait.

114. (A) $bâ€™Pb$
The variance of the selection index reflects the amount of variation in the calculated index scores across the population. It is mathematically determined by multiplying the transposed vector of index weights by the phenotypic variance-covariance matrix and then by the original vector of weights. This variance is a key component in calculating the accuracy and the expected genetic response of the index.

115. (C) Be lowered to prevent degradation of the correlated trait
When two traits have an antagonistic genetic correlation, selecting strongly for one will cause a decline in the other. In a selection index, the weight for a trait will be adjusted downward if its improvement would cause a disproportionately large and economically damaging loss in a negatively correlated trait. The index balances these relationships to maximize the total economic progress of the animal.

116. (A) 100
For ease of interpretation, selection index scores are often standardized so that the average individual in the population has a score of one hundred. This provides a clear reference point for breeders, where scores above one hundred indicate individuals that are genetically superior to the population average, and scores below one hundred represent individuals that are below average for the overall breeding objective.

117. (C) Phenotypic variances
The aggregate genotype is a purely genetic concept representing the total economic merit of an individual's breeding values. It is defined by the traits included in the breeding objective and their relative economic weights. While phenotypic variances are necessary to construct the selection index used to predict the aggregate genotype, they are not part of the definition of the aggregate genotype itself.

118. (D) A is false but R is true.
The simple daughter average is a biased method of sire evaluation because it fails to account for the genetic merit of the dams and the environmental differences between herds. A sire whose daughters are raised in a superior environment will appear genetically better than he truly is. The method only works accurately under the unrealistic assumption that all sires are mated to identical, average dams.

119. (D) $I = 2D - M$
The Equal Parent Index is based on the principle that an offspring inherits exactly half of its genes from each parent. Therefore, the daughter's average performance is the average of the sire's and the dam's genetic contributions. To estimate the sire's merit, the formula multiplies the daughter average by two and subtracts the dam average, theoretically isolating the sire's genetic influence.

120. (A) Perfect inheritance without any regression to the population mean
A fundamental flaw of the Equal Parent Index is its assumption that traits are perfectly inherited without accounting for the environmental noise

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The frequency of favorable alleles at the start determines how much improvement can be made before they are fixed. The effective population size (N_e) influences the rate of genetic drift, which can cause the accidental loss of valuable alleles, especially when selection is very intense in small breeding groups.

191. (A) Extreme phenotypes selected by humans often possess lower natural reproductive fitness.
Artificial selection often pushes animals toward phenotypic extremes that are not favored by natural selection. For example, selecting for extremely high growth rates or milk yields may lead to physiological stress and reduced fertility. As the population mean moves further from its natural optimum, the pressure from natural selection increases, eventually stalling further progress when the two opposing selective forces reach an equilibrium state.

192. (D) Produces a rapid response if natural selection was an factor
If a population is at a plateau because natural selection is opposing artificial selection, applying selection in the opposite direction usually results in a very fast response. This is because both artificial and natural selection are now working in the same direction, quickly moving the population mean toward the natural optimum. This rapid change demonstrates that significant genetic variation was still present but was previously held in a balanced state.

193. (B) All favorable alleles are either fixed or lost due to drift.
In an idealized population where no new mutations occur, the ultimate limit to selection is reached when there is no longer any additive genetic variance for the trait. This happens when all the alleles that contribute to higher performance have either been fixed in the population or have been lost through genetic drift. At this point, the population is genetically uniform for the selected trait, and no further progress is possible.

194. (A) A strong negative genetic correlation with essential fitness
Continued selection for high egg production can reach a limit if the physiological demands of laying more eggs begin to severely compromise the hen's health or reproductive ability. This negative correlation between production and fitness means that natural selection for survival will act against the most productive individuals. The plateau occurs because the genetic gain from artificial selection is balanced by the fitness loss, preventing further increases in egg numbers.

195. (B) II, III and V
Genetic slippage is the decline in performance observed when selection is relaxed, often indicating a conflict between human breeding goals and natural fitness. It is frequently caused by the breakdown of favorable epistatic combinations of genes that were maintained only through intense selection pressure. This phenomenon highlights that some of the progress achieved in highly selected lines is unstable and dependent on continuous and focused selection.

196. (D) Decreases genetic variance through linkage disequilibrium
The Bulmer effect describes the immediate reduction in additive genetic variance that occurs when directional truncation selection is applied to a population. This reduction is not due to a change in allele frequencies but rather the creation of negative linkage disequilibrium among alleles at different loci. This phenomenon means that the actual response to selection in the early generations will be lower than predicted by the base population heritability.

197. (C) Negative linkage disequilibrium generated among trait-enhancing alleles
Truncation selection favors individuals with superior phenotypes, who tend to have favorable alleles across many loci. However, among those selected, there is a negative correlation between alleles at different loci. An individual with a very good allele at one locus needs fewer good alleles elsewhere to be selected. This creates negative linkage disequilibrium, which reduces the overall additive genetic variance available for the next generation of breeding.

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198. (B) No, it changes covariance between loci via linkage balance
The Bulmer effect does not permanently remove alleles from the population; instead, it changes how they are associated with each other. It creates a state of linkage disequilibrium that reduces the genetic variance. This is a reversible change in the covariance between loci. As long as selection continues, this reduced variance persists, but the underlying alleles remain present and can

249. (C) Increase susceptibility to stress if specific genes are ignored
Intense selection for lean meat and muscle growth in pigs has historically been linked to the Porcine Stress Syndrome, caused by the Halothane gene. While selection for leanness improves carcass quality, it can inadvertently increase the frequency of this gene, making pigs more susceptible to stress-induced death and poor meat quality. Modern breeders now use genetic testing to ensure that selection for lean yield does not compromise animal welfare.

250. (A) Egg production (number) and egg weight
In layer poultry, there is a well-known antagonistic relationship between the number of eggs a hen lays and the average size of those eggs. hens that lay very large numbers of eggs tend to produce slightly smaller eggs. breeders must manage this correlation by selecting for total egg mass or by using specialized sire and dam lines to achieve the desired balance between quantity and size for the market.

251. (D) Heavy musculature, strong feet/legs, and endurance levels
Breeding for draught purpose cattle focuses on traits that enhance physical work capacity. This includes selecting for large body size, heavy muscle development, and a strong skeletal structure, particularly in the feet and legs. Additionally, traits like endurance and a calm temperament are prioritized to ensure the animals can perform heavy labor over long periods. These characteristics differ significantly from those emphasized in specialized dairy or meat breeds.

252. (B) Select for total yield as it drives total component mass
Because of the negative correlation between milk volume and fat percentage, the most effective way to increase the total amount of fat produced is to select for high overall milk yield. While the percentage of fat might decline slightly, the massive increase in total milk volume more than compensates, resulting in a higher total yield of fat in kilograms. This approach is commonly used in breeding objectives focused on total solid production.

253. (C) Skeletal integrity and cardiovascular capacity in birds
In broiler chickens, selecting for extremely rapid growth has led to significant health challenges. The birds' skeletal systems and hearts often struggle to keep pace with their rapidly increasing muscle mass. This can result in leg problems, lameness, and cardiovascular failure. To address this, modern broiler breeding programs now include traits for bone strength and heart health alongside growth and feed efficiency to improve bird welfare and survival.

254. (D) Reduce the incidence of downgraded and broken eggs produced
Maintaining high eggshell quality is a major goal in poultry breeding. Thicker and stronger shells are essential for protecting the egg during transport and handling. By selecting for better shell quality, breeders can significantly reduce the number of cracked or broken eggs, which are economically worthless. This becomes increasingly important as hens age and their ability to produce strong shells naturally declines during their laying cycle.

255. (A) Milk production and draught capability
Dual-purpose cattle breeds are developed to provide both milk for human consumption and draught power for agricultural work. In regions like South Asia, breeds like the Sahiwal and Haryana are prized for this balance. The breeding objective focuses on maintaining adequate milk yields while ensuring the bulls remain strong and capable of pulling plows and carts, making these animals highly versatile and valuable to small-scale farmers.

256. (B) A decline in maternal traits like fertility and milk
Focusing exclusively on terminal sire traits, such as fast growth and high carcass lean yield, can be detrimental if those animals are also used to produce replacement females. There is often a negative correlation between extreme meat production and maternal traits like fertility and milk production. If not managed, this can lead to a population of cows or sows that are efficient at producing meat but poor at successfully raising offspring.

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207. (A) Overestimate the genetic gain
If a breeder ignores the Bulmer effect, they will likely use the higher genetic variance from the unselected base population to predict future progress. However, since the actual variance is reduced by selection-induced linkage disequilibrium, the real response will be smaller than expected. This leads to an overestimation of the genetic gain, resulting in biased predictions and potentially flawed economic planning for the long-term breeding program.

208. (D) Breaking down the selection-induced linkage disequilibrium
Recombination during meiosis is the biological process that counteracts the Bulmer effect. While truncation selection creates negative associations between alleles at different loci, recombination reshuffles these alleles, breaking down the disequilibrium. The equilibrium genetic variance in a selected population is reached when the rate at which selection creates these negative associations is exactly equal to the rate at which recombination destroys them in each generation.

209. (B) Distinguish genetic trends from environmental trends over time
The primary purpose of a control population in a selection experiment is to act as a baseline. Because environmental factors like nutrition, weather, and management can change over time, they can affect the phenotypic mean of the selected line. By measuring a contemporaneous unselected control line, breeders can separate these environmental shifts from the actual genetic progress achieved through selection, ensuring an accurate evaluation of the breeding program.

210. (A) Maintain a large effective size to minimize drift and inbreeding
To be an effective baseline, a control population must remain as genetically stable as possible. This is achieved by maintaining a large effective population size, which minimizes the effects of genetic drift and the accumulation of inbreeding. A stable control population ensures that any changes in its phenotypic mean are purely environmental, providing a reliable reference for measuring the genetic gain in the selected line.

211. (C) Repeat-mating design
A repeat-mating design is a specialized strategy used to estimate environmental trends without the need for a separate, unselected control line. In this design, the same parents are mated in consecutive years to produce multiple groups of offspring. Since the parents' genetics remain the same, any differences in the performance of their offspring born in different years can be attributed directly to environmental changes between those years.

212. (D) Progeny from same parents born and reared in consecutive years
In a repeat-mating design, the environmental trend is estimated by comparing the performance of offspring produced by the same pair of parents in different years. For example, the difference between the weaning weights of calves born in year one and year two from the same sire and dam reflects the change in the environment. This method effectively isolates environmental noise from the genetic evaluation process.

213. (C) Every sire leaves one son and every dam leaves one daughter
To maintain a stable genetic base and minimize drift in a control population, breeders often use a structured mating scheme where each parent is replaced by exactly one of its offspring. Specifically, every sire leaves one son and every dam leaves one daughter for the next generation. This approach ensures a very equal genetic contribution from all individuals, which maximizes the effective population size and preserves the original genetic variance.

214. (C) 6 units
The actual genetic response is calculated by subtracting the change in the control population from the change in the selected line. In this case, the selected line increased by ten units, but four of those units were due to improved nutrition, as shown by the control line. Therefore, the genetic improvement achieved through selection is ten minus four, which equals six units. This provides an unbiased measure of progress.

215. (D) Be identical to the base population from which the selected line is derived
For a control population to be valid, it should ideally have the same genetic starting point as the selected line. This means it should be derived from the same base population and have similar initial allele frequencies and genetic variance. Starting from an identical base ensures that any divergence between the two lines over time is due

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solely to the selection pressure applied to the experimental group.

216. (A) Completely halting genetic drift and mutation in the samples
Cryopreservation provides an ideal way to maintain a genetic control because frozen semen or embryos are biologically inactive. This completely halts genetic drift, mutation, and the accumulation of inbreeding that can occur in live populations. When these frozen samples are used in the future, they represent the exact genetic makeup of the original base population, providing a perfect and cost-effective reference for measuring long-term genetic progress.

217. (C) I and III
Control populations must be kept in the same environment as the selected lines to ensure that both groups experience identical environmental trends. This is essential for accurately estimating realized heritability and genetic gain. However, they must not undergo the same selection as the experimental line; instead, they should be mated randomly to maintain a stable genetic mean and act as a neutral baseline for the entire selection experiment.

218. (A) Its genetic mean remains constant over time
The use of a randombred control population is based on the fundamental assumption that its genetic mean does not change significantly over the course of the experiment. By minimizing selection, drift, and inbreeding, the control is intended to stay genetically representative of the original base population. Any observed changes in the control's performance are therefore assumed to be caused by shifts in the environment or management conditions.

219. (D) Minimize inbreeding while maintaining stable genetic variance
The Gowe mating system is a cyclical pedigree design used in poultry to maintain a stable control population. It is specifically designed to minimize the rate of inbreeding and the effects of genetic drift by ensuring that no close relatives are mated together across generations. This preserves the original genetic variance and allele frequencies of the base population, making it a reliable and long-term reference for selection studies.

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220. (B) Biased (over- or under-estimated)
If a control population experiences significant genetic drift, its phenotypic mean will change due to random genetic shifts rather than environmental factors alone. This introduces bias into the calculation of genetic response for the selected line. Depending on the direction of the drift, the estimated genetic gain could be either artificially inflated or deflated, leading to incorrect conclusions about the effectiveness of the selection program.

221. (C) The accumulative cost and accumulation of inbreeding or drift
Maintaining a live animal control population is expensive and logistically challenging. Over many generations, even with careful mating, these small populations are susceptible to the gradual accumulation of inbreeding and random genetic drift. These factors can alter the genetic baseline, making it a less accurate reference point. This makes modern alternatives, like using frozen genetic material, increasingly attractive for establishing stable long-term controls in animal breeding.

222. (D) 6-week body weight
Mice have been a primary laboratory model for studying quantitative genetics, with body weight at six weeks of age being one of the most frequently selected traits. This trait is easy to measure, exhibits moderate heritability, and provides a clear model for investigating the response to selection, the effects of inbreeding, and the nature of genetic variation in a mammalian species under controlled laboratory conditions.

223. (A) Maternal effects providing superior pre-weaning environments
In mouse selection experiments, the response is often faster in the high-weight line than in the low-weight line. This asymmetry is partly due to maternal effects, where mothers selected for larger size provide a better environment for their pups through superior milk production and care. This creates a positive correlation between the mother's genetics and the environment she provides, enhancing the response in the upward direction.

224. (B) Corn (maize) selected for high and low oil/protein content
The Illinois experiment is the longest-running selection study in history, beginning in eighteen ninety-six. It involves selecting corn for high and low levels of oil and protein. Over more than a century and a hundred generations, the experiment has demonstrated the incredible capacity for continued genetic response in quantitative traits, fueled by the recombination of existing variation and the occurrence of new mutations.

225. (B) It has a short generation interval and high reproductive rate
Tribolium castaneum, the flour beetle, is an excellent model for quantitative genetics because it can be reared in large numbers with very short generation intervals of about one month. This allows for many selection cycles to be completed in a short period. Their high reproductive rate and ease of management make them ideal for empirically testing breeding theories and comparing the efficiency of different selection strategies.

226. (A) Efficiency of recurrent selection and individual selection
Flour beetles were used in landmark experiments to compare different breeding methods, such as individual mass selection and recurrent selection for crossbred performance. These studies helped to validate the principles of heterosis and the effectiveness of selecting for combining ability. The results from these insect models provided valuable insights that were later applied to improve selection schemes in commercial livestock and poultry industries.

227. (C) Extreme phenotypic divergence from bidirectional selection
The Virginia chicken lines were established to study the long-term effects of selecting for high and low eight-week body weight. Over dozens of generations, this divergent selection has created extreme phenotypic differences between the two lines, with the high-growth birds becoming several times larger than the low-growth birds. This experiment remains a classic example of the power of consistent directional selection to transform a population's phenotype.

228. (D) New mutations contributing to quantitative genetic variance
Long-term selection experiments often show a continued response far beyond what was thought possible based on the initial genetic variance. This persistent progress is largely attributed to the occurrence of new mutations that create fresh genetic variation. While each mutation may have a small effect, their accumulation over many generations allows the population to continue evolving and reaching new phenotypic heights well past the original limits.

229. (C) Reproductive traits such as egg production and fertility levels
A consistent finding in poultry selection for rapid growth is the presence of an antagonistic genetic correlation with reproductive performance. As birds are selected to grow larger and faster, their egg production, fertility, and hatchability often decline. This creates a challenge for breeders, who must use specialized lines and multi-trait selection to balance the need for efficient meat production with the requirement for healthy reproductive offspring.

230. (B) The effective population size of the selected animal lines
Laboratory experiments have confirmed that the total response and the selection limit are heavily dependent on the effective population size. Larger populations maintain more genetic variation and are less affected by the random loss of favorable alleles due to drift. This allows them to respond to selection for more generations and reach a higher ultimate phenotypic level compared to smaller populations subjected to the same intensity.

231. (B) III only
Landmark selection experiments have provided critical validation for many breeding theories. While mouse studies highlighted the complexity of maternal effects, and Tribolium validated selection index efficiency, the poultry experiments clearly showed that selection for growth often has detrimental, not beneficial, effects on reproductive fitness. This conflict between production and reproduction is a fundamental challenge that animal breeders must manage through careful multi-trait selection and crossbreeding strategies.

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232. (A) Exhaustion of additive genetic variance in the selected line
When a plateaued line is crossed with another population and then resumes responding to selection, it demonstrates that the limit was due to a lack of genetic variation. The cross introduces new alleles, providing the additive genetic variance necessary for further progress. This proves that the biological capacity for improvement was not reached; rather, the selection process had simply run out of selectable genetic material.

233. (B) Short-term divergent selection experiments in lab models like mice and Drosophila
The concept of realized heritability was developed and refined through the analysis of data from numerous short-term selection experiments in laboratory animals. These studies provided the empirical evidence that heritability could be accurately estimated by observing the actual progress achieved in high and low selection lines. This retrospective approach became a standard tool for evaluating the effectiveness of selection in both laboratory and livestock populations.

234. (A) Highly genetically correlated with litter size in a complex way
Selection for litter size in mice revealed that the trait is influenced by both the mother's own reproductive capacity and the environment she provides for her offspring. There is often a complex genetic relationship between the number of pups born and the mother's ability to successfully rear them to weaning. These findings emphasize that improving litter-based traits requires accounting for both direct and maternal genetic components.

235. (D) Determines the specificity of immune response to antigens
The Major Histocompatibility Complex is a critical set of genes in the immune system of all vertebrates. It encodes proteins that appear on the surface of cells and help the body recognize and respond to foreign pathogens, such as viruses and bacteria. Because it determines how effectively an animal's immune system identifies specific antigens, genetic variation within the MHC is a primary factor in disease resistance and susceptibility.

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236. (B) B-complex
In poultry, the Major Histocompatibility Complex is known as the B-complex. This genetic region is highly polymorphic and plays a vital role in the bird's ability to resist various diseases, including viral infections like Marek's disease. Breeders have long studied the B-complex to identify specific alleles associated with superior immunity, allowing for the genetic improvement of health and survival in commercial poultry flocks.

237. (C) An antagonistic genetic correlation with overall milk yield
Breeding for mastitis resistance in dairy cattle is difficult because high-producing cows are often more susceptible to the disease. There is an antagonistic genetic correlation between milk yield and the animal's natural resistance to udder infections. This means that selecting solely for increased production can inadvertently lead to higher mastitis rates, requiring breeders to use balanced selection indexes that include both yield and health-related traits.

238. (D) Somatic Cell Score or Somatic Cell Count in milk
Somatic Cell Count is the most common indicator used for indirect selection against mastitis in dairy cattle. Cows with infections tend to have higher concentrations of white blood cells in their milk. Because SCC has a strong positive genetic correlation with clinical mastitis and is easy to measure during routine milk recording, it serves as a reliable proxy for identifying and selecting for genetic resistance to the disease.

239. (A) MHC B-complex
Marek's disease is a highly contagious viral infection in chickens that causes tumors and paralysis. Extensive research has shown that genetic resistance to this disease is strongly influenced by specific alleles within the MHC B-complex. By identifying and selecting for these favorable genotypes, poultry breeders have been able to significantly reduce the impact of the disease and improve the overall resilience of commercial bird populations.

240. (B) Low to moderate (<0.3)
Traits related to disease resistance and health in livestock generally have low to moderate heritability. This means that a large portion of the variation in these traits is due to environmental

factors and exposure to pathogens rather than genetics. Despite this, consistent selection using large datasets and advanced statistical models can still achieve significant and permanent genetic improvement in a population's overall level of resistance.

241. (B) It offers a permanent and cumulative population improvement
While vaccines and antibiotics provide temporary protection, breeding for disease resistance results in permanent genetic changes that are passed to future generations. These improvements are cumulative, meaning that each generation of selection adds to the population's overall resilience. This genetic approach reduces the long-term reliance on chemical treatments and provides a more sustainable and cost-effective way to manage animal health in commercial production systems.

242. (A) I, II and III
Genetic resistance to disease is a complex area involving several key relationships. Somatic cell count is a reliable indicator for mastitis, and the bovine MHC is closely related to the human immune system genes. The antagonism between high milk production and udder health is well-documented. Successfully improving resistance requires understanding these correlations and utilizing both direct and indirect traits within a comprehensive and balanced breeding objective.

243. (C) BoLA (Bovine Leukocyte Antigen)
The Major Histocompatibility Complex in cattle is specifically referred to as the BoLA system, which stands for Bovine Leukocyte Antigen. This complex is highly variable and is located on chromosome twenty-three. It plays a fundamental role in the bovine immune system, and specific BoLA alleles have been associated with resistance or susceptibility to important diseases like mastitis, leukemia, and various parasitic infections.

244. (D) Binary data nature and incomplete exposure to the pathogen
Direct selection for disease resistance is difficult because records are often binary; an animal is either sick or healthy. Furthermore, if the pathogen is not present in the environment, even susceptible animals will appear healthy. This lack of complete exposure and the simplistic nature of the data make it hard to accurately estimate breeding values, leading breeders to rely on more continuous and reliably measured indicator traits.

245. (C) Avoiding intentional exposure of candidates to pathogens
Genomic selection is highly beneficial for improving disease resistance because it allows breeders to identify resistant animals using their DNA alone. This avoids the ethical and practical problems of intentionally exposing breeding candidates to dangerous pathogens to see if they survive. By using a reference population that has experienced the disease, breeders can accurately select for resistance in young animals before they ever encounter the infection.

246. (A) 136, 154, and 171
In sheep breeding, genetic resistance to scrapie, a fatal neurodegenerative disease, is primarily determined by variation at three specific positions in the PrP gene. These are codons one hundred and thirty-six, one hundred and fifty-four, and one hundred and seventy-one. By testing for the presence of specific alleles at these sites, breeders can identify sheep with high natural resistance and selectively breed them to eliminate the disease from their flocks.

247. (D) A multi-trait index with weighted values for yield and SCS
To improve mastitis resistance while maintaining milk production, breeders use a selection index that includes both traits. By assigning appropriate economic weights to yield and somatic cell score, the index finds the optimal balance. This allows for genetic progress in both areas, ensuring that cows are both highly productive and naturally healthier, which maximizes the overall profitability and sustainability of the dairy enterprise over the long term.

248. (A) Negative (antagonistic)
In dairy cattle, there is generally a negative genetic correlation between the total volume of milk produced and the percentage of fat it contains. As cows are selected for higher milk yields, the concentration of fat tends to decrease. Breeders who wish to improve both must use selection indexes that account for this antagonism, focusing on the total yield of fat in kilograms rather than just the percentage.

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be reshuffled in subsequent generations of the population.

199. (D) Gradually recover over a few generations as linkage breaks
Because the Bulmer effect is caused by linkage disequilibrium rather than changes in allele frequencies, it is a temporary phenomenon. If the selection pressure is removed, the negative associations between alleles at different loci will be gradually broken down by recombination during meiosis. Over a few generations of random mating, the additive genetic variance will return to its original level as the population returns to a state of linkage equilibrium.

200. (A) Lower than predicted by the base population heritability
When predicting selection response, using the heritability of the unselected base population often leads to an overestimation of the progress in subsequent generations. This is because the Bulmer effect reduces the genetic variance almost immediately after selection starts. Therefore, the actual response in the second and later generations is typically lower than the initial prediction, as the population is working with a reduced pool of additive variation.

201. (C) The selection intensity and the trait's heritability
The magnitude of the reduction in genetic variance due to the Bulmer effect is determined by how intense the selection is and how much of the phenotypic variance is genetic. Higher selection intensity and higher heritability lead to a greater degree of linkage disequilibrium being generated. This results in a larger initial drop in the additive genetic variance and a more significant adjustment needed for accurate response predictions in the breeding program.

202. (A) Asymptotic variance
Under continuous and consistent truncation selection, the reduction in additive genetic variance due to the Bulmer effect eventually stabilizes. The population reaches a new equilibrium where the creation of linkage disequilibrium by selection is perfectly balanced by its breakdown through recombination. This stable level of variance is known as the asymptotic variance, and it is this value that determines the long-term rate of genetic progress in the program.

203. (D) Elite breeding schemes utilizing intense selection and BLUP animal models
The Bulmer effect is most relevant in modern, highly structured breeding programs that use intense selection pressure and advanced statistical models like BLUP. In these systems, the rapid reduction in variance can significantly impact the accuracy of genetic evaluations and the prediction of progress. Failing to account for this effect can lead to biased breeding values and unrealistic expectations for the rate of genetic improvement over time.

204. (B) By utilizing the pedigree and relationship matrix in BLUP
Advanced statistical methods like the BLUP Animal Model are designed to handle the Bulmer effect automatically. By using the complete relationship matrix and the pedigree, the model accounts for the changes in genetic variance and covariance caused by selection and linkage. This allows the model to provide unbiased estimates of breeding values even when the population is undergoing intense directional selection that reduces the available genetic variation.

205. (C) Less likely to have favorable alleles at other loci compared to a random combination
In a population under truncation selection, negative linkage disequilibrium means that favorable alleles at different loci are "repelled" from each other within the selected group. If an individual has an exceptionally good allele at one locus, it is statistically more likely to have less favorable alleles at other loci and still be selected. This negative association is what causes the overall reduction in the population's additive genetic variance for the trait.

206. (III, I, IV, II)
The process starts with a base population undergoing intense directional selection. This truncation selection favors specific allele combinations, which inadvertently creates negative linkage disequilibrium. This association reduces the amount of additive genetic variance available for the next generation. As selection continues over several generations, this variance eventually stabilizes at a new, lower asymptotic level where the creation and breakdown of linkage associations are in balance.

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257. (B) Backfat thickness and loin eye area in meat-producing animals
Ultrasound technology is a valuable tool for meat animal breeders because it allows for the non-invasive measurement of carcass traits on live breeding candidates. By measuring backfat thickness and the size of the loin muscle, breeders can estimate an animal's carcass quality and lean meat yield without having to slaughter it. This information enables more accurate selection and faster genetic progress for improved meat characteristics in the population.

258. (A) Using specialized male and female lines for commercial hybrids
To overcome the antagonistic relationship between egg number and egg size, commercial poultry breeding uses a crossbreeding system. Specialized female lines are selected primarily for high egg numbers, while male lines are selected for larger egg size or other complementary traits. When these lines are crossed, the resulting commercial hybrid layers exhibit an optimal combination of both traits, achieving a balance that would be difficult to reach within a single purebred population.

259. (C) Body size, bone structure, and muscularity levels
Draught power in cattle is a function of the animal's physical strength and leverage. Therefore, it is positively correlated with traits like total body weight, large bone structure, and well-developed musculature. Breeding for draught involves selecting for these structural characteristics to ensure the animals have the power and durability needed for heavy work. These traits are often visually and genetically distinct from the leaner, more angular features of specialized dairy cattle.

260. (D) Protein and fat yield
When the market shifts toward cheese production, the economic value of milk components like protein and fat increases relative to the total fluid volume. To maximize profit under this pricing system, the selection index must be adjusted to place more weight on the total yield of these solids. This encourages the breeding of cows that produce milk with higher concentrations of the proteins and fats necessary for efficient cheese manufacturing.

261. (C) Total feed consumed / Total weight gain
Feed Conversion Ratio is a measure of an animal's efficiency in converting feed into body mass. It is calculated by dividing the total amount of feed an animal eats during a specific period by the amount of weight it gains. A lower ratio is more desirable, as it means the animal required less feed to produce each unit of growth, which is a major factor in the profitability of meat production.

262. (B) Higher feed efficiency
In livestock production, a lower Feed Conversion Ratio value is a sign of superior efficiency. It indicates that the animal is highly effective at utilizing nutrients for growth, requiring less total feed to achieve a specific weight gain. improving FCR through selection is a key goal in the poultry, pig, and beef industries, as feed is typically the largest single cost in the production of meat animals.

263. (D) Actual feed intake and expected intake based on growth data
Residual Feed Intake is an alternative measure of efficiency that compares how much an animal actually eats to what it is predicted to eat based on its size and growth rate. It is the difference between the observed feed intake and the expected intake. Animals that eat less than predicted have a negative RFI and are considered more efficient, as they require less maintenance energy for their level of production.

264. (A) Efficient, consuming less feed than expected for its size and growth
An animal with a negative Residual Feed Intake value is highly efficient because it consumes less feed than the average animal of the same weight and growth rate. This negative value indicates that the individual has lower maintenance requirements or better metabolic efficiency. Selecting for negative RFI allows breeders to improve the efficiency of the herd without unexpectedly changing the animals' size or rate of growth.

265. (C) Being independent of production traits used in the calculation
A theoretical advantage of Residual Feed Intake is that it is mathematically independent of the production traits, such as body weight and growth, used to calculate the expected intake. This allows breeders to select for improved

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metabolic efficiency without inadvertently changing the size or growth characteristics of the population. Unlike FCR, which is a ratio, RFI provides a cleaner measure of the genetic variation in maintenance energy requirements.

266. (A) Residual Feed Intake
Calculating Residual Feed Intake requires precise data on how much each individual animal eats every day. This necessitates the use of expensive and specialized equipment, such as electronic feed bunks that recognize individual animals via ear tags and record their intake. Because of the high cost of this technology, RFI is typically measured only in central testing stations or elite nucleus herds rather than on commercial farms.

267. (D) Moderate (0.20 to 0.40)
Research in beef cattle and pigs has shown that Residual Feed Intake is a moderately heritable trait. with heritability values typically ranging from zero point two to zero point four, there is significant genetic variation that can be exploited through selection. This means that consistent breeding for low RFI can lead to permanent improvements in the feed efficiency of the population, reducing costs and the environmental impact of livestock production.

268. (B) Reduced overall feed intake with no change in growth rates
The primary result of selecting for favorable, negative Residual Feed Intake is a reduction in the total amount of feed consumed by the herd. Because RFI is adjusted for growth, this improvement in efficiency does not come at the expense of daily gain or final body weight. Consequently, the herd becomes more profitable by maintaining the same level of production while significantly lowering the most expensive input, which is feed.

269. (C) Metabolic body weight and average daily gain of the animal
To calculate the expected feed intake for an RFI analysis, a multiple regression model is used. The two most important factors in this model are the animal's metabolic body weight, which reflects its maintenance energy needs, and its average daily gain, which reflects the energy needed for growth. By accounting for these factors, the model can identify which individuals are eating more or less than expected for their specific performance level.

270. (D) Selection for rapid early growth rate
In the poultry industry, huge improvements in feed conversion have been achieved over the past several decades. most of this progress was an indirect result of intense selection for rapid early growth. Faster-growing birds reach their market weight sooner, which means they spend fewer days consuming feed for maintenance. This reduction in the total lifetime maintenance energy requirement has been the primary driver of improved FCR in commercial broilers.

271. (A) Differences in digestibility, metabolic rate, and activity
Genetic variation in Residual Feed Intake is rooted in the fundamental biological processes of the animal. Individuals with negative RFI tend to have better nutrient digestibility, lower basal metabolic rates, and reduced physical activity. By selecting for these more efficient individuals, breeders are essentially improving the animal's internal energy management, allowing more of the consumed nutrients to be used for production rather than being wasted as heat or maintenance.

272. (A) -0.3 kg/day
Residual Feed Intake is calculated by subtracting the expected feed intake from the actual feed intake. For this pig, subtracting the expected intake of two point eight kilograms from the actual intake of two point five kilograms results in an RFI of negative zero point three kilograms per day. This negative value indicates that the pig is more efficient than the average, as it consumes less feed than predicted.

NODIA

273. (B) Asymmetric changes in the numerator and denominator traits
Because Feed Conversion Ratio is a ratio of feed intake to weight gain, selecting directly for it can lead to unpredictable results. The ratio can be improved by either decreasing feed intake or increasing weight gain. Often, selection pressure is not applied equally to both parts of the ratio, leading to asymmetric genetic changes that might not align with the breeder's ultimate goals for the animal's growth and intake characteristics.

274. (A) Genetic divergence between populations based on multiple traits
The Mahalanobis D2 statistic is a powerful tool used to measure the overall difference, or genetic divergence, between different populations or breeds. It combines information from several

phenotypic traits at once, providing a single numerical value that represents the total distance between the groups. This statistic is essential for understanding the relationships between breeds and for making decisions about conservation and crossbreeding.

275. (C) Phenotypic correlation between variables via covariance data
Unlike simple distance measures that treat every trait as independent, Mahalanobis distance accounts for the fact that many traits are correlated. It uses the variance-covariance matrix to adjust for these relationships, ensuring that redundant information from highly correlated traits does not disproportionately influence the final distance calculation. This makes it a more accurate and robust measure of the true divergence between complex biological groups like animal breeds.

276. (D) Pooled within-group variance-covariance matrix
Calculating the Mahalanobis D2 statistic requires the inversion of the pooled within-group variance-covariance matrix. This matrix represents the average level of variation and correlation between traits within the populations being compared. Inverting this matrix is the mathematical step that standardizes the traits and adjusts for their correlations, allowing for a fair and multi-dimensional comparison of the differences between the means of the various groups.

277. (C) $D^2 = d\hat{a}\text{€}^{\text{TM}}S^{\{-1\}}d$
The mathematical formula for Mahalanobis distance involves three components. First, the difference between the mean vectors of the two populations is calculated. This difference vector is then multiplied by the inverse of the pooled covariance matrix and finally by the transposed difference vector. This calculation results in the D2 statistic, which represents the squared distance between the two groups in a multi-dimensional space defined by the traits.

278. (B) Tocher's optimization method
After calculating the D2 values for a set of breeds, breeders often use Tocher's method to group them into distinct clusters. This hierarchical clustering technique identifies groups of populations that are more similar to each other than they are to those in other clusters. This helps in visualizing the genetic structure of a species and identifying which breeds are most closely related or most divergent.

279. (D) They have high divergence and distinct phenotypic features
A large Mahalanobis D2 value indicates that two breeds are phenotypically very different across the suite of traits measured. In the context of conservation, this suggests that the breeds have high genetic divergence and may possess unique characteristics or adaptations. Identifying such divergent populations is important for preserving the total genetic diversity of a species and ensuring that distinct and valuable genetic resources are not lost.

280. (A) Morphological traits being influenced by environmental factors
A limitation of using Mahalanobis distance based on morphological traits is that these characteristics are influenced by the environment. Factors like nutrition and climate can cause populations to appear more similar or different than they are genetically. While D2 is excellent for describing phenotypic divergence, it must be interpreted carefully if the populations being compared were raised in significantly different management systems or geographical regions.

281. (C) Principal Component Analysis (PCA)
Principal Component Analysis is a statistical technique often used alongside distance measures to simplify complex data. It transforms a set of correlated phenotypic traits into a smaller number of uncorrelated variables called principal components. These components capture the most important variation in the data, making it easier to visualize the divergence between populations and identify which traits contribute most to the differences between different animal groups.

NODIA

282. (A) The minimum D^2 value
Tocher's clustering method is an iterative process that begins by finding the pair of populations with the smallest Mahalanobis distance. These two are grouped into the first cluster. The method then continues to add other populations to the cluster or start new clusters based on their average distances to existing groups. This approach ensures that populations within a cluster are as similar as possible based on the measured traits.

300. (B) A loss of rare alleles and increased genetic drift, altering genetic distance

Genetic bottlenecks and founder effects occur when a new population is started by a small number of individuals. This process leads to a significant reduction in genetic variation and the random loss of many alleles, especially those that were already rare. This increased genetic drift causes the allele frequencies of the new population to diverge rapidly from the original group, resulting in a larger genetic distance over a short period.

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will be exactly one point zero, reflecting the perfect correspondence between the genetic compositions of the two populations.

292. (D) Highly polymorphic and codominantly inherited
Microsatellite markers were a mainstay of genetic distance studies because they are highly variable, often having many different alleles at a single locus. This high polymorphism provides great statistical power for detecting differences between populations. Additionally, their codominant inheritance allows for the direct identification of both alleles in a diploid individual, which is essential for accurately calculating allele frequencies and heterozygosity within and between different animal breeds.

293. (C) Heterozygosity within groups compared to the total population
The calculation of $F_{\{st\}}$ is based on the partitioning of genetic variation within and between subpopulations. It compares the average heterozygosity found within each subpopulation to the expected heterozygosity of the total population if it were mating randomly as a single group. The difference between these two values represents the reduction in heterozygosity caused by the population structure and the divergence of allele frequencies between the groups.

294. (B) $\frac{H_T - H_S}{H_T}$
The mathematical formula for $F_{\{st\}}$ uses the expected heterozygosity of the total population and the average heterozygosity of the subpopulations. It is calculated as the difference between the total heterozygosity and the subpopulation heterozygosity, divided by the total heterozygosity. This ratio expresses the proportion of the total genetic variation that is attributable to the differences between the subpopulations rather than the variation within them.

295. (D) Biallelic
Single Nucleotide Polymorphisms have become the preferred markers for modern genetic studies. Unlike microsatellites, most SNPs have only two possible alleles, making them biallelic. While each individual SNP provides less information than a multi-allelic microsatellite, they are extremely abundant throughout the genome and can be analyzed in very large numbers using automated technologies. This allows for a much more detailed and accurate assessment of genetic distance and population structure.

296. (A) Prioritizing them for conservation to maintain global diversity
In conservation genetics, breeds that show high $F_{\{st\}}$ values when compared to others are often prioritized because they represent unique genetic lineages. These populations frequently carry rare alleles that are not found elsewhere. Preserving these divergent breeds is essential for maintaining the overall genetic diversity of the species, which is critical for long-term health, resilience, and the ability to adapt to future environmental or market changes.

297. (C) Inbreeding of individuals relative to their own subpopulation
$F_{\{is\}}$ is a fixation index that measures the degree of inbreeding within a specific subpopulation. It reflects the reduction in heterozygosity of an individual relative to what would be expected under random mating within that group. A positive $F_{\{is\}}$ value indicates that mating between relatives is occurring more frequently than random, while a negative value suggests that the subpopulation is more heterozygous than expected, possibly due to outbreeding.

NODIA

298. (A) Pairwise genetic distances between all targeted populations
Phylogenetic trees are used to visualize the evolutionary relationships between different populations or breeds. They are constructed using a matrix that contains the genetic distance between every possible pair of groups in the study. Algorithms like Neighbor-Joining use these distances to build a branching structure where more closely related populations are placed on nearby branches, providing a clear map of how the breeds have diverged over time.

299. (B) 0.20
Using the $F_{\{st\}}$ formula, the value is calculated by subtracting the subpopulation heterozygosity of zero point four from the total heterozygosity of zero point five, which equals zero point one. This difference is then divided by the total heterozygosity of zero point five. The resulting $F_{\{st\}}$ of zero point two indicates that twenty percent of the total genetic variation in the population is due to the differences between the subpopulations.

2019

50. Consider the following statements about PCR primer design:

I. Primers should have a GC content of 40-60%.

II. The melting temperatures (T_m) of forward and reverse primers should be within 1-2 degrees C.

III. Primer-dimers occur when primers share extensive complementary sequences.

IV. A "GC clamp" at the 3' end ensures weak binding.

V. Optimal primer length is typically 50-60 nucleotides.

Which of the above statement(s) is/are CORRECT?

(A) I, II and IV
(B) I, II and III
(C) II, III and V
(D) I, III and V

2022

51. After capillary transfer in Southern blotting, how is the DNA permanently fixed to a nylon membrane?

(A) By baking at 80 degrees Celsius or UV crosslinking
(B) By boiling the membrane in water
(C) By freezing at -80 degrees Celsius
(D) By soaking in ethidium bromide

2019

52. Which membrane type exhibits the highest binding capacity for nucleic acids in blotting techniques?

(A) Nitrocellulose
(B) Polyvinylidene fluoride (PVDF)
(C) Cellulose acetate
(D) Positively charged nylon

2015

53. The process of blocking a membrane before hybridization in Southern blotting is intended to:

(A) Prevent specific binding of the probe
(B) Reduce non-specific background binding of the probe to the membrane
(C) Denature the probe completely
(D) Facilitate capillary transfer

2007

54. What is the standard concentration range for magnesium ions (Mg2+) in a conventional PCR reaction?

(A) 0.1 to 0.5 mM
(B) 1.5 to 2.5 mM
(C) 10 to 15 mM
(D) 50 to 100 mM

2003

55. Match the PCR component (List I) with its respective function (List II).

List I: (PCR component)

P. dNTPs
Q. Taq Polymerase
R. Mg2+
S. Buffer (KCl/Tris)

List II: (Function)

1. Provides optimal pH and monovalent salt environment
2. Acts as a cofactor for the enzyme
3. Synthesizes the new DNA strand
4. Provides the building blocks for elongation

(A) P-4, Q-3, R-2, S-1
(B) P-3, Q-1, R-4, S-2
(C) P-2, Q-4, R-1, S-3
(D) P-1, Q-2, R-3, S-4

2024

56. At what temperature does the denaturation step typically occur in a standard PCR cycle?

(A) 55-60 degrees Celsius
(B) 72 degrees Celsius
(C) 94-98 degrees Celsius
(D) 105 degrees Celsius

2017

57. High concentrations of primer-dimers in a PCR reaction typically lead to which outcome?

(A) Exponential increase in target amplicon yield
(B) Reduction in the yield of the desired target amplicon
(C) Improved fidelity of the Taq polymerase
(D) Prevention of template degradation

2018

58. The formula $Tm = 4(G+C)+2(A+T)$ is widely used for what purpose in molecular biology?

(A) Calculating the elongation time for Taq polymerase
(B) Estimating the melting temperature of short oligonucleotides
(C) Determining the molecular weight of an amplicon
(D) Assessing the processivity of restriction enzymes

2006

59. What happens if the annealing temperature in a PCR reaction is set too low?

(A) Non-specific amplification and multiple

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CHAPTER 08
Genetic Laboratory Techniques

2023

1. What is the primary function of proteinase K in genomic DNA extraction from blood samples?
(A) To digest histones and cell membrane proteins
(B) To precipitate nucleic acids out of the aqueous phase
(C) To lyse erythrocytes prior to leukocyte isolation
(D) To solubilize the lipid bilayer of the cell membrane

2012

2. During phase separation using phenol-chloroform-isoamyl alcohol, which layer contains the genomic DNA?
(A) The lower organic phase
(B) The interphase between organic and aqueous layers
(C) The upper aqueous phase
(D) The bottommost layer containing precipitated proteins

2004

3. What is the precise role of isoamyl alcohol in the phenol-chloroform extraction protocol?
(A) It reduces foaming at the interphase during centrifugation
(B) It facilitates the unfolding of complex proteins
(C) It acts as a chelating agent for divalent cations
(D) It neutralizes the pH of the phenol solution

2013

4. Which chemical is most commonly used for the precipitation of DNA from an aqueous solution?
(A) Sodium dodecyl sulfate
(B) Glacial acetic acid
(C) Ammonium chloride
(D) Absolute ethanol

2018

5. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): Semen samples require the addition of dithiothreitol (DTT) for effective genomic DNA extraction.
Reason (R): DTT reduces disulfide bonds present in the protamine complexes of sperm heads.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

NODIA

2003

6. The Lysis of erythrocytes in whole blood prior to DNA extraction is typically achieved using which condition?
(A) High concentrations of chaotropic salts
(B) Incubation with strong anionic detergents
(C) Treatment with hypotonic buffer solutions
(D) Digestion with specific restriction endonucleases

2024

7. Which detergent is routinely utilized to solubilize cell membranes during leukocyte lysis?
(A) Triton X-100
(B) Tween 20
(C) CHAPS
(D) Sodium dodecyl sulfate (SDS)

2013

8. In alcohol precipitation of DNA, what is the function of adding monovalent cations like sodium or acetate?
(A) To neutralize the negative charge on the phosphate backbone
(B) To increase the dielectric constant of the solvent mixture
(C) To denature residual nucleases during the final wash step
(D) To facilitate the binding of proteinase K to the template

2019

9. Which sample requires the most rigorous digestion protocol due to highly condensed chromatin?
(A) Peripheral blood lymphocytes
(B) Semen

2022

30. Consider the following statements regarding Agarose Gel Electrophoresis (AGE):
I. DNA migrates towards the anode.
II. TBE buffer has higher buffering capacity than TAE.
III. High voltage improves resolution of very large fragments.
IV. Glycerol in loading dye increases sample density.
Which of the above statement(s) is/are CORRECT?
(A) I, II and IV
(B) II, III and IV
(C) I, III and IV
(D) I and II

2021

31. Under standard neutral pH conditions in AGE, the overall electrical charge of a DNA molecule is:
(A) Positive, due to histones
(B) Negative, due to the phosphate backbone
(C) Neutral, due to the pairing of bases
(D) Variable, depending on GC content

2014

32. Which phenomenon occurs if the applied voltage gradient is too high during agarose gel electrophoresis?
(A) Rapid reversal of the migration direction
(B) Immediate precipitation of high-weight DNA
(C) Complete depletion of all tracking dyes
(D) Smearing due to thermal gradient formation

2016

33. The fluorescent emission of ethidium bromide is maximized when the molecule is:
(A) Intercalated between the nitrogenous bases of double-stranded DNA
(B) Dissolved in distilled water
(C) Bound to the ribose sugars of single-stranded RNA
(D) Exposed to visible white light

2023

34. What dictates the choice between TAE and TBE buffers for resolving PCR amplicons?
(A) TAE is used for small amplicons, TBE for large genomic segments
(B) TAE prevents DNA denaturation better than TBE
(C) TBE is preferred for smaller fragments due to better resolving power
(D) TBE is required whenever downstream enzymatic reactions are planned

2005

35. Match the restriction endonuclease type (List I) with its specific property (List II).
List I: (Restriction endonuclease type)
P. Type I
Q. Type II
R. Type III
S. Type IV
List II: (Specific property)
1. Cleaves at specific sites within the recognition sequence
2. Cleaves modified (e.g., methylated) DNA
3. Cleaves randomly far from the recognition site
4. Cleaves a short distance from the recognition site
(A) P-3, Q-1, R-4, S-2
(B) P-1, Q-2, R-3, S-4
(C) P-4, Q-3, R-1, S-2
(D) P-2, Q-4, R-1, S-3

2014

36. Which type of restriction enzyme is predominantly used in recombinant DNA technology due to its predictable cleavage?
(A) Type I
(B) Type II
(C) Type III
(D) Type IV

2013

37. Restriction enzymes exhibiting "star activity" undergo which functional change?
(A) They lose all cleavage ability
(B) They cleave non-specifically under suboptimal conditions
(C) They methylate their own recognition sites
(D) They act as ligases instead of nucleases

2014

38. The sequence 5'-GAATTC-3' is recognized by EcoRI. This type of sequence is characterized mathematically as a:
(A) Tandem repeat
(B) Hairpin loop
(C) Palindrome
(D) Homopolymeric tract

2014

39. Which requirement is mandatory for the cleavage activity of Type II restriction endonucleases?
(A) ATP
(B) S-adenosyl methionine
(C) NADH
(D) Mg2+ ions

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(D) 320 nm

2008

20. Select the correct sequence of steps for fluorometric DNA quantification.
(A) Add dye to sample, incubate, measure fluorescence, calculate concentration from standard curve
(B) Prepare standard curve, add dye to unknown, incubate, measure fluorescence
(C) Measure intrinsic fluorescence, add dye, compare to blank, plot standard curve
(D) Blank instrument, measure $A_{\{260\}}$, add fluorophore, measure emission

2022

21. Which intercalating dye is frequently utilized in fluorometers for highly sensitive double-stranded DNA quantification?
(A) Trypan Blue
(B) PicoGreen
(C) Coomassie Brilliant Blue
(D) Xylene Cyanol

2012

22. What causes an artificially high $A_{\{260\}}$ reading during DNA quantification?
(A) Complete removal of RNA
(B) Depletion of background salts
(C) Presence of free nucleotides or single-stranded RNA
(D) Use of a quartz cuvette

2025

23. An $\frac{A_{260}}{A_{280}}$ ratio of 2.1 is obtained for a nucleic acid extract. What is the most appropriate inference?
(A) The sample is pure DNA
(B) The sample has severe phenol contamination
(C) The sample contains high levels of humic acid
(D) The sample is predominantly RNA

2010

24. Why does RNA absorb more UV light at 260 nm than an equal mass of double-stranded DNA?
(A) Single-stranded molecules lack base-stacking shielding effects
(B) RNA contains uracil instead of thymine in its primary sequence
(C) Ribose sugars absorb UV light stronger than deoxyribose moieties
(D) RNA molecules are inherently longer than typical genomic DNA

2008

25. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): TAE buffer provides superior resolution for large DNA fragments compared to TBE buffer.
Reason (R): TAE has a lower ionic strength and buffering capacity, causing faster migration of large fragments.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2025

26. Which property determines the migration rate of DNA in agarose gel electrophoresis under a uniform electric field?
(A) Base composition
(B) Molecular weight
(C) Sugar-phosphate linkages
(D) Nuclear origin

2001

27. What is the primary function of tracking dyes such as bromophenol blue in agarose gel electrophoresis?
(A) To monitor the progress of the electrophoretic run
(B) To stain the DNA molecules for visualization under UV light
(C) To increase the density of the sample for well loading
(D) To neutralize the charge of the DNA backbone

NODIA

2002

28. Which chemical is an alternative to ethidium bromide and intercalates DNA with a lower mutagenic profile?
(A) Silver nitrate
(B) Coomassie blue
(C) GelRed
(D) Acridine orange

2009

29. Increasing the agarose concentration in a gel is recommended for which specific purpose?
(A) Resolving very large DNA fragments
(B) Decreasing the running time
(C) Preventing RNA degradation
(D) Resolving small DNA fragments

283. (D) Standardizes measurement scales for different types of traits
One of the strengths of the D2 statistic is that it standardizes the measurements of different traits, such as weight in kilograms and length in centimeters. By utilizing the covariance matrix, it converts all traits into a common dimensionless scale. This allows breeders to combine very different types of information into a single, comprehensive measure of divergence, providing a holistic view of the phenotypic differences between breeds.

284. (B) Zero
Mahalanobis distance is a measure of the difference between the means of two groups. If two populations have identical average values for every single trait included in the analysis, there is no divergence between them in the multi-dimensional space. Consequently, the calculated D2 value would be exactly zero. This indicates that, based on the specific traits measured, the two populations are phenotypically indistinguishable from each other.

285. (C) Euclidean distance
Mahalanobis distance is essentially a generalized form of the more common Euclidean distance. While Euclidean distance measures the straight-line distance between two points, Mahalanobis distance adds a layer of complexity by accounting for the variances of the traits and the correlations between them. It can be thought of as the distance between two groups after they have been standardized and the redundant information from correlations has been removed.

286. (D) Canonical Discriminant Analysis
Canonical Discriminant Analysis is a statistical procedure that is closely related to the use of Mahalanobis distance. It is designed to identify the linear combinations of traits that best separate two or more predefined groups. This analysis helps to reveal which phenotypic characteristics are the most important for distinguishing between different breeds or populations, providing insights into the specific features that define their unique genetic and morphological divergence.

287. (A) Population differentiation due to structure and divergence
Wright's fixation index, specifically $F_{\{st\}}$, is a fundamental statistic used in population genetics to measure the degree of genetic differentiation between subpopulations. It quantifies how much of the total genetic variation is due to differences in allele frequencies between the groups. High $F_{\{st\}}$ values indicate significant divergence and limited gene flow, while low values suggest that the subpopulations are genetically very similar to each other.

288. (B) No genetic differentiation; subpopulations share identical allele frequencies
An $F_{\{st\}}$ value of zero means that there is no genetic differentiation between the groups being compared. This indicates that the allele frequencies are identical across all subpopulations, suggesting that they belong to a single, panmictic population with high levels of gene flow. In this state, there is no genetic evidence of structure or isolation, and individuals from different groups are genotypically indistinguishable at the population level.

289. (A) Average number of codon substitutions per locus between groups
Nei's standard genetic distance is a measure of the accumulated genetic differences between two populations since they diverged from a common ancestor. It is specifically designed to estimate the average number of codon substitutions that have occurred at each locus. This distance increases linearly with time under the assumption of neutral evolution, making it a valuable tool for reconstructing the evolutionary history and relationships of different breeds.

290. (A) $D = -\ln(I)$
Nei's genetic identity, represented by "I", and genetic distance, represented by "D", are mathematically related. The distance is calculated as the negative natural logarithm of the identity. Genetic identity measures the degree of similarity in allele frequencies between two populations, ranging from zero to one. By taking the negative log, this similarity is transformed into a distance measure that increases as the populations become more divergent.

291. (C) 1.0
Genetic identity is a measure of the overlap in allele frequencies between two groups. If two populations have exactly the same frequencies for all alleles at every locus studied, they are genetically identical according to this metric. In such a case, the value of Nei's genetic identity

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2013

40. Arrange the standard steps of a Southern Blotting procedure in the correct sequence:
I. Restriction digestion of genomic DNA
II. Transfer to nitrocellulose/nylon membrane
III. Agarose gel electrophoresis
IV. Hybridization with labeled probe
V. Alkali denaturation
(A) I, III, V, II, IV
(B) I, III, II, V, IV
(C) III, I, V, II, IV
(D) I, V, III, II, IV

2025

41. What is the fundamental mechanism distinguishing Type II restriction endonucleases from Type I?
(A) Type II enzymes possess both activities in a single polypeptide
(B) Type II enzymes cleave at recognition sites without requiring ATP
(C) Type II enzymes require ATP for translocation along the DNA strands
(D) Type II enzymes specifically cleave only single-stranded DNA templates

2006

42. EcoRV produces "blunt ends" upon cleavage. What does this indicate about its restriction mechanism?
(A) It leaves a 5' overhang on both DNA strands
(B) It cuts the DNA strands symmetrically at the exact center of the recognition site
(C) It cleaves only the coding strand
(D) It removes bases completely to leave a gap

2023

43. Why are bacterial genomes protected from cleavage by their endogenous restriction endonucleases?
(A) The recognition sequences are specifically methylated by corresponding methyltransferases
(B) The restriction sites are mutated
(C) Endogenous DNA is masked by histone-like proteins
(D) The endonucleases are maintained in an inactive state

2004

44. The nomenclature of restriction enzyme HindIII is derived from:
(A) Helicobacter intestinalis
(B) Halobacterium indicum
(C) Haemophilus influenzae strain d
(D) Haemophilus introgression

2004

45. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): Nylon membranes are generally preferred over nitrocellulose for Southern blotting.
Reason (R): Nylon membranes possess higher tensile strength and allow for multiple reprobings.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2010

46. During Southern blotting, what is the purpose of treating the agarose gel with sodium hydroxide prior to transfer?
(A) To neutralize the gel pH
(B) To crosslink the DNA to the gel matrix
(C) To denature the double-stranded DNA into single strands
(D) To degrade any contaminating RNA

2016

47. Which transfer method relies primarily on the upward flow of buffer driven by paper towels?
(A) Electroblotting
(B) Capillary blotting
(C) Vacuum blotting
(D) Positive pressure blotting

2002

48. In non-radioactive probe labeling for Southern blotting, digoxigenin (DIG) is commonly detected using:
(A) Autoradiography film exposure
(B) Direct fluorescence under UV light
(C) Scintillation counting
(D) Antibody-enzyme conjugates and colorimetric/chemiluminescent substrates

2024

49. Depurination of high molecular weight DNA with dilute HCl prior to alkali treatment in Southern blotting achieves what result?
(A) It fragments large DNA to facilitate efficient transfer from the gel to the membrane
(B) It crosslinks the DNA permanently
(C) It translates the negative charge for better binding
(D) It prevents probe self-ligation

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(C) Buccal swabs
(D) Hair follicles

2023

10. Consider the following statements regarding DNA extraction:
I. Phenol denatures proteins effectively.
II. Chloroform increases the density of the organic phase.
III. EDTA acts as a cofactor for DNase enzymes.
Which of the above statement(s) is/are INCORRECT?
(A) I and II
(B) III only
(C) II and III
(D) I and III

2019

11. What is the consequence of vigorous vortexing during the precipitation of high-molecular-weight genomic DNA?
(A) Mechanical shearing of the DNA strands
(B) Enhanced removal of RNA contaminants
(C) Improved dissolution of DNA pellets
(D) Immediate phase inversion

2009

12. Which cellular component is selectively eliminated during the initial steps of blood DNA isolation?
(A) Granulocytes
(B) Monocytes
(C) Erythrocytes
(D) Lymphocytes

2017

13. An absorbance ratio (A260/A280) of 1.2 in a purified DNA sample strongly indicates contamination by which substance?
(A) RNA
(B) Phenol
(C) Carbohydrates
(D) Proteins

2018

14. What absorbance wavelength is universally used to quantify the concentration of nucleic acids?
(A) 230 nm
(B) 280 nm
(C) 260 nm
(D) 320 nm

2004

15. Match the absorbance characteristics (List I) with their corresponding interpretation (List II).
List I: (Absorbance characteristics)
P. $\frac{A_{260}}{A_{280}} = 1.8$
Q. $\frac{A_{260}}{A_{280}} = 2.0$
R. $\frac{A_{260}}{A_{230}} < 1.5$
S. High absorbance at 320 nm
List II: (Interpretation)
1. Pure RNA
2. Pure DNA
3. Particulate contamination
4. Salt or solvent contamination
(A) P-2, Q-1, R-4, S-3
(B) P-1, Q-2, R-3, S-4
(C) P-2, Q-4, R-1, S-3
(D) P-3, Q-1, R-2, S-4

NODIA

2003

16. In spectrophotometry, an optical density (OD) of 1 at 260 nm corresponds to what concentration of double-stranded DNA?
(A) 33 micrograms per ml
(B) 40 micrograms per ml
(C) 50 micrograms per ml
(D) 60 micrograms per ml

2024

17. Fluorometric quantification of DNA is generally preferred over spectrophotometry for which reason?
(A) It specifically measures dsDNA without RNA interference
(B) It is significantly less expensive for high-throughput labs
(C) It requires no standard curve preparation during the run
(D) It simultaneously assesses protein contamination in the mix

2013

18. A low $\frac{A_{260}}{A_{230}}$ ratio frequently points to the presence of which contaminant from the extraction process?
(A) Intact histones
(B) Ribosomal RNA
(C) Guanidine thiocyanate
(D) Degraded peptides

2008

19. Background scattering in a spectrophotometer reading is typically corrected by subtracting the absorbance at which wavelength?
(A) 230 nm
(B) 260 nm
(C) 280 nm

banding occur
(B) Primers fail to bind to the template entirely
(C) The Taq polymerase is irreversibly denatured
(D) The amplicons become heavily methylated

2001

60. Select the correct sequence of phases observed in a standard real-time PCR amplification plot.
(A) Plateau phase, Exponential phase, Linear phase
(B) Baseline phase, Exponential phase, Linear phase, Plateau phase
(C) Linear phase, Plateau phase, Baseline phase
(D) Exponential phase, Baseline phase, Plateau phase

2003

61. Taq polymerase lacks which enzymatic activity, contributing to its relatively high error rate compared to modern high-fidelity polymerases?
(A) 5' to 3' polymerase activity
(B) 5' to 3' exonuclease activity
(C) DNA helicase activity
(D) 3' to 5' exonuclease proofreading activity

2017

62. Which additive is commonly used to resolve secondary structures in GC-rich templates during PCR?
(A) Ethylenediaminetetraacetic acid (EDTA)
(B) Sodium dodecyl sulfate (SDS)
(C) Dimethyl sulfoxide (DMSO)
(D) Phenol

2017

63. A fundamental requirement for identifying a single nucleotide polymorphism via PCR-RFLP is:
(A) The polymorphism must alter the sequence of the PCR primers
(B) The polymorphism must create or abolish a restriction enzyme recognition site
(C) The polymorphism must change the amino acid sequence of the protein
(D) The restriction enzyme must cleave outside the amplicon

2006

64. In a PCR-RFLP assay for a diallelic locus, how many distinct banding patterns are typically expected to represent all possible genotypes?
(A) One
(B) Two
(C) Three
(D) Four

2023

65. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): Heterozygous individuals in a PCR-RFLP assay display a banding pattern that is a composite of both homozygous patterns.
Reason (R): Heterozygotes possess both alleles, leading to a mixture of cleaved and uncleaved amplicons following restriction digestion.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2011

66. A 500 bp amplicon contains a polymorphic restriction site exactly in the middle. Digestion of a homozygous wild-type sample (site present) will yield:
(A) A single 500 bp band
(B) Three bands: 500 bp, 250 bp, and 250 bp
(C) Two bands of 250 bp each (appearing as one thick band)
(D) Smearing indicating complete degradation

2017

67. Partial digestion in a PCR-RFLP assay is most likely caused by which factor?
(A) Insufficient restriction enzyme concentration or incubation time
(B) Use of highly purified DNA
(C) Excessive Taq polymerase activity
(D) Extended agarose gel run time

2005

68. Which matrix is most suitable for resolving very small difference in restriction fragment sizes (e.g., < 10 bp difference) in PCR-RFLP?
(A) 0.8% Agarose
(B) Nitrocellulose membrane
(C) Sephadex columns
(D) Polyacrylamide gel

2005

69. When designing a PCR-RFLP assay, the restriction enzyme should ideally be selected such that:
(A) It cuts the amplicon into hundreds of small fragments
(B) It cleaves one allele but leaves the alternative allele intact
(C) It recognizes a sequence independent of the mutation

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2018

108. In RH mapping, physical distances between markers are calculated based on the frequency of:
(A) Meiotic crossing over
(B) Spontaneous mutations during cell culture
(C) Co-retention of the markers in the hybrid panel
(D) Chromosomal translocations in the host

2001

109. Which mapping function is strictly used to measure map distances in Radiation Hybrid mapping?
(A) CentiMorgans (cM)
(B) LOD scores
(C) Kilobase pairs (kb)
(D) CentiRays (cR)

2011

110. Consider the following statements regarding cloning vectors:
I. Plasmids typically carry inserts up to 10 kb.
II. Cosmids possess cohesive end (cos) sites for phage packaging.
III. YACs are utilized for cloning extremely large DNA fragments (>1000 kb).
IV. BACs replicate using mammalian origins of replication exclusively.
Which of the above statement(s) is/are CORRECT?
(A) I, II and III
(B) I, II and IV
(C) II, III and IV
(D) I, III and IV

2016

111. The origin of replication (ori) in a plasmid vector determines:
(A) The copy number of the plasmid in the host cell
(B) The antibiotic resistance profile
(C) The maximum size of the insert DNA
(D) The efficiency of blue-white screening

2008

112. Cosmids are specialized vectors that combine features of plasmids and which other biological entity?
(A) Retroviruses
(B) Adenoviruses
(C) Bacteriophage lambda
(D) Yeast artificial chromosomes

2012

113. Which cloning vector is most appropriate for constructing a genomic library of a large mammalian genome?
(A) Standard pUC19 plasmid
(B) Bacteriophage M13
(C) Bacterial Artificial Chromosome (BAC)
(D) Expression vector pET

2022

114. In recombinant DNA technology, "competent cells" refer to bacterial cells that:
(A) Are immune to viral infection
(B) Can produce active restriction enzymes
(C) Have high spontaneous mutation rates
(D) Have been treated to uptake extracellular plasmid DNA

2023

115. Consider the following features of cloning methods:
I. Calcium chloride treatment neutralizes repulsion between DNA and the cell membrane.
II. Electroporation uses a brief electrical pulse to create transient membrane pores.
III. T4 DNA ligase catalyzes phosphodiester bond formation between 5'-phosphate and 3'-hydroxyl groups.
IV. Heat shock promotes the exit of plasmid DNA from the cell.
V. Transformation efficiency is usually higher with electroporation than with chemical methods.
Which of the above statement(s) is/are INCORRECT?
(A) I and II
(B) III and V
(C) IV only
(D) II, IV and V

2003

116. Blue-white colony screening relies on the insertional inactivation of which specific gene?
(A) Ampicillin resistance gene (bla)
(B) Beta-galactosidase gene (lacZ)
(C) Tetracycline resistance gene (tetR)
(D) Green fluorescent protein gene (gfp)

2025

117. In a blue-white screening assay, white colonies represent:
(A) Un-transformed host cells lacking the vector
(B) Host cells containing the non-recombinant (empty) vector
(C) Host cells containing the recombinant vector

NODIA

2015

79. Bridge amplification is a critical cluster generation step characteristic of which sequencing technology?
(A) Sanger
(B) Illumina
(C) PacBio
(D) Nanopore

2009

80. Arrange the essential steps of an Illumina NGS workflow in the correct order:
I. Library preparation (fragmentation and adapter ligation)
II. Cluster generation via bridge amplification
III. Sequencing by synthesis
IV. Data analysis and read alignment
(A) I, II, III, IV
(B) II, I, III, IV
(C) I, III, II, IV
(D) II, III, I, IV

2013

81. Colchicine is used during chromosome preparation from peripheral blood lymphocytes specifically to:
(A) Arrest cells in metaphase by inhibiting spindle fiber formation
(B) Stimulate T-cell proliferation
(C) Induce hypotonic swelling of the cells
(D) Fix the chromosomal structure permanently

2019

82. Which mitogen is routinely added to livestock blood cultures to stimulate the division of T-lymphocytes for karyotyping?
(A) Lipopolysaccharide (LPS)
(B) Concanavalin A
(C) Phytohemagglutinin (PHA)
(D) Pokeweed mitogen

2007

83. During chromosome preparation, what is the primary purpose of treating cells with a hypotonic solution (e.g., 0.075 M KCl)?
(A) To cause cells to swell, aiding in chromosome spreading upon dropping
(B) To crosslink DNA and proteins
(C) To dissolve the nuclear membrane chemically
(D) To stain the chromosomes for G-banding

2016

84. Carnoy's fixative, standardly used in cytogenetics, is composed of which chemicals in a 3:1 ratio?
(A) Ethanol and Formaldehyde
(B) Acetone and Methanol
(C) Chloroform and Isoamyl alcohol
(D) Methanol and Glacial Acetic Acid

2002

85. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): Dropping the fixed cell suspension onto cold, wet slides improves the spreading of metaphase chromosomes.
Reason (R): The rapid evaporation of the fixative and the mechanical impact cause the swollen cells to burst, dispersing the chromosomes.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2019

86. How are chromosomes typically prepared from bone marrow compared to peripheral blood?
(A) They require 72 hours of mitogen stimulation
(B) They must be digested with collagenase first
(C) They can be analyzed directly without prior in vitro culture stimulation
(D) They require exclusively meiotic isolation protocols

2013

87. The standard diploid chromosome number ($2n$) for domestic cattle (Bos taurus) is:
(A) 46
(B) 54
(C) 60
(D) 78

2021

88. G-banding of chromosomes is most commonly achieved by treating the slide with which proteolytic enzyme prior to Giemsa staining?
(A) Trypsin
(B) Pepsin
(C) Proteinase K
(D) Collagenase

2016

89. In G-banded chromosomes, the dark bands generally correspond to genomic regions that are:
(A) GC-rich, gene-dense, and replicate early
(B) AT-rich, gene-poor, and replicate late
(C) Exclusively composed of ribosomal RNA genes
(D) Centromeric heterochromatin only

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2008

90. Consider the following statements regarding chromosome banding:

I. R-banding produces a pattern opposite to G-banding.

II. C-banding specifically stains constitutive heterochromatin, such as centromeres.

III. Q-banding requires a fluorescence microscope for visualization.

IV. G-banding is ineffective for detecting structural aberrations.

Which of the above statement(s) is/are CORRECT?

(A) I, II and III
(B) I, II and IV
(C) II, III and IV
(D) I, III and IV

2003

91. Which banding technique is particularly useful for identifying the Y chromosome in certain mammalian species due to its bright fluorescence?

(A) Q-banding
(B) G-banding
(C) C-banding
(D) NOR-banding

2007

92. The standard nomenclature for describing a Robertsonian translocation in cattle between chromosomes 1 and 29 is denoted as:

(A) t(1;29)
(B) inv(1;29)
(C) rob(1;29)
(D) del(1;29)

2007

93. R-banding typically involves heat denaturation in a specific buffer prior to staining. The dark bands observed represent regions that are:

(A) AT-rich
(B) Telomeric only
(C) Highly methylated
(D) GC-rich

2011

94. A structural chromosomal aberration involving a segment that has been flipped 180 degrees within the same chromosome is called:

(A) Duplication
(B) Deletion
(C) Inversion
(D) Translocation

2007

95. Match the FISH probe type (List I) with its primary diagnostic utility (List II).

List I: (FISH probe type)

P. Whole-chromosome paint
Q. Centromeric probe
R. Telomeric probe
S. Locus-specific probe

List II: (Diagnostic utility)

1. Detection of sub-microscopic terminal deletions
2. Identification of specific gene microdeletions or amplifications
3. Rapid enumeration of specific chromosomes (aneuploidy)
4. Characterization of complex translocations and marker chromosomes

(A) P-4, Q-3, R-1, S-2
(B) P-1, Q-2, R-3, S-4
(C) P-3, Q-1, R-4, S-2
(D) P-2, Q-4, R-1, S-3

2005

96. Fluorescence In Situ Hybridization (FISH) differs from conventional chromosome banding primarily because FISH:

(A) Does not require metaphase chromosomes
(B) Utilizes radioactive isotopes for visualization
(C) Can only be performed on live cells
(D) Detects specific nucleic acid sequences rather than general chromatin density

2014

97. During the FISH protocol, what is the critical purpose of heating the chromosome slides and the probe to approximately 72 degrees Celsius?

(A) To denature the double-stranded DNA into single strands
(B) To crosslink the fluorophores permanently
(C) To digest excess proteins masking the target
(D) To evaporate residual formamide

2018

98. Which chemical is routinely included in FISH hybridization buffers to lower the melting temperature (Tm) of DNA, allowing hybridization at lower temperatures?

(A) Dimethyl sulfoxide (DMSO)
(B) Dextran sulfate
(C) Formamide
(D) Cot-1 DNA

NODIA

2010

99. The inclusion of Cot-1 DNA in a FISH hybridization mixture serves to:

(A) Suppress non-specific binding of the probe

to repetitive genomic sequences
(B) Enhance the fluorescence signal intensity
(C) Act as a counterstain for the chromosomes
(D) Increase the viscosity of the buffer

2003

100. Consider the following statements about PRINS (Primed In Situ Labeling):
I. It utilizes unlabeled oligonucleotide primers.
II. It requires in situ DNA synthesis by a DNA polymerase.
III. It incorporates labeled nucleotides directly at the target site.
IV. It involves hybridization of a large, pre-labeled probe.
V. It is generally faster than traditional FISH protocols.
Which of the above statement(s) is/are CORRECT?
(A) I, II, III and V
(B) II, III, IV and V
(C) I, III, IV and V
(D) I, II, III and IV

2003

101. What is the fundamental difference between FISH and PRINS methodologies?
(A) FISH requires metaphase spreads, whereas PRINS works only on interphase nuclei
(B) FISH uses pre-labeled probes, while PRINS utilizes a polymerase to incorporate labeled nucleotides in situ
(C) FISH detects RNA, whereas PRINS exclusively detects DNA
(D) PRINS does not require thermal denaturation of the target DNA

2001

102. In Somatic Cell Hybrid (SCH) panel mapping, cell lines are typically created by fusing cells from two different species. Which fusion agent is classically used?
(A) Sodium dodecyl sulfate (SDS)
(B) Dithiothreitol (DTT)
(C) Polyethylene glycol (PEG)
(D) Colchicine

2014

103. Synteny testing in SCH mapping relies on the principle that:
(A) Both species' chromosomes are retained equally
(B) Recombination occurs frequently between the chromosomes of the two species
(C) Lethal irradiation destroys the recipient genome completely
(D) Chromosomes of one species (e.g., livestock) are randomly lost in the hybrid, allowing correlation of marker retention

2007

104. Which selection medium is traditionally used to isolate hybrid cells from unfused parental cells in SCH construction, assuming complementation of genetic deficiencies?
(A) HAT (Hypoxanthine-Aminopterin-Thymidine) medium
(B) LB broth with ampicillin
(C) DMEM with 10% Fetal Bovine Serum
(D) MacConkey agar

2004

105. Consider the following statements regarding SCH mapping:
I. It determines the physical distance in base pairs between markers.
II. Two markers are syntenic if they are consistently retained or lost together in hybrid lines.
III. The statistical analysis of retention frequencies assigns markers to specific chromosomes.
Which of the above statement(s) is/are INCORRECT?
(A) I only
(B) II only
(C) III only
(D) I and III

2008

106. Radiation Hybrid (RH) mapping fundamentally differs from SCH mapping in that RH mapping:
(A) Does not involve the fusion of cells
(B) Uses lethal doses of X-rays or gamma rays to fragment the donor genome before fusion
(C) Relies exclusively on naturally occurring meiotic recombination
(D) Uses human donor cells exclusively

2021

107. The resolution of a Radiation Hybrid (RH) map is primarily determined by:
(A) The dosage of radiation applied to the donor cells
(B) The concentration of the selection drug in the medium
(C) The number of chromosomes in the recipient cell
(D) The specific DNA polymerase used for marker typing

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(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2002

146. The common enzyme-substrate pair HRP and TMB utilized in ELISA yields a product of which color prior to adding the stop solution?
(A) Yellow
(B) Blue
(C) Red
(D) Green

2010

147. What is the fundamental purpose of the "stop solution" (e.g., dilute sulfuric acid) in an HRP-TMB ELISA?
(A) To denature the target antigen
(B) To halt the enzymatic reaction and convert the blue product to a measurable yellow color
(C) To wash away unbound secondary antibodies
(D) To precipitate the immune complexes

2004

148. Northern blotting is specifically utilized for the detection and semi-quantification of:
(A) Specific DNA sequences
(B) Specific RNA molecules
(C) Complex protein mixtures
(D) Lipid bilayers

2019

149. Why is formaldehyde or glyoxal frequently included in the agarose gel for Northern blotting?
(A) To stain the RNA for visual detection
(B) To inhibit RNase enzymes and keep the RNA denatured (preventing secondary structures)
(C) To crosslink the RNA to the membrane
(D) To increase the electrical conductivity of the buffer

2014

150. Match the molecular biology technique (List I) with the target molecule it detects (List II).
List I: (Molecular biology technique)
P. Southern Blotting
Q. Northern Blotting
R. Western Blotting
S. PCR-RFLP
List II: (Target molecule)
1. RNA expression
2. DNA sequences/polymorphisms
3. Restriction fragment patterns
4. Specific proteins
(A) P-2, Q-1, R-4, S-3
(B) P-1, Q-2, R-3, S-4
(C) P-3, Q-4, R-1, S-2
(D) P-4, Q-3, R-2, S-1

2017

151. In Western blotting, the role of Sodium Dodecyl Sulfate (SDS) during PAGE is to:
(A) Preserve the tertiary structure of the proteins
(B) Impart a uniform negative charge to proteins and denature them into linear chains
(C) Act as the specific primary antibody
(D) Transfer the proteins to the PVDF membrane

2010

152. Which membrane is commonly favored in Western blotting due to its high protein binding capacity and physical durability?
(A) Standard agarose
(B) Polyacrylamide
(C) Polyvinylidene fluoride (PVDF)
(D) Cellulose acetate

2016

153. Western blots are most commonly "probed" using:
(A) Fluorescently labeled oligonucleotide primers
(B) Radioactively labeled cDNA
(C) Specific primary antibodies followed by enzyme-conjugated secondary antibodies
(D) SYBR Green dye

2007

154. In real-time quantitative PCR (qPCR), what does the C_t (Cycle threshold) value represent?
(A) The total number of cycles performed
(B) The cycle number at which the fluorescence signal significantly exceeds background levels
(C) The concentration of the primers used
(D) The final maximum fluorescence achieved

2025

155. A lower C_t value in a qPCR assay directly correlates with:
(A) A higher initial concentration of the target nucleic acid
(B) A lower initial concentration of the target nucleic acid
(C) Extensive primer-dimer formation
(D) Degradation of the Taq polymerase

NODIA

2011

156. The SYBR Green dye used in qPCR functions by:
(A) Binding non-specifically to all single-

with an insert
(D) Cells that have died due to antibiotic selection

2017

118. The chemical X-gal used in blue-white screening is a chromogenic substrate that turns blue when cleaved by:
(A) Taq polymerase
(B) Beta-lactamase
(C) Beta-galactosidase
(D) T4 DNA ligase

2011

119. Recombination frequencies in linkage mapping are fundamentally limited to a maximum theoretical value of:
(A) 0.1 (10%)
(B) 0.5 (50%)
(C) 1.0 (100%)
(D) Infinite

2009

120. In genetic linkage mapping, a LOD score of 3.0 indicates that:
(A) Linkage is 1000 times more likely than independent assortment
(B) Linkage is 3 times more likely than independent assortment
(C) The recombination fraction is exactly 0.03
(D) The genes are located on three different chromosomes

2003

121. Which mapping function accounts for the occurrence of double crossovers without assuming crossover interference?
(A) Kosambi function
(B) Haldane function
(C) Morgan function
(D) LOD function

2007

122. Linkage disequilibrium (LD) refers to:
(A) The random assortment of alleles at two unlinked loci
(B) The non-random association of alleles at two or more loci in a population
(C) The complete absence of meiotic crossing over in a population
(D) The physical uncoupling of genes located on the same chromosome

2004

123. Which marker type is predominantly used in modern livestock Genome-Wide Association Studies (GWAS) due to its abundance and ease of high-throughput genotyping?
(A) Microsatellites
(B) Single Nucleotide Polymorphisms (SNPs)
(C) RFLPs
(D) Minisatellites

NODIA

2002

124. EDTA is the preferred anticoagulant for blood collection destined for DNA isolation because it:
(A) Promotes rapid coagulation, concentrating the DNA
(B) Chelates Mg2+ and Ca2+ ions, inhibiting endogenous DNase activity
(C) Stains the leukocytes for easy visual identification
(D) Directly lyses the red blood cells upon contact

2002

125. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): FTA cards are highly useful for long-term storage of DNA from blood samples at room temperature.
Reason (R): The chemicals impregnated in the FTA card immediately lyse cells, denature proteins, and protect DNA from nucleases and UV degradation.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2021

126. "Chain of custody" in forensic DNA fingerprinting ensures:
(A) The DNA strands remain unbroken during extraction
(B) A documented, unbroken record of sample possession from collection to analysis
(C) The linkage of genetic markers on the same chromosome
(D) The sequential activation of PCR enzymes

2019

127. Microsatellites, or Short Tandem Repeats (STRs), are highly effective for parentage verification primarily because they exhibit:
(A) Strict biallelic distribution
(B) High levels of length polymorphism and heterozygosity in populations

(C) High mutation rates leading to complete loss of Mendelian inheritance
(D) Complete linkage disequilibrium with all known phenotypes

2025

128. If an offspring possesses an STR allele that is absent in both the biological mother and the alleged sire, the most appropriate forensic conclusion is:
(A) The alleged sire is confirmed as the biological father
(B) The alleged sire is excluded as the biological father
(C) The mother is excluded as the biological mother
(D) A de novo mutation has definitively occurred in the sire's somatic cells

2012

129. The FAO/ISAG recommended molecular markers for defining breed descriptors in livestock heavily utilize:
(A) Mitochondrial DNA exclusively
(B) A standardized panel of highly polymorphic microsatellite loci
(C) A single unique SNP for every breed
(D) Whole-genome long-read sequencing exclusively

2003

130. Consider the following statements regarding population genetic diversity:
I. Observed heterozygosity (H_o) is a measure of genetic variation.
II. $F_{\{ST\}}$ measures population differentiation based on allele frequencies.
III. Phylogenetic trees represent the evolutionary relationships among breeds.
Which of the above statements are CORRECT?
(A) I and II only
(B) II and III only
(C) I and III only
(D) I, II, and III

2024

131. Inbreeding within a specific livestock population will generally lead to:
(A) An increase in observed heterozygosity
(B) A decrease in observed heterozygosity
(C) The rapid creation of new SNP alleles
(D) No change in genotype frequencies

2010

132. The Wright's F-statistic, $F_{\{IS\}}$, specifically measures:
(A) Genetic differentiation between distinct sub-populations
(B) The reduction in heterozygosity due to inbreeding within a sub-population
(C) The total genetic variance across the entire global species
(D) The mutation rate of a given locus

2018

133. Which methodology visually maps the genetic distances and evolutionary divergence between multiple livestock breeds?
(A) Southern Blotting
(B) Phylogenetic tree construction (e.g., Neighbor-Joining trees)
(C) Karyotyping
(D) Real-time PCR amplification plots

2001

134. Vitrification in cryopreservation of germplasm is characterized by:
(A) Slow, controlled ice crystal formation
(B) The conversion of a liquid directly into a glass-like amorphous solid without ice crystallization
(C) The rapid boiling of liquid nitrogen
(D) The exclusive use of extracellular cryoprotectants

2007

135. Match the cryoprotectant property (List I) with its corresponding characteristic (List II).
List I: (Cryoprotectant property)
P. Intracellular cryoprotectant
Q. Extracellular cryoprotectant
R. Glycerol
S. Egg yolk
List II: (Characteristic)
1. Crosses the cell membrane to prevent intracellular ice formation
2. Standardly used permeating agent in bull semen freezing
3. Non-permeating agent that protects the cell membrane externally
4. Provides external lipid protection against cold shock
(A) P-1, Q-3, R-2, S-4
(B) P-3, Q-1, R-4, S-2
(C) P-2, Q-4, R-1, S-3
(D) P-4, Q-2, R-3, S-1

2010

136. During slow freezing protocols, what is the primary cause of cell death if the cooling rate is too slow?

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(A) Lethal intracellular ice crystal formation
(B) Severe osmotic stress and cellular dehydration (solution effect)
(C) Immediate rupture of the nuclear envelope
(D) Denaturation of the cryoprotectant

2009

137. Which of the following is a classic non-permeating (extracellular) cryoprotectant?
(A) Dimethyl sulfoxide (DMSO)
(B) Glycerol
(C) Ethylene glycol
(D) Sucrose

2010

138. The addition of DMSO during cell freezing prevents cellular damage primarily by:
(A) Lowering the freezing point and disrupting crystalline ice lattice formation
(B) Providing metabolic energy to the cells during freezing
(C) Increasing the thermal conductivity of the liquid nitrogen
(D) Crosslinking the plasma membrane lipids

2011

139. Liquid nitrogen (LN2), routinely used for ultra-low temperature storage of biological samples, boils at what temperature?
(A) -80 degrees Celsius
(B) -150 degrees Celsius
(C) -196 degrees Celsius
(D) -273 degrees Celsius

2015

140. Consider the following statements about germplasm storage:
I. LN2 tanks operate as large Dewar flasks with a high-vacuum insulating jacket.
II. Safe thawing of bull semen straws typically involves a warm water bath (37 degrees C).
III. Frequent opening of LN2 tanks has no effect on static holding time.
IV. Post-thaw viability is assessed via sperm motility and acrosome integrity.
V. Cryovials must be loosely capped to prevent explosion during thawing.
Which of the above statement(s) is/are INCORRECT?
(A) I and II
(B) III and V
(C) II, IV and V
(D) I, III and V

2019

141. The condition known as "cold shock" in spermatozoa is fundamentally caused by:
(A) Phase transitions and lateral phase separations of membrane lipids during rapid chilling
(B) The toxic effects of accumulating metabolic byproducts at low temperatures
(C) Immediate freezing of intracellular water prior to cryoprotectant equilibration
(D) Evaporation of the seminal plasma

2001

142. A direct ELISA fundamentally requires which configuration of antibodies?
(A) Unlabeled primary antibody and enzyme-labeled secondary antibody
(B) Enzyme-labeled primary antibody binding directly to the immobilized antigen
(C) Two antibodies binding to different epitopes on the same antigen (sandwich)
(D) An antibody recognizing a specific enzyme substrate

2003

143. Which ELISA format is most sensitive and appropriate for detecting extremely low concentrations of a specific protein antigen in serum?
(A) Direct ELISA
(B) Indirect ELISA
(C) Sandwich ELISA
(D) Competitive ELISA

2001

144. In a competitive ELISA detecting a small molecule (e.g., a steroid hormone), a high signal (strong color) indicates:
(A) A high concentration of the target hormone in the sample
(B) A low concentration of the target hormone in the sample
(C) Complete degradation of the enzyme
(D) The absence of the primary antibody

2005

145. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): The indirect ELISA offers greater signal amplification than the direct ELISA.
Reason (R): Multiple enzyme-labeled secondary antibodies can bind to a single unlabeled primary antibody.
(A) Both A and R are true and R is the correct explanation of A.

NODIA

(D) It digests the primer sequences exclusively

2011

70. Consider the following statements regarding PCR-RFLP:
I. It is heavily utilized for genotyping known SNPs.
II. It requires expensive fluorescently labeled probes.
III. It relies on specific restriction endonucleases.
Which of the above statement(s) is/are CORRECT?
(A) I and II
(B) I and III
(C) II and III
(D) I, II, and III

2018

71. The detection limit of a PCR-RFLP assay on an agarose gel is primarily constrained by:
(A) The half-life of Taq polymerase
(B) The melting temperature of the primers
(C) The size of the host organism's genome
(D) The sensitivity of the DNA intercalating dye used

2018

72. In Sanger sequencing, chain termination is accomplished through the incorporation of which modified nucleotide?
(A) Dideoxynucleotide triphosphate (ddNTP)
(B) Deoxynucleotide triphosphate (dNTP)
(C) Ribonucleotide triphosphate (rNTP)
(D) Fluorophore-labeled dNTP

2001

73. What key structural feature do ddNTPs lack, which prevents further strand extension in Sanger sequencing?
(A) 5' phosphate group
(B) 2' hydroxyl group
(C) 3' hydroxyl group
(D) Nitrogenous base

2010

74. Which Next-Generation Sequencing (NGS) platform utilizes a "sequencing by synthesis" methodology relying on reversible dye-terminators?
(A) PacBio (SMRT sequencing)
(B) Illumina
(C) Oxford Nanopore
(D) 454 Pyrosequencing

2008

75. Match the sequencing platform (List I) with its underlying detection chemistry/principle (List II).
List I: (Sequencing platform)
P. Sanger Sequencing
Q. Pyrosequencing
R. Ion Torrent
S. PacBio
List II: (Principle)
1. Detection of pyrophosphate release via light emission
2. Detection of hydrogen ion release (pH change)
3. Capillary electrophoresis of ddNTP-terminated fragments
4. Single-molecule real-time monitoring of zero-mode waveguides
(A) P-3, Q-1, R-2, S-4
(B) P-1, Q-2, R-3, S-4
(C) P-3, Q-4, R-1, S-2
(D) P-2, Q-3, R-4, S-1

2006

76. A major advantage of Pacific Biosciences (PacBio) sequencing over Illumina sequencing in livestock genomics is its ability to:
(A) Generate billions of very short, highly accurate reads
(B) Sequence metabolic proteins directly alongside DNA
(C) Produce long reads for resolving complex genomic repeats
(D) Completely bypass the use of a DNA polymerase

2002

77. In the context of NGS, what does the term "read depth" or "coverage" refer to?
(A) The length of an individual sequence read
(B) The physical depth of the sequencing flow cell
(C) The percentage of GC content in the sequenced genome
(D) The average number of times a specific genomic nucleotide is sequenced

2007

78. Pyrosequencing detects nucleotide incorporation by measuring light produced from an enzymatic cascade involving:
(A) Taq polymerase and SYBR Green
(B) Proteinase K and alkaline phosphatase
(C) ATP sulfurylase and luciferase
(D) Horseradish peroxidase and TMB

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stranded DNA
(B) Binding specifically to double-stranded DNA and emitting fluorescence
(C) Cleaving a specific reporter probe via exonuclease activity
(D) Absorbing UV light and emitting heat

2010

157. What is the primary disadvantage of using SYBR Green chemistry over TaqMan probes in qPCR?
(A) SYBR Green is significantly more expensive
(B) SYBR Green requires complex probe design
(C) SYBR Green detects all double-stranded DNA, including non-specific products and primer-dimers
(D) SYBR Green cannot be used for relative quantification

2024

158. TaqMan probes rely on which specific property of Taq polymerase to generate a fluorescent signal?
(A) 3' to 5' exonuclease proofreading
(B) 5' to 3' exonuclease activity
(C) Terminal transferase activity
(D) Strand displacement activity

2009

159. The phenomenon utilized in TaqMan probes where the proximity of a quencher suppresses the fluorescence of a reporter dye is called:
(A) Fluorescence Resonance Energy Transfer (FRET)
(B) Induced photobleaching within the well
(C) Regulated microbial bioluminescence
(D) Chemiluminescence based on pH change

2016

160. Consider the following statements about relative quantification in qPCR:
I. It compares the expression of a target gene to a reference (housekeeping) gene.
II. The $2^{-\Delta\Delta C_t}$ method is widely used.
III. It requires absolute standard curves of known concentrations for every sample.
IV. It assumes the amplification efficiencies of the target and reference genes are approximately equal.
Which of the above statement(s) is/are CORRECT?
(A) I, II and IV
(B) I, II and III
(C) II, III and IV
(D) I, III and IV

2013

161. A melt curve analysis is typically performed post-amplification in which type of qPCR assay?
(A) TaqMan probe assays exclusively
(B) SYBR Green assays
(C) Northern blots
(D) End-point PCR-RFLP

2012

162. The purpose of a melt curve analysis in qPCR is to:
(A) Determine the exact sequence of the amplicon
(B) Confirm the specificity of amplification by checking for a single, specific melting peak
(C) Measure the efficiency of the reverse transcriptase step
(D) Denature the primers to prevent further extension

2011

163. If the efficiency of a qPCR reaction is 100%, the amount of target DNA will increase by what factor during each cycle of the exponential phase?
(A) It will triple (3-fold)
(B) It will double (2-fold)
(C) It will quadruple (4-fold)
(D) It will increase by 10-fold

2011

164. Which of the following is commonly used as a reference (housekeeping) gene for normalizing gene expression data in livestock qPCR?
(A) GAPDH
(B) Insulin
(C) Myostatin
(D) Casein

2012

165. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): In RNA-based qPCR (RT-qPCR), a "No Reverse Transcriptase" (NRT) control is crucial.
Reason (R): The NRT control detects potential contamination of the RNA sample with residual genomic DNA.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

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(A) Fluorophore-conjugated dUTPs (e.g., FITC-dUTP)
(B) Dideoxynucleotides (ddNTPs)
(C) Unmodified ATP only
(D) Ribonucleotides (rNTPs)

2025

187. The term "chromosome painting" refers to the application of which specific type of FISH probe?
(A) A universal centromere probe
(B) A single, highly specific 20-bp oligonucleotide
(C) A complex pool of probes derived from an entire single isolated chromosome
(D) A probe targeting only ribosomal RNA clusters

2011

188. In PRINS methodology, the visual signal is localized to the chromosomes via:
(A) The enzymatic incorporation of labeled nucleotides by Taq polymerase directly onto the slide
(B) The direct binding of a 10,000 bp fluorescent probe
(C) Autoradiography
(D) Silver staining of nucleolar organizer regions

2025

189. A major advantage of Somatic Cell Hybrid (SCH) panels in early livestock genome mapping was:
(A) The ability to map genes without finding polymorphic variants within the livestock species
(B) The precise measurement of physical distance in base pairs
(C) The extremely high resolution down to single-nucleotide levels
(D) The bypass of any cell culture requirements

2015

190. In a Radiation Hybrid panel, the frequency at which a donor chromosome fragment is retained in the recipient cell clone averages around:
(A) 0.1% to 1%
(B) 10% to 50%
(C) 90% to 95%
(D) 100%

2002

191. A key structural requirement of a Yeast Artificial Chromosome (YAC) vector that distinguishes it from a bacterial plasmid is the presence of:
(A) Telomeres and a centromere
(B) An ampicillin resistance gene
(C) A strong T7 bacteriophage promoter
(D) A multiple cloning site (MCS)

2006

192. During recombinant DNA ligation using T4 DNA ligase, what cofactor is absolutely essential for the reaction?
(A) NAD+
(B) ATP
(C) GTP
(D) FAD

2024

193. The calculation of genetic map distance in centiMorgans (cM) assumes that 1 cM is approximately equal to:
(A) A 1% recombination frequency
(B) A 10% recombination frequency
(C) Exactly 1 million base pairs
(D) One chiasma per chromosome

2025

194. In the context of linkage mapping, what does "phase" refer to?
(A) The arrangement of alleles on homologous chromosomes (coupling or repulsion)
(B) The stage of mitosis the cells are in
(C) The ratio of physical distance to genetic distance
(D) The statistical significance of the LOD score

2012

195. The primary purpose of applying FTA cards for blood collection in the field is to:
(A) Perform immediate PCR without extraction
(B) Safely transport samples at ambient temperature without cold chain logistics
(C) Separate red blood cells from white blood cells visually
(D) Quantify the DNA concentration directly on the card

2009

196. When verifying parentage using microsatellite markers, a "mismatch" at a single locus out of 15 loci is generally considered:
(A) A potential mutation event requiring further analysis before exclusion
(B) Absolute proof of non-paternity
(C) Absolute proof of paternity
(D) An artifact of DNA degradation

2002

197. Animal identification based on DNA profiling fundamentally relies on the principle that:
(A) All animals within a breed are genetically identical

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template DNA strands
(B) Non-specific amplification and primer-dimer formation before denaturation
(C) The premature melting of highly GC-rich template regions
(D) Evaporation of the reaction mixture during early cycling

2022

178. What determines the final size of the amplicon generated in a standard PCR reaction?
(A) The inherent processivity of the Taq polymerase
(B) The physical distance between the 5' ends of the bound forward and reverse primers
(C) The concentration of the dNTPs
(D) The size of the original genomic template

2017

179. A common application of PCR-RFLP in dairy cattle breeding is genotyping for the A1/A2 beta-casein polymorphism. This polymorphism involves:
(A) A single nucleotide change leading to an amino acid substitution (Pro/His) that alters a restriction site
(B) A large deletion in the beta-casein promoter
(C) An inversion of the entire beta-casein gene
(D) Variable numbers of tandem repeats in intron 1

2012

180. Consider the following statements about DNA sequencing platforms:
I. Sanger sequencing handles 1 sample per capillary lane.
II. Illumina uses reversible dye terminators.
III. PacBio detects proton release.
IV. NGS allows massive multiplexing via barcoding.
V. Pyrosequencing reads are highly prone to homopolymer errors.
Which of the above statement(s) is/are CORRECT?
(A) I, II, IV and V
(B) II, III, IV and V
(C) I, II, III and V
(D) I, III, IV and V

2001

181. In an Illumina sequencing run, "adapters" ligated to the ends of DNA fragments serve what primary purpose?
(A) They bind to complementary oligos on the flow cell surface for cluster generation
(B) They encode the restriction sites for final cleavage
(C) They act as the DNA polymerase during synthesis
(D) They fluorescently label the fragments

2009

182. Metaphase arresting agents like colchicine function by binding to which intracellular structural component?
(A) Tubulin dimers
(B) Actin microfilaments
(C) Histone octamers
(D) Nuclear lamins

2008

183. To prepare high-quality chromosome spreads from bone marrow, which step is routinely omitted compared to blood culture?
(A) Extended mitogen-stimulated culture
(B) Hypotonic treatment
(C) Carnoy's fixation
(D) Slide dropping

2012

184. The International System for Cytogenetic Nomenclature of Domestic Animals (ISCNDA) standardizes:
(A) The specific PCR primers for every gene
(B) The naming and numbering of chromosome bands for accurate karyotype description
(C) The feed rations for experimental livestock
(D) The sequence of all mitochondrial genomes

2010

185. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): C-banding techniques selectively stain the constitutive heterochromatin at the centromeres.
Reason (R): Centromeric heterochromatin is resistant to alkali extraction, while euchromatin is not.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

NODIA

2016

186. Fluorescently labeled probes used in FISH can be directly synthesized by incorporating which type of modified nucleotides during nick translation or PCR?

2025

206. In an Indirect ELISA meant to diagnose a viral infection in a cow, what is typically coated onto the bottom of the microtiter plate well?
(A) Purified viral antigen
(B) Bovine serum
(C) Enzyme-linked anti-bovine antibodies
(D) Substrate solution

2009

207. A critical requirement for a successful Sandwich ELISA is that the target antigen must:
(A) Be a very small molecule with only one epitope
(B) Have at least two distinct binding sites (epitopes) for the capture and detection antibodies
(C) Be a single-stranded nucleic acid
(D) Be completely denatured prior to assay

2002

208. In Western Blotting, after blocking the PVDF membrane, it is typically incubated with the primary antibody. This primary antibody is specific to:
(A) The target protein of interest
(B) The enzyme conjugated to the secondary antibody
(C) The SDS used in the gel
(D) The blocking buffer proteins

2023

209. The detection method utilizing luminol and hydrogen peroxide in Western Blotting is known as:
(A) Enhanced Chemiluminescence (ECL)
(B) Colorimetric detection
(C) Autoradiography
(D) Fluorescent resonance

2014

210. Why is the $\frac{A_{260}}{A_{280}}$ ratio of pure RNA higher (typically ~2.0) than that of pure DNA (typically ~1.8)?
(A) Uracil absorbs more UV light at 260 nm than thymine
(B) Ribose absorbs more strongly than deoxyribose at 280 nm
(C) RNA extraction protocols completely eliminate all proteins
(D) RNA lacks standard histones

2009

2018

211. Which method provides the most reliable measurement of extremely low concentrations (< 1 ng/uL) of double-stranded DNA?
(A) PicoGreen-based fluorometry
(B) UV Spectrophotometry at 260 nm
(C) Standard agarose gel electrophoresis
(D) Bradford assay

2008

212. In agarose gel electrophoresis, larger DNA fragments migrate slower through the gel matrix because they:
(A) Bind more ethidium bromide
(B) Have a lower charge-to-mass ratio than smaller fragments
(C) Experience greater frictional resistance within the agarose pores
(D) Are repelled strongly by the cathode

2016

213. Restriction enzymes belong to which broader class of enzymes?
(A) Hydrolases (specifically Endonucleases)
(B) Transferases
(C) Ligases
(D) Oxidoreductases

2021

214. Which restriction endonucleases create DNA fragments with exactly matching complementary overhangs?
(A) Enzymes producing "blunt" ends
(B) Enzymes that cleave outside their recognition site randomly
(C) Isoschizomers that cleave identical staggered sequences
(D) Type I enzymes

2016

215. What is the fundamental difference between Southern and Northern blotting transfers?
(A) Southern transfers DNA; Northern transfers RNA
(B) Southern requires nitrocellulose; Northern strictly requires nylon
(C) Southern uses electricity; Northern exclusively uses vacuum
(D) Southern blots are never probed; Northern blots are probed

2005

216. During probe hybridization, increasing the temperature of the hybridization buffer will:
(A) Increase the stringency of the reaction, reducing non-specific binding
(B) Decrease the stringency of the reaction
(C) Instantly denature the target on the membrane
(D) Prevent the probe from finding any

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(B) Except for monozygotic twins, the combined multilocus genotype of every individual is unique
(C) Microsatellites mutate at extremely low rates
(D) Blood and semen carry different genomic DNA profiles

2021

198. The term "polymorphism information content" (PIC) is used to evaluate a genetic marker's:
(A) Usefulness in linkage analysis based on the number and frequency of alleles
(B) Physical size in base pairs
(C) Susceptibility to restriction enzyme cleavage
(D) Melting temperature during PCR

2023

199. Molecular characterization of livestock breeds frequently uses F-statistics. A highly negative $F_{\{IS\}}$ value typically implies:
(A) An excess of heterozygotes, possibly due to outbreeding or selective advantage
(B) High levels of inbreeding
(C) A high degree of population subdivision
(D) Total loss of genetic diversity

2022

200. Match the term (List I) with its definition in population genetics (List II).
List I: (Term)
P. Hardy-Weinberg Equilibrium
Q. Linkage Disequilibrium
R. Heterozygosity
S. Bottleneck effect
List II: (Definition)
1. Presence of different alleles at a locus
2. Non-random association of alleles at different loci
3. Constant allele frequencies over generations without evolutionary forces
4. Drastic reduction in population size leading to loss of diversity
(A) P-3, Q-2, R-1, S-4
(B) P-1, Q-2, R-4, S-3
(C) P-2, Q-3, R-1, S-4
(D) P-3, Q-1, R-2, S-4

2022

201. Which cryoprotectant is universally considered the standard permeating agent for the deep freezing of mammalian spermatozoa?
(A) Glycerol
(B) Dimethyl sulfoxide (DMSO)
(C) Propylene glycol
(D) Methanol

2019

202. Egg yolk is included in many semen cryopreservation extenders primarily because it:
(A) Provides complex lipids and lipoproteins that protect the sperm plasma membrane from cold shock
(B) Acts as the primary energy source for frozen sperm
(C) Lowers the freezing point of the extender below that of liquid nitrogen
(D) Stimulates sperm capacitation prior to freezing

2019

203. During the cryopreservation of livestock embryos, the seeding step involves:
(A) Artificially inducing extracellular ice formation at mild sub-zero temperatures
(B) Plunging the embryos directly into liquid nitrogen
(C) Adding the maximum concentration of cryoprotectant
(D) Washing out the cryoprotectant post-thaw

2004

204. What is the fundamental difference between slow freezing and vitrification of embryos?
(A) Vitrification requires ultra-rapid cooling rates to form an amorphous solid, completely avoiding ice crystal formation
(B) Slow freezing uses extremely high cryoprotectant concentrations, while vitrification uses very low concentrations
(C) Slow freezing avoids the use of liquid nitrogen
(D) Vitrification can only be performed at 4 degrees Celsius

2015

205. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): Assessing post-thaw sperm motility immediately upon thawing provides a complete picture of fertilizing capacity.
Reason (R): Spermatozoa must possess progressive motility to successfully navigate the female reproductive tract.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

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2024

166. A spectrophotometer uses a prism or diffraction grating primarily to:
(A) Isolate specific wavelengths of light from a broad-spectrum source
(B) Focus the light beam into the cuvette
(C) Amplify the intensity of the light
(D) Detect the transmitted photons

2001

167. Which type of cuvette is absolutely required for measuring UV absorbance at 260 nm?
(A) Standard glass
(B) Optical plastic (polystyrene)
(C) Quartz
(D) Borosilicate

2012

168. To extract intact, high-quality RNA from tissues, the homogenization buffer strongly relies on which chemical to inhibit endogenous RNases?
(A) Guanidinium thiocyanate
(B) EDTA
(C) Tris-HCl
(D) Calcium chloride

2019

169. What is the standard voltage gradient typically applied during standard analytical Agarose Gel Electrophoresis?
(A) 1-5 V/cm
(B) 10-20 V/cm
(C) 50-100 V/cm
(D) 200-300 V/cm

2025

170. Arrange the following cloning vectors in order of INCREASING insert capacity:
I. BAC
II. YAC
III. Plasmid
IV. Cosmid
(A) III, IV, I, II
(B) III, I, IV, II
(C) IV, III, I, II
(D) III, IV, II, I

2004

171. A restriction enzyme recognizes a 4-bp sequence (e.g., Sau3AI). Assuming a random, equal distribution of nucleotides, how frequently will this site appear in the genome on average?
(A) Once every 256 bp
(B) Once every 1024 bp
(C) Once every 4096 bp
(D) Once every 65,536 bp

2025

172. The presence of isoschizomers implies that two different restriction enzymes:
(A) Recognize entirely different sequences but produce the same overhangs
(B) Recognize the exact same sequence
(C) Have the same optimal temperature but require different buffers
(D) Are isolated from the exact same bacterial strain

2005

173. Capillary transfer in Southern blotting typically takes how long to achieve complete transfer of large genomic fragments?
(A) 5 to 10 minutes
(B) 1 to 2 hours
(C) 12 to 24 hours (overnight)
(D) 3 to 5 days

2015

174. Which hybridization stringency condition will favor the binding of a probe to sequences with imperfect complementarity (e.g., cross-species hybridization)?
(A) Low temperature, high salt concentration
(B) High temperature, low salt concentration
(C) High temperature, high salt concentration
(D) Low temperature, low salt concentration

2006

175. Radioactive probes for Southern blotting are frequently labeled using which specific isotope incorporated into dNTPs?
(A) Carbon-14
(B) Tritium (H-3)
(C) Phosphorus-32
(D) Sulfur-35

NODIA

2004

176. PCR amplification of very long targets (e.g., >5 kb) generally requires modifications to standard protocols. Which of the following is typically implemented?
(A) Decreasing the extension temperature to 68 degrees Celsius
(B) Increasing the denaturation time to 5 minutes per cycle
(C) Using purely standard Taq polymerase without proofreading capability
(D) Eliminating magnesium from the buffer

2003

177. The "hot-start" PCR method is primarily designed to prevent:
(A) The rapid enzymatic degradation of the

complementary sequence

2008

217. In the context of PCR, what is an amplicon?
(A) The specific segment of DNA synthesized during the reaction
(B) The restriction enzyme used for digestion
(C) The apparatus used for thermal cycling
(D) The fluorescent dye used for tracking

2016

218. The "plateau phase" in standard endpoint PCR is typically reached due to:
(A) Depletion of reaction components (dNTPs, primers) and loss of polymerase activity
(B) Infinite exponential growth
(C) The temperature dropping too low
(D) Continuous addition of template DNA

2008

219. PCR-RFLP relies on successful amplification followed by complete enzymatic digestion. If a mutation destroys a restriction site, the expected result for that allele is:
(A) The amplicon remains uncut, producing a single large band
(B) The amplicon cuts in multiple places, producing a smear
(C) The amplicon completely degrades
(D) No PCR amplification occurs

2009

220. Arrange the following steps of a standard DNA fingerprinting (microsatellite) analysis in the correct order:
I. Multiplex PCR amplification of STR loci
II. Isolation of genomic DNA from the sample
III. Capillary electrophoresis and fragment sizing
IV. Allele calling and profile generation
(A) I, II, III, IV
(B) II, I, III, IV
(C) II, III, I, IV
(D) I, III, II, IV

2001

221. High-throughput genotyping using SNP microarrays involves:
(A) Sequencing the entire genome fragment by fragment
(B) Hybridization of sample DNA to millions of locus-specific probes attached to a solid surface
(C) Southern blotting of the entire genome
(D) RFLP digestion of the entire genome

2002

222. The term "coverage" in Next Generation Sequencing implies:
(A) The average number of sequence reads that align to a specific reference base
(B) The physical area of the flow cell covered by clusters
(C) The percentage of the genome that is completely unknown
(D) The amount of fluorescent dye applied

2022

223. What specific feature of the PacBio SMRT sequencing technology permits the sequencing of extremely long DNA fragments?
(A) Single-molecule real-time monitoring of a continuous polymerase within a Zero-Mode Waveguide
(B) The utilization of highly advanced capillary tubes
(C) Massive chemical shearing of DNA
(D) Reliance on restriction enzyme mapping

2002

224. Which technique allows for the direct observation of the physical location of a gene on a specific chromosome band?
(A) FISH (Fluorescence In Situ Hybridization)
(B) High-resolution melting analysis
(C) PCR-RFLP
(D) Northern Blotting

2018

225. A key difference between G-banding and C-banding is that C-banding:
(A) Consistently stains the highly condensed constitutive heterochromatin, predominantly at centromeres
(B) Stains only AT-rich euchromatin
(C) Completely denatures the DNA leaving only the protein backbone
(D) Requires fluorescent microscopy

2016

226. During karyotype analysis of domestic animals, what morphological characteristic is primarily used to identify and pair homologous chromosomes?
(A) Total chromosome length and centromere position
(B) The exact sequence of telomeres
(C) The rate of meiotic crossing over
(D) The specific alleles present on the chromosome

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2010

227. In PRINS (Primed In Situ Labeling), the specificity of the genomic target detection is fundamentally determined by:
(A) The sequence of the specific oligonucleotide primer utilized
(B) The choice of fluorochrome
(C) The concentration of the DNA polymerase
(D) The size of the metaphase spread

2016

228. Radiation Hybrid maps express distances in centiRays (cR). A distance of 1 $cR_{\{10000\}}$ indicates a 1% probability of:
(A) A radiation-induced chromosome break occurring between two markers after an exposure of 10,000 rads
(B) A crossover occurring during meiosis
(C) Two cells fusing successfully
(D) A marker mutating during culture

2017

229. A standard plasmid cloning vector typically contains a multiple cloning site (MCS). What is its function?
(A) It contains a dense array of unique restriction enzyme sites for easy insertion of foreign DNA
(B) It dictates the copy number of the plasmid
(C) It provides resistance to ampicillin
(D) It initiates transcription of the inserted gene

2024

230. During the transformation of E. coli, a brief 42 degrees Celsius heat shock step is applied. What is its physiological effect?
(A) It creates a thermal gradient that sweeps plasmid DNA through the transiently altered cell membrane
(B) It permanently denatures the bacterial DNA
(C) It boils the cell wall completely away
(D) It activates the beta-lactamase enzyme

2007

231. In genetic linkage analysis, recombination frequency is calculated by dividing the number of recombinant offspring by:
(A) The total number of offspring
(B) The number of parental offspring
(C) The number of chromosomes in the species
(D) The base pair length of the chromosome

2001

232. Which scenario strongly indicates a violation of Hardy-Weinberg equilibrium within a livestock population?
(A) Intense artificial selection for a specific production trait
(B) Large population size
(C) Random mating
(D) No migration or mutation

2017

233. The genetic variation observed between different breeds of cattle (e.g., Holstein vs. Brahman) can be quantified using which specific statistical metric?
(A) $F_{\{ST\}}$ (Fixation index among subpopulations)
(B) Relative humidity
(C) LOD score
(D) Thermal melting point

2016

234. In forensic DNA analysis, why is the analysis of multiple STR loci necessary rather than just one?
(A) Multiple loci drastically increase the discriminatory power, minimizing the probability of identical profiles by chance
(B) Single STR loci are impossible to amplify
(C) Single loci always mutate during PCR
(D) STRs are only found on the sex chromosomes

2014

235. The fundamental principle behind the vitrification of oocytes or embryos is the prevention of:
(A) Lethal ice crystal formation using high cooling rates
(B) The denaturation of critical metabolic protein complexes
(C) DNA fragmentation during the first meiotic division
(D) Evaporation of the storage medium over long periods

2008

236. Why must liquid nitrogen dewars be stored in well-ventilated areas?
(A) Because evaporating nitrogen gas rapidly displaces oxygen, presenting a severe asphyxiation hazard
(B) To prevent the liquid nitrogen from boiling
(C) To ensure ambient temperatures remain above 25 degrees Celsius
(D) To allow sunlight to sterilize the tanks

2022

237. The integrity of the sperm acrosome post-thawing is frequently assessed using:
(A) Fluorescent staining techniques such as FITC-PNA or CTC
(B) Standard agar plating

NODIA

(C) Southern blotting
(D) Phenol-chloroform extraction

2010

238. In a sandwich ELISA setup, the "capture" antibody is bound to:
(A) The solid-phase surface of the microtiter plate well
(B) The target antigen directly
(C) The specific enzyme used for detection
(D) The stop solution

2012

239. Alkaline phosphatase (AP) is frequently used in ELISAs. Which of the following is a common colorimetric substrate for AP?
(A) p-Nitrophenyl phosphate (pNPP)
(B) Tetramethylbenzidine (TMB)
(C) Luminol
(D) X-gal

2019

240. The transfer of proteins from a PAGE gel to a membrane in Western blotting typically requires:
(A) An applied electric current (electroblotting) perpendicular to the gel
(B) High vacuum pressure
(C) Strong capillary action with salt buffers
(D) Simple gravity diffusion overnight

2003

241. The following question consists of two statements: Assertion (A) and Reason (R). Choose the correct answer from the options below:
Assertion (A): In RT-qPCR, using gene-specific primers during the reverse transcription step enhances the specificity of the assay.
Reason (R): Gene-specific primers exclusively convert the target mRNA into cDNA, ignoring ribosomal and transfer RNAs.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2011

242. In a real-time PCR assay, if Sample A has a C_t of 20 and Sample B has a C_t of 23 for the same target (assuming 100% efficiency), what is the relative difference in initial template concentration?
(A) Sample A has approximately 8 times (2^3) more template than Sample B
(B) Sample A has 3 times more template than Sample B
(C) Sample B has 3 times more template than Sample A
(D) Sample B has approximately 8 times more template than Sample A

2004

243. The "baseline" in a qPCR amplification plot represents:
(A) The background fluorescence level during the initial cycles before measurable amplification occurs
(B) The phase of exponential product generation
(C) The final concentration of the amplicon
(D) The temperature of the annealing step

2002

244. Genomic DNA isolation from semen samples is particularly challenging because:
(A) Compacted sperm chromatin is crosslinked with disulfide bonds
(B) A complete lack of a functional nucleus within mature cells
(C) The DNA is highly degraded immediately upon ejaculation
(D) Semen contains massive quantities of digestive RNases

2024

245. When preparing DNA from avian whole blood, the yield is exceptionally high per milliliter compared to mammalian blood because:
(A) Avian erythrocytes are nucleated, unlike mature mammalian erythrocytes
(B) Avian genomes are significantly larger than mammalian genomes
(C) Avian blood lacks plasma proteins
(D) Avian DNA is exclusively single-stranded

2003

246. Which specific role does RNase A play during genomic DNA extraction protocols?
(A) It specifically degrades contaminating RNA, leaving the DNA intact
(B) It stabilizes the RNA for concurrent extraction
(C) It acts as a primary buffer for pH control
(D) It actively digests histone proteins

2009

247. If an extraction protocol calls for the use of "TE buffer" to resuspend the final DNA pellet, what are the primary components of this buffer?
(A) Tris-HCl and EDTA
(B) Triton X-100 and Ethanol
(C) Toluene and Ethidium Bromide

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(D) Trypsin and EGTA

2002

248. Measuring the $\frac{A_{260}}{A_{280}}$ ratio provides an assessment of DNA purity. A ratio of 1.4 suggests:
(A) Significant protein contamination
(B) The DNA is highly pure
(C) Significant RNA contamination
(D) Complete DNA degradation

2003

249. A researcher quantifies a DNA sample and obtains an absorbance of 0.5 at 260 nm. Assuming a path length of 1 cm, what is the concentration?
(A) 25 ug/mL
(B) 12.5 ug/mL
(C) 50 ug/mL
(D) 100 ug/mL

2019

250. Arrange the sequence of steps for creating a standard Recombinant Plasmid:
I. Digestion of plasmid and insert with the same restriction enzyme
II. Ligation of the insert into the plasmid using T4 DNA ligase
III. Transformation of the recombinant plasmid into competent E. coli
IV. Isolation of plasmid DNA and PCR amplicon
(A) I, II, III, IV
(B) IV, I, II, III
(C) IV, II, I, III
(D) I, IV, II, III

2018

251. The primary advantage of a NanoDrop spectrophotometer over standard cuvette-based spectrophotometers is:
(A) It requires a significantly smaller sample volume (usually 1-2 uL) and no cuvettes
(B) It does not utilize UV light
(C) It automatically sequences the DNA
(D) It inherently distinguishes between DNA and RNA

2017

252. Which concentration of agarose is most appropriate for resolving DNA fragments spanning from 500 to 1000 base pairs?
(A) 0.5%
(B) 1.2%
(C) 3.0%
(D) 5.0%

2005

253. The visualization of DNA bands in agarose gels depends on the fluorescence of intercalating dyes. This fluorescence requires excitation by:
(A) Ultraviolet (UV) light
(B) Infrared light
(C) Visible white light
(D) X-rays

NODIA

2022

254. When interpreting a restriction digestion on an agarose gel, an undigested plasmid control typically runs:
(A) Faster than the completely digested linear form due to its supercoiled conformation
(B) As a single band representing the linear form
(C) Much slower, at the very top of the well
(D) Invisibly, as it cannot bind ethidium bromide

2018

255. BamHI recognizes a specific 6-base pair palindromic sequence. What defines a palindrome in double-stranded DNA?
(A) The sequence reads the same on one strand from 5' to 3' as it does on the complementary strand from 5' to 3'
(B) The sequence reads the same on one strand from 5' to 3' as it does on the complementary strand from 3' to 5'
(C) It consists entirely of alternating G and C residues
(D) It forms a permanent hair-pin loop structure

2018

256. A limitation of using nitrocellulose membranes in Southern Blotting compared to nylon is that nitrocellulose:
(A) Is brittle and tends to shatter, making reprobing difficult
(B) Cannot bind DNA fragments
(C) Requires highly radioactive probes exclusively
(D) Autofluoresces heavily under UV light

2011

257. In Southern hybridization, the "probe" is fundamentally a:
(A) Labeled single-stranded nucleic acid sequence complementary to the target of interest
(B) Monoclonal antibody specific for a DNA-binding protein
(C) Specific restriction enzyme
(D) Fluorescent intercalating dye

2017

258. PCR relies fundamentally on temperature cycling. The annealing temperature is predominantly dictated by the:
(A) Length and sequence composition (T_m) of the specific primers
(B) Brand of the thermal cycler
(C) Specific activity of the Taq polymerase
(D) Concentration of the template DNA

2013

259. A standard PCR cycle is typically repeated how many times to achieve sufficient amplification for agarose gel visualization?
(A) 5-10 times
(B) 15-20 times
(C) 25-35 times
(D) 50-70 times

2005

260. During a PCR-RFLP assay, incomplete restriction enzyme digestion can yield misleading genotyping results. This issue can often be mitigated by:
(A) Increasing the incubation time or utilizing a higher concentration of the restriction enzyme
(B) Adding extra EDTA to the digestion mix
(C) Running the agarose gel at a much higher voltage
(D) Decreasing the magnesium concentration

2001

261. The high accuracy of modern automated Sanger sequencing relies heavily on:
(A) Fluorescently labeled ddNTPs that allow for a single-tube reaction and capillary electrophoresis
(B) Four separate reaction tubes run in four separate gel lanes
(C) Massive parallelization of billions of templates
(D) The complete exclusion of standard dNTPs

2001

262. Which NGS platform utilizes semiconductor technology to directly translate chemically encoded information (pH changes) into digital data?
(A) Ion Torrent
(B) Illumina
(C) PacBio SMRT
(D) Oxford Nanopore

2006

263. When performing metaphase chromosome preparations, peripheral blood must be cultured for roughly 72 hours. What occurs during this period?
(A) The added mitogen stimulates the T-lymphocytes to proliferate and enter mitosis
(B) The red blood cells naturally undergo apoptosis
(C) The DNA is chemically denatured
(D) The chromosomes naturally undergo G-banding

2009

264. The primary goal of applying a hypotonic solution during chromosome preparation is to:
(A) Swell the cells, causing the chromosomes to spread widely apart when the cells are burst onto a slide
(B) Prevent premature sister chromatid separation
(C) Shrink the nucleus for better contrast
(D) Dissolve the remaining erythrocytes

2010

265. What distinguishes Q-banding from G-banding?
(A) Q-banding relies on quinacrine mustard and fluorescence microscopy, whereas G-banding uses Giemsa and brightfield microscopy
(B) Q-banding specifically highlights only the centromeres
(C) Q-banding requires no prior enzymatic treatment
(D) Q-banding can only be performed on plant chromosomes

2013

266. A Robertsonian translocation typically involves the fusion of two chromosomes at which precise location?
(A) Their centromeres (specifically in acrocentric chromosomes)
(B) Their telomeres
(C) Within their specific euchromatic bands
(D) At the nucleolar organizing region

2025

267. Fluorescence In Situ Hybridization (FISH) can be employed to directly detect:
(A) The gross structural location of a specific DNA sequence or entire chromosome on a metaphase spread
(B) The presence of a specific single nucleotide polymorphism
(C) The exact sequence of an uncharacterized

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locations. Type two restriction enzymes are the primary tool for this purpose because they recognize specific palindromic sequences and cleave precisely at or within those sites. This predictability allows researchers to generate fragments with known ends that can be easily ligated into plasmids or other cloning vectors.

37. (B) They cleave non-specifically under suboptimal conditions
Restriction enzymes are highly specific under optimal laboratory conditions, but this specificity can break down in certain environments. Star activity refers to the relaxation of the recognition sequence requirement, often caused by high glycerol concentrations, incorrect pH, or suboptimal salt levels. When this occurs, the enzyme begins to cut at sequences that are similar but not identical to its target.

38. (C) Palindrome
Many restriction endonucleases recognize DNA sequences characterized by a specific type of symmetry. A palindromic sequence reads the same on both strands when each is read in the five-prime to three-prime direction. This arrangement is common for enzymes that function as homodimers, as it allows each identical subunit to bind to one side of the symmetrical site on the double helix simultaneously.

39. (D) $Mg^{\{2+\}}$ ions
Type two restriction endonucleases require specific environmental conditions and cofactors to catalyze the hydrolysis of phosphodiester bonds. While these enzymes do not require energy from adenosine triphosphate, they strictly depend on the presence of divalent magnesium ions. These ions help position the DNA within the active site of the enzyme and facilitate the chemical reaction that breaks the DNA strand.

40. (A) I, III, V, II, IV
Southern blotting follows a logical sequence to identify specific DNA fragments within a complex genome. The process starts with enzymatic digestion and electrophoretic separation of the fragments. After separation, the DNA must be denatured into single strands before being transferred to a membrane. Finally, a labeled probe is hybridized to the membrane to detect the specific sequences of interest through complementarity.

41. (B) Type II enzymes cleave at recognition sites without requiring ATP
The classification of restriction enzymes is based on their mechanism of action and energy requirements. Unlike Type one enzymes, which use adenosine triphosphate to move along the DNA before cutting randomly, Type two enzymes are simpler and more predictable. They cleave the DNA directly at their specific recognition sites and do not require external energy sources to perform their catalytic function.

42. (B) It cuts the DNA strands symmetrically at the exact center of the recognition site
Some restriction enzymes cut the DNA double helix differently than others. While many leave staggered overhangs, or sticky ends, enzymes like EcoRV cleave both strands at the same position within the recognition sequence. This symmetrical cutting results in fragments with blunt ends, which lack single-stranded overhangs. These fragments are useful in certain cloning procedures but are generally more difficult to ligate.

43. (A) The recognition sequences are specifically methylated by corresponding methyltransferases
Bacteria protect their own genetic material from their endogenous restriction enzymes using a sophisticated modification system. For every restriction enzyme, the bacterium also produces a corresponding methyltransferase that adds a methyl group to a specific base within the recognition site. This chemical modification prevents the restriction enzyme from binding to the host DNA, while allowing it to destroy unmethylated viral DNA.

NODIA

44. (C) Haemophilus influenzae strain d
The naming convention for restriction enzymes follows a standardized system based on the organism of origin. The first letter represents the genus, and the next two represent the species. Additional characters identify the specific strain and the order in which the enzyme was discovered in that organism. In this case, the name refers to the third enzyme isolated from Haemophilus influenzae.

45. (A) Both A and R are true and R is the correct explanation of A.
Nylon membranes have largely replaced nitrocellulose in many blotting applications because of their superior physical properties.

exclusively
(D) Restriction maps of the Y chromosome

2012

278. Cryopreservation relies on effectively minimizing both intracellular ice formation and "solution effects" (severe osmotic stress). This is best achieved by:
(A) Optimizing cooling rates in the presence of cryoprotectants
(B) Using pure distilled water as a primary freezing medium
(C) Instantly boiling the cells prior to liquid nitrogen immersion
(D) Withholding all external lipids from the extension buffer

2019

279. Which parameter represents a critical metric of post-thaw viability for cryopreserved spermatozoa intended for artificial insemination?
(A) The proportion of progressively motile sperm and the physical integrity of the acrosome
(B) The concentration of the DNA in the head
(C) The length of the tail
(D) The strict absence of any seminal plasma

2003

280. Which of the following is commonly used as a blocking agent in ELISA to prevent non-specific binding of antibodies to the plastic surface?
(A) Bovine Serum Albumin (BSA)
(B) Sodium Azide
(C) Sulfuric acid
(D) Polyethylene glycol

2006

281. After the addition of stop solution in a TMB-based ELISA, the resulting yellow color is typically measured at which absorbance wavelength?
(A) 260 nm
(B) 280 nm
(C) 450 nm
(D) 600 nm

2022

282. What is the primary role of methanol in the transfer buffer used for Western blotting?
(A) It increases the solubility of high molecular weight proteins
(B) It facilitates the binding of proteins to the membrane by removing SDS
(C) It provides the electrical charge to the proteins
(D) It acts as a protease inhibitor

2023

283. In standard qPCR analysis, the primary threshold line is set:
(A) In the middle of the linear amplification phase on a log scale, significantly above the background noise
(B) Below the baseline fluorescence
(C) At the exact plateau level
(D) At cycle zero

2010

284. In real-time PCR, the purpose of a passive reference dye like ROX is to:
(A) Act as an internal control for cDNA synthesis
(B) Normalize for non-PCR related fluctuations in fluorescence signal
(C) Specifically detect the target amplicon
(D) Increase the melting temperature of the primers

NODIA

2022

285. In livestock breeding, genomic DNA isolation from hair follicles relies heavily on which specific region of the hair?
(A) The follicular root bulb
(B) The distal tip
(C) The shaft
(D) The cuticle

2025

286. What is the fundamental role of TBE buffer in agarose gel electrophoresis compared to TAE?
(A) It has a higher buffering capacity and is less prone to exhaustion during prolonged, high-voltage electrophoretic runs
(B) It specifically prevents DNA from running backward
(C) It strictly stains the DNA orange
(D) It acts as a tracking dye

2025

287. If a DNA sample is diluted 1:100 and the absorbance at 260 nm is 0.2, what is the concentration of the original DNA stock (assuming $1 OD = 50 ug/ml$)?
(A) 10 ug/mL
(B) 200 ug/mL
(C) 1000 ug/mL
(D) 5000 ug/mL

2006

288. In conventional PCR, the denaturation step (usually 94-98 degrees Celsius) serves to:
(A) Break the hydrogen bonds between complementary base pairs, yielding single-stranded templates

ANSWERS

1. (A) To digest histones and cell membrane proteins
Proteinase K serves as a critical serine protease in genomic extraction protocols. Its primary function involves the enzymatic digestion of structural proteins, specifically histones that package DNA and various membrane-bound proteins. By degrading these protein components, the enzyme effectively releases nucleic acids into the solution while simultaneously inactivating endogenous nucleases that could otherwise degrade the target genomic material.

2. (C) The upper aqueous phase
Organic solvent extraction utilizes the differing solubilities of cellular components to isolate genetic material. During phenol-chloroform-isoamyl alcohol treatment, the mixture separates into distinct layers based on density and polarity. Nucleic acids remain in the top aqueous layer because they are highly polar and hydrophilic. Proteins denature and accumulate at the interphase, while lipids dissolve in the lower organic phase.

3. (A) It reduces foaming at the interphase during centrifugation
Liquid-liquid extraction protocols involve vigorous mixing that often generates air bubbles within the sample. Isoamyl alcohol is specifically included in the phenol-chloroform mixture to act as an antifoaming agent. By reducing surface tension, it prevents the formation of a stable foam layer at the interphase during centrifugation, thereby facilitating the clean recovery of the upper aqueous DNA layer.

4. (D) Absolute ethanol
Precipitation of genetic material from a solution requires reducing its solubility in the surrounding solvent. High-grade alcohol is commonly added to the aqueous extract to decrease the dielectric constant of the medium. This change promotes the formation of ionic bonds between the phosphate backbone and available cations, causing the nucleic acid molecules to aggregate and precipitate out of the solution.

5. (A) Both A and R are true and R is the correct explanation of A.
Semen extraction protocols necessitate the use of dithiothreitol because sperm DNA is exceptionally compacted by protamines rather than standard histones. These protamine complexes are stabilized by numerous disulfide cross-links that resist standard lysis buffers. The reducing agent breaks these chemical bonds, allowing the proteinase to access and digest the proteins, which ultimately facilitates the release of high-quality genomic DNA.

6. (C) Treatment with hypotonic buffer solutions
Isolating leukocytes from whole blood often begins with the selective destruction of red blood cells. Using a buffer with a low solute concentration relative to the cytoplasm creates an osmotic gradient. Water enters the erythrocytes rapidly, causing them to swell and eventually burst. Because white blood cells are more resistant to these osmotic changes, they remain intact for subsequent collection.

7. (D) Sodium dodecyl sulfate (SDS)
Efficient lysis of nucleated cells requires the disruption of lipid bilayers and the denaturation of structural proteins. Sodium dodecyl sulfate is a powerful anionic detergent frequently used for this purpose in molecular biology. It solubilizes membrane lipids and unfolds proteins by disrupting non-covalent bonds, effectively releasing the genomic contents of the nucleus into the lysis buffer for further purification.

8. (A) To neutralize the negative charge on the phosphate backbone
DNA molecules are naturally surrounded by a shell of water molecules that prevent aggregation in aqueous solutions. Adding monovalent salt ions provides positively charged cations that interact with the negatively charged phosphate groups on the DNA backbone. This neutralization reduces the repulsive forces between DNA molecules, allowing them to clump together and precipitate more efficiently when alcohol is later added.

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and population structure among different breeds

(B) Calculate the exact sequence of individual SNPs

(C) Estimate the molecular weight of extracted genomic DNA

(D) Determine the optimal cooling rate for embryo freezing

2021

299. During slow cooling protocols in cryopreservation, what phenomenon is managed by "seeding"?

(A) Supercooling of the extracellular medium, mitigated by deliberately inducing ice crystal formation just below the freezing point

(B) The formation of intracellular ice at -196 degrees Celsius

(C) The immediate evaporation of liquid nitrogen

(D) The cross-linking of surface proteins

2001

300. In absolute quantification using real-time qPCR, the concentration of an unknown target sample is determined by:

(A) Visual comparison of band intensity on an agarose gel

(B) The direct measurement of total SYBR Green fluorescence at the end of the reaction

(C) Normalizing to three internal housekeeping genes

(D) Comparing its C_t value to a standard curve generated from a dilution series of known template concentrations

****

NODIA

(B) Break the covalent bonds between adjacent nucleotides
(C) Digest any contaminating proteins
(D) Inactivate the Taq polymerase

2012

289. In PCR-RFLP, what is the purpose of including an "internal control" restriction site within the amplicon that is non-polymorphic?
(A) To ensure the restriction enzyme was active and digestion went to completion
(B) To increase the number of alleles detected
(C) To act as a primer for the next round of PCR
(D) To prevent non-specific amplification

2014

290. The concept of "sequencing by synthesis" implies that the nucleotide sequence is read:
(A) In real-time as a DNA polymerase incorporates specific nucleotides onto a growing complementary strand
(B) By sequentially degrading the DNA molecule from one end
(C) By viewing the molecule directly with an electron microscope
(D) By hybridizing specific restriction enzymes to the molecule

2019

291. Cytogenetic preparation from peripheral blood involves a hypotonic solution treatment. If the hypotonic treatment duration is excessively long, what is the most likely consequence?
(A) The cells will rupture prematurely in the tube, leading to scattered, unanalyzable chromosomes
(B) The cells will fail to burst upon dropping
(C) The DNA will heavily methylate
(D) The chromosomes will artificially double in size

2011

292. In the context of karyotypic analysis, what is an ideogram?
(A) A schematic, diagrammatic representation of a karyotype showing typical banding patterns
(B) A chemical stain used for G-banding
(C) A specific mutation in a chromosome
(D) A photograph of an unbanded metaphase spread

2005

293. Which technique is most appropriate for precisely identifying the chromosomal origin of a small "marker chromosome" of unknown identity?
(A) Fluorescence In Situ Hybridization (FISH) with specific chromosomal paints
(B) Routine G-banding
(C) Standard PCR
(D) Restriction digestion

2003

294. In Somatic Cell Genetics, what is the primary purpose of the HAT medium?
(A) To selectively allow the survival of hybrid cells while parental cells die due to biochemical deficiencies
(B) To selectively kill only the hybrid cells
(C) To chemically fuse the parental cells
(D) To stain the chromosomes

2013

295. Which type of cloning vector utilizes the 'cos' sites of bacteriophage lambda to package large DNA inserts (up to 45 kb)?
(A) Cosmid
(B) Plasmid
(C) YAC
(D) BAC

2009

296. A LOD score is a standard statistical parameter in linkage mapping representing the:
(A) Base-10 logarithm of the odds that two loci are physically linked rather than unlinked
(B) Total number of recombinants observed
(C) Linear distance between a marker and a centromere
(D) Exact frequency of double crossovers

2010

297. In DNA fingerprinting for parentage verification, a "null allele" at a microsatellite locus generally refers to:
(A) An allele that fails to amplify during PCR due to a mutation in the primer binding site, potentially causing a false apparent homozygosity
(B) An allele that physically lacks any repetitive sequence
(C) An allele that contains only AT base pairs
(D) A sequence that codes for no known protein

2017

298. F-statistics (e.g., $F_{\{ST\}}$) are utilized extensively in livestock genomics primarily to:
(A) Quantify the degree of genetic differentiation

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9. (B) Semen
Different biological samples possess varying levels of chromatin condensation and structural complexity. Mature sperm cells contain DNA that is extremely tightly packed with protamines instead of the usual histone proteins found in somatic cells. This unique structural arrangement requires more aggressive chemical treatment and specific reducing agents during the lysis step to ensure the complete release and recovery of the genomic DNA.

10. (B) III only
The use of ethylenediaminetetraacetic acid in molecular biology serves to protect nucleic acids by chelating divalent metal ions like magnesium. Because deoxyribonucleases require these ions as essential cofactors for their catalytic activity, sequestering them effectively inhibits enzymatic degradation of the DNA. Therefore, describing this chemical as a cofactor for such enzymes is inaccurate as it functions specifically as an inhibitor.

11. (A) Mechanical shearing of the DNA strands
High-molecular-weight genomic DNA is physically fragile due to its extreme length. When the solution is subjected to intense mechanical forces, such as rapid vortexing, the resulting hydrodynamic stress causes the long double-stranded molecules to break. This fragmentation, known as shearing, results in shorter DNA pieces, which can negatively impact downstream applications like long-read sequencing or the analysis of large fragments.

12. (C) Erythrocytes
Whole blood consists of diverse cell types, but in mammals, only the white blood cells contain nuclei and genomic DNA. Therefore, the first stage of isolation involves removing the more numerous red blood cells. By selectively lysing these cells and removing the released hemoglobin and cytoplasmic proteins, researchers can concentrate the leukocytes, which provide the actual template for the extraction process.

13. (D) Proteins
Purified nucleic acids absorb ultraviolet light at specific wavelengths, and the ratio of these measurements indicates sample cleanliness. An absorbance ratio significantly lower than the standard threshold for DNA suggests the presence of contaminants that absorb strongly at higher wavelengths. Proteins typically exhibit peak absorbance near two hundred eighty nanometers due to aromatic amino acids, leading to a reduced ratio when present.

14. (C) 260 nm
Quantification of nucleic acids relies on the specific absorption of ultraviolet light by the nitrogenous bases. Maximum light absorption for both DNA and RNA occurs at a wavelength of two hundred sixty nanometers. By measuring the amount of light absorbed at this precise point using a spectrophotometer, researchers can accurately calculate the concentration of genetic material in a purified sample.

15. (A) P-2, Q-1, R-4, S-3
Spectrophotometric analysis provides detailed information about the purity and composition of a sample. A ratio of one point eight indicates pure DNA, while a ratio of two point zero suggests pure RNA. Low values at other wavelengths often signify salt or solvent residues. Furthermore, measurements at three hundred twenty nanometers detect light scattering, which points to the presence of particulate matter.

16. (C) 50 micrograms per ml
Spectrophotometry uses the Beer-Lambert law to correlate light absorption with the quantity of a substance in solution. For double-stranded DNA, a standard unit of optical density at two hundred sixty nanometers is equivalent to a specific mass concentration. By convention, an absorbance reading of one corresponds to fifty micrograms of DNA per milliliter, providing a simple conversion for quantification.

NODIA

17. (A) It specifically measures dsDNA without RNA interference
Fluorometric methods use specialized dyes that only emit light when bound to specific molecules. Unlike spectrophotometry, which measures total absorbance of all nucleic acids at two hundred sixty nanometers, fluorometry can distinguish between double-stranded DNA and other contaminants like single-stranded RNA or proteins. This specificity makes it a more accurate choice for quantifying DNA intended for sensitive genomic applications like library preparation.

genome
(D) The rate of mRNA transcription in real time

2016

268. Which enzyme is the catalytic driver of the PRINS (Primed In Situ Labeling) technique?
(A) RNA Polymerase
(B) Taq DNA Polymerase
(C) Reverse Transcriptase
(D) T4 DNA Ligase

2007

269. The principle of Somatic Cell Hybrid mapping assumes that over successive cell culture passages, the hybrid line will:
(A) Preferentially and randomly lose the chromosomes of one specific parent species (e.g., the livestock species in a rodent-livestock hybrid)
(B) Sequentially duplicate its own genome
(C) Undergo massive homologous recombination
(D) Develop complete resistance to HAT medium

2016

270. In Radiation Hybrid mapping, the donor cells are subjected to lethal irradiation. The resulting fragmented chromosomes are then "rescued" by:
(A) Fusion with a non-irradiated recipient rodent cell line
(B) Immediate transformation into competent E. coli
(C) PCR amplification of the entire genome
(D) Capillary electrophoresis

2018

271. When selecting a cloning vector to map an entire large genomic region (e.g., 200 kb), which vector is most appropriate?
(A) Bacterial Artificial Chromosome (BAC)
(B) Standard pUC19
(C) Bacteriophage Lambda
(D) Standard Cosmid

2001

272. In recombinant DNA protocols, T4 DNA ligase functions to repair which specific structural feature of the DNA backbone?
(A) Phosphodiester bonds between a 3'-OH and a 5'-PO4
(B) Hydrogen bonds between base pairs
(C) Disulfide bonds in the major groove
(D) Glycosidic bonds

2007

273. According to Haldane's mapping function, what happens to the relationship between recombination frequency and actual genetic map distance as the distance increases?
(A) The recombination frequency underestimates the true map distance due to undetected double crossovers
(B) They remain strictly identical and linear indefinitely
(C) The genetic distance physically shrinks
(D) The recombination frequency exceeds 100%

2017

274. In quantitative trait locus (QTL) mapping, Linkage Disequilibrium (LD) is heavily utilized. LD is best described as:
(A) A statistical correlation between specific alleles at two distinct loci
(B) The complete physical separation of two linked genes
(C) The mutation of a microsatellite marker
(D) A failure in PCR amplification

2022

275. For forensic DNA analysis, what is the primary benefit of depositing biological samples onto specialized FTA paper cards?
(A) It facilitates immediate cell lysis and firmly binds the DNA, preventing degradation by nucleases and microbes during room-temperature storage
(B) It automatically sizes the DNA fragments
(C) It enhances the activity of restriction enzymes
(D) It sequences the DNA by chemical degradation

2014

276. In parentage testing using microsatellites, a sire can be definitively excluded if:
(A) The offspring possesses obligate paternal alleles at multiple loci that are entirely absent in the alleged sire's genotype
(B) The offspring and sire share 99% of alleles across all loci
(C) The offspring is heterozygous at all tested loci
(D) The sire is homozygous at all tested loci

2004

277. The FAO/ISAG recommended marker panels for defining genetic diversity in livestock breeds primarily consist of:
(A) Standardized panels of highly polymorphic Short Tandem Repeats (microsatellites)
(B) Morphological trait scores
(C) Complete mitochondrial genome sequences

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27. (A) To monitor the progress of the electrophoretic run
Tracking dyes are small, colored molecules added to the sample buffer before loading. Because they migrate at predictable rates through the gel alongside DNA, they allow researchers to visually monitor the progress of the electrophoresis without exposing the gel to ultraviolet light. These dyes ensure that the run is stopped before the smaller DNA fragments reach the end of the gel.

28. (C) GelRed
Traditional methods for visualizing DNA in gels utilize ethidium bromide, which is a potent mutagen. Modern alternatives like GelRed have been developed to offer similar sensitivity with a safer profile. These dyes are designed to be much larger and more polar, preventing them from crossing cell membranes easily. They function by intercalating into the DNA double helix and fluorescing under ultraviolet light.

29. (D) Resolving small DNA fragments
The resolution of a gel is determined by the size of the pores within the agarose matrix. Increasing the concentration of agarose creates a denser network with smaller pores, which provides better resistance for separating very small DNA fragments or PCR products. Conversely, lower concentrations are used when the goal is to allow larger genomic fragments to migrate and separate effectively.

30. (A) I, II and IV
DNA carries a net negative charge and naturally moves toward the positive anode when placed in an electric field. The choice of buffer and additives also influences the result; TBE provides superior buffering for long runs, while glycerol increases sample density to ensure it sinks into the well. High voltage, however, usually decreases resolution for very large fragments by causing smearing.

31. (B) Negative, due to the phosphate backbone
The chemical structure of DNA consists of a backbone made of alternating sugar and phosphate groups. Each phosphate group carries a negative charge at physiological and standard electrophoretic pH levels. This consistent negative charge along the entire length of the molecule allows DNA to migrate predictably toward the positive electrode in an electric field, regardless of the specific sequence of bases.

32. (D) Smearing due to thermal gradient formation
Applying excessive voltage during electrophoresis generates significant heat within the gel and buffer. This temperature increase can cause the agarose matrix to soften and creates uneven thermal gradients that disrupt the uniform movement of the DNA bands. As a result, the fragments do not migrate in tight groups, leading to blurred or smeared results that are difficult to interpret accurately.

33. (A) Intercalated between the nitrogenous bases of double-stranded DNA
Ethidium bromide is a fluorescent dye whose emission properties change based on its environment. When the molecule is free in an aqueous solution, its fluorescence is relatively weak. However, when it wedges itself between the stacked bases of a double-stranded DNA molecule, the hydrophobic environment significantly enhances its fluorescence. This property allows for the specific visualization of DNA bands within a gel.

34. (C) TBE is preferred for smaller fragments due to better resolving power
The selection of an electrophoresis buffer depends on the size of the DNA fragments being analyzed. TBE buffer interacts with the agarose matrix to create smaller effective pore sizes, which provides superior resolution for small fragments like PCR amplicons. While TAE is better for large genomic DNA, TBE is the standard choice for high-resolution analysis of short, specific amplification products.

35. (A) P-3, Q-1, R-4, S-2
Restriction endonucleases are categorized based on their subunit composition and cleavage behavior. Type one enzymes cut randomly at a distance from their recognition site, while Type two enzymes are most useful because they cleave precisely within the target sequence. Type three enzymes cut a short distance away, and Type four enzymes specifically target DNA that has undergone chemical modifications like methylation.

36. (B) Type II
Recombinant DNA technology relies on the ability to cut DNA at predictable and specific

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18. (C) Guanidine thiocyanate
The secondary purity ratio comparing absorbance at two hundred sixty and two hundred thirty nanometers is highly sensitive to extraction reagents. Contaminants such as carbohydrates, salts, and chaotropic agents used during lysis typically absorb light strongly at the shorter wavelength. A low ratio often suggests that residues like guanidine thiocyanate from the purification process remain in the final DNA or RNA sample.

19. (D) 320 nm
Particulate matter and bubbles in a sample cause light to scatter rather than being absorbed by the target molecules. Because nucleic acids do not absorb light at three hundred twenty nanometers, any reading at this wavelength is considered background noise or scattering. Subtracting this value from the primary absorbance measurements helps researchers correct for these physical artifacts and obtain more accurate concentrations.

20. (B) Prepare standard curve, add dye to unknown, incubate, measure fluorescence
Quantification through fluorescence requires comparing the emission of an unknown sample to known references. The process begins by creating a standard curve using samples of precise concentrations. After mixing the fluorescent dye with the unknown and allowing it to bind, the intensity of the light emitted is measured. This value is then interpolated on the curve to determine the concentration.

21. (B) PicoGreen
Highly sensitive quantification of double-stranded DNA is often achieved using specialized fluorophores. PicoGreen is an asymmetrical cyanine dye that exhibits a massive increase in fluorescence intensity upon binding to double-stranded molecules. Because it ignores single-stranded RNA and free nucleotides, it provides an exceptionally accurate measurement of DNA quantity, even in samples containing significant amounts of common laboratory contaminants.

22. (C) Presence of free nucleotides or single-stranded RNA
Spectrophotometric quantification at two hundred sixty nanometers is not specific to intact genomic DNA. All nitrogenous bases, including those found in degraded RNA fragments and individual nucleotides, absorb light at this wavelength. Therefore, if a sample contains significant RNA contamination or has undergone degradation, the total absorbance will be higher than the actual DNA concentration would normally suggest.

23. (D) The sample is predominantly RNA
The absorbance ratio at two60 and two80 nanometers serves as a primary indicator of nucleic acid purity. While pure double-stranded DNA typically yields a ratio around one point eight, pure RNA exhibits a higher ratio, often exceeding two point zero. Consequently, a reading of two point one strongly suggests that the preparation is heavily contaminated with or consists mostly of RNA.

24. (A) Single-stranded molecules lack base-stacking shielding effects
Nucleic acids exhibit ultraviolet absorption due to the conjugated double bond systems within their nitrogenous bases. Double-stranded DNA molecules show lower absorbance than single-stranded molecules like RNA because the stacked arrangement of base pairs in the double helix shields the chromophores. This phenomenon, known as the hypochromic effect, results in RNA absorbing more light per unit mass than native double-stranded genomic DNA.

25. (B) Both A and R are true but R is not the correct explanation of A.
Different buffering systems impact the resolution and migration speed of DNA during electrophoresis. While TAE is preferred for separating large fragments, this property is primarily related to its lower ionic strength and the way it interacts with the gel matrix, rather than its buffering capacity. TBE offers better stability and resolution for smaller fragments but can inhibit certain downstream enzymatic reactions.

26. (B) Molecular weight
During agarose gel electrophoresis, the gel matrix acts as a molecular sieve through which DNA molecules must pass. Since all DNA molecules possess a nearly identical negative charge-to-mass ratio, their migration speed is determined by their physical size. Smaller fragments move more easily through the pores, while larger molecules are more hindered, allowing separation based solely on their overall length.

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They are more durable, less prone to tearing when wet, and possess a higher binding capacity for nucleic acids. Furthermore, nylon membranes can withstand the harsh conditions required to remove a probe, allowing the same blot to be reused multiple times for different targets.

46. (C) To denature the double-stranded DNA into single strands
Successful hybridization in Southern blotting requires that the target DNA on the membrane be accessible to the probe. Because the DNA in the gel is double-stranded, it must be treated with a strong base like sodium hydroxide. This alkali treatment breaks the hydrogen bonds between base pairs, converting the DNA into single strands that can then bind to the labeled probe.

47. (B) Capillary blotting
Capillary transfer is a traditional method for moving DNA from an electrophoresis gel to a membrane. It uses the flow of a concentrated salt buffer, which is drawn upward through the gel and membrane by a stack of dry paper towels. As the buffer moves, it carries the DNA fragments out of the gel and traps them onto the surface of the membrane.

48. (D) Antibody-enzyme conjugates and colorimetric/chemiluminescent substrates
Non-radioactive detection systems utilize chemical labels that can be recognized by specific binding proteins. Digoxigenin is a common hapten used to label DNA probes. Once the probe hybridizes to the target, it is detected using an anti-digoxigenin antibody conjugated to an enzyme. This enzyme then processes a substrate to produce a visible color or a light signal that can be captured.

49. (A) It fragments large DNA to facilitate efficient transfer from the gel to the membrane
High-molecular-weight DNA fragments move very slowly out of an agarose gel during the blotting process. Treating the gel with a dilute acid causes depurination, which weakens the DNA backbone. Subsequent treatment with a base then breaks the DNA at these points. This fragmentation reduces the size of the fragments, allowing them to transfer to the membrane much more rapidly and efficiently.

50. (B) I, II and III
Designing effective PCR primers involves balancing several physical and chemical properties. Ideal primers should have a moderate GC content and matching melting temperatures to ensure they bind efficiently under the same conditions. It is also critical to avoid complementary sequences that could cause the primers to bind to each other. Overly long primers or those with weak three-prime ends are generally avoided.

51. (A) By baking at 80 degrees Celsius or UV crosslinking
Once DNA has been transferred to a membrane, it must be permanently attached to prevent it from washing away during the hybridization steps. This fixation is achieved by exposing the membrane to ultraviolet light, which creates covalent bonds between the DNA and the membrane, or by heating it. These methods ensure the genetic material remains localized on the surface throughout the procedure.

52. (D) Positively charged nylon
Different membrane materials exhibit varying affinities for nucleic acids. Positively charged nylon membranes are particularly effective because they utilize both hydrophobic interactions and ionic attraction to the negatively charged DNA backbone. This dual binding mechanism results in a very high binding capacity, making them ideal for detecting low-abundance sequences in Southern and Northern blotting applications.

53. (B) Reduce non-specific background binding of the probe to the membrane
Membranes used in blotting are designed to bind nucleic acids with high affinity. To prevent the labeled probe from sticking randomly to the empty spaces on the membrane, a blocking step is performed using non-specific DNA or proteins. This ensures that the probe only remains on the membrane where it has found a perfectly complementary target sequence, significantly improving the signal-to-noise ratio.

54. (B) 1.5 to 2.5 mM
Magnesium ions are essential for the catalytic activity of DNA polymerase and influence the stability of primer-template interactions. In most standard PCR reactions, the concentration of these ions is carefully optimized within a narrow range. Too little magnesium results in

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92. (C) rob(1;29)
Chromosomal abnormalities are described using a standardized international nomenclature. A Robertsonian translocation is a specific type of rearrangement where two acrocentric chromosomes fuse at their centromeres to form a single larger chromosome. This is a common and important finding in cattle, particularly involving chromosomes one and twenty-nine, and is correctly denoted by the prefix that identifies the type of translocation.

93. (D) GC-rich
R-banding, or reverse banding, provides a pattern that is the inverse of the more common G-banding. This technique involves heat treatment that specifically denatures the AT-rich regions of the chromosomes. When the slides are then stained, the remaining GC-rich regions appear as dark bands. This method is particularly useful for studying the ends of chromosomes, which are often rich in genes and GC content.

94. (C) Inversion
Structural changes in chromosomes can take many forms, depending on how the DNA segments are rearranged. An inversion occurs when a single chromosome breaks in two places and the segment between the breaks is reinserted in the opposite orientation. While the total amount of genetic material remains the same, this rearrangement can disrupt genes and lead to problems during meiosis and reproduction.

95. (A) P-4, Q-3, R-1, S-2
Different types of fluorescent probes are used to investigate various aspects of chromosome structure and number. Whole-chromosome paints can identify complex rearrangements, while centromeric probes are used to count specific chromosomes. Locus-specific probes can detect the loss or gain of individual genes, and telomeric probes help identify deletions at the ends of chromosomes. Together, these tools provide a detailed map of genomic health.

96. (D) Detects specific nucleic acid sequences rather than general chromatin density
Conventional banding techniques rely on the general properties of chromatin to produce patterns. In contrast, FISH utilizes the specificity of DNA hybridization. By using a labeled probe with a known sequence, researchers can pinpoint the exact physical location of a gene or DNA segment on a chromosome. This provides much higher resolution and allows for the detection of very small genetic changes.

97. (A) To denature the double-stranded DNA into single strands
Successful hybridization in any technique requires that the target DNA and the probe be able to bind to each other. Because both are naturally double-stranded, they must be separated into single strands using heat. This denaturation step is a critical part of the procedure, as it allows the complementary sequences to find each other and form a stable hybrid when the temperature is lowered.

98. (C) Formamide
The temperature required to separate DNA strands is often high enough to damage the delicate structure of chromosomes on a slide. Formamide is added to the hybridization buffer to lower the melting temperature of the DNA. This allows researchers to perform the denaturation and hybridization steps at lower temperatures, which preserves the physical integrity of the chromosomes while still ensuring efficient probe binding.

99. (A) Suppress non-specific binding of the probe to repetitive genomic sequences
Many parts of the genome contain highly repetitive sequences that can cause probes to bind non-specifically. To prevent this, researchers use blocking DNA, such as the Cot-one fraction, which is enriched for these repetitive elements. This DNA binds to the repetitive sequences on the probe and the target, ensuring that the remaining probe only hybridizes to the specific, unique target of interest.

100. (A) I, II, III and V
PRINS is a modern alternative to traditional hybridization methods that utilizes the power of DNA polymerase. This technique uses short, unlabeled primers that bind to a specific target in the genome. The enzyme then extends these primers on the slide, incorporating labeled nucleotides directly at the target site. This method is often faster and can be more sensitive than using large, pre-labeled probes.

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64. (C) Three
In a standard diallelic system, there are two possible versions of a gene. An individual can be homozygous for either allele or heterozygous, possessing one of each. When the PCR products are digested, the two homozygous types will each produce a single distinct pattern. The heterozygote will contain both versions of the DNA, resulting in a unique composite pattern that includes all possible fragments.

65. (A) Both A and R are true and R is the correct explanation of A.
Heterozygous individuals possess two different versions of a genetic locus on their homologous chromosomes. During PCR-RFLP, both alleles are amplified simultaneously. When the resulting mixture of DNA is treated with a restriction enzyme, the allele with the site will be cut while the other remains intact. This produces a banding pattern that contains fragments from both the cleaved and uncleaved versions.

66. (C) Two bands of 250 bp each (appearing as one thick band)
When a restriction enzyme cuts a DNA fragment exactly in the middle, it produces two new fragments of equal length. In an electrophoresis gel, fragments move based on their size. Since both resulting pieces are identical in weight, they will migrate to the same position. This often results in a single, unusually bright or thick band that represents the total mass of both fragments.

67. (A) Insufficient restriction enzyme concentration or incubation time
Complete digestion is essential for accurate genotyping in RFLP assays. If the reaction conditions are not optimal, such as having too little enzyme or not allowing enough time for the reaction, some of the DNA molecules may remain uncut. This results in the presence of both the original fragment and the digestion products in the same sample, which can lead to incorrect interpretations.

68. (D) Polyacrylamide gel
Agarose gels are excellent for separating large DNA fragments but lack the resolution needed for very small differences. Polyacrylamide gels have much smaller and more uniform pores, which allows them to resolve DNA fragments that differ by only a few nucleotides. This high level of precision makes them the preferred choice for detailed analysis of small restriction fragments and sequencing products.

69. (B) It cleaves one allele but leaves the alternative allele intact
The goal of a PCR-RFLP assay is to distinguish between different genetic variants. To achieve this, the selected restriction enzyme must be sensitive to the mutation of interest. Ideally, the enzyme should recognize a sequence that is present in one version of the gene but absent in the other. This ensures that the two alleles produce clearly different patterns after the digestion step.

70. (B) I and III
PCR-RFLP is a cost-effective and straightforward method for genotyping known polymorphisms. It relies on the use of specific restriction enzymes to detect changes in DNA sequences. Unlike some modern techniques, it does not require expensive fluorescent probes or specialized equipment, as the results can be easily visualized on a standard agarose gel after amplification and enzymatic digestion have been completed.

71. (D) The sensitivity of the DNA intercalating dye used
The ability to see the results of a PCR-RFLP assay depends on the visualization method. While the PCR process can produce many copies of the DNA, the final bands must be bright enough to be detected. The sensitivity of the dye used to stain the DNA, such as ethidium bromide, determines the minimum amount of DNA required for a band to be visible.

72. (A) Dideoxynucleotide triphosphate (ddNTP)
Sanger sequencing utilizes specialized nucleotides to stop the growth of a DNA chain at specific points. These dideoxynucleotides are added to the reaction in small amounts alongside standard nucleotides. When the DNA polymerase incorporates one of these modified bases into the growing strand, the synthesis reaction is terminated, resulting in a collection of fragments of varying lengths that represent the sequence.

73. (C) 3' hydroxyl group
DNA synthesis requires a specific chemical group at the end of the growing strand to form a bond with the next nucleotide. Dideoxynucleotides are specifically engineered to lack this hydroxyl group at the three-prime position. Once a

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modified nucleotide is added, there is no place for the next base to attach, which effectively stops the elongation of that particular DNA molecule during sequencing.

74. (B) Illumina
Modern high-throughput sequencing often uses a method where the sequence is read as it is being built. Illumina technology utilizes reversible terminators that allow only a single fluorescently labeled nucleotide to be added at a time. After the color is recorded, the terminator is chemically removed, allowing the next base to be added. This cycle is repeated millions of times simultaneously.

75. (A) P-3, Q-1, R-2, S-4
Different sequencing technologies utilize unique chemical and physical principles to decode genetic information. Sanger sequencing relies on fragment separation by size, while pyrosequencing and Ion Torrent detect chemical byproducts of nucleotide incorporation like light or pH changes. Advanced single-molecule methods like PacBio monitor the activity of individual polymerase molecules in real time to generate exceptionally long sequence reads for genomic analysis.

76. (C) Produce long reads for resolving complex genomic repeats
Long-read sequencing technologies provide a significant advantage for assembling complex genomes. Many livestock species have repetitive regions that are difficult to resolve using short reads. PacBio technology generates much longer sequences, which can span across these repeats and provide a more accurate scaffold for the entire genome. This helps researchers better understand the structure and variation of the livestock genetic map.

77. (D) The average number of times a specific genomic nucleotide is sequenced
In next-generation sequencing, the accuracy of the results depends on how many times each base is read. Read depth refers to the total number of overlapping sequences that cover a particular position in the genome. Higher coverage provides greater confidence in the data, as it allows researchers to distinguish between real genetic variations and random errors made during the sequencing process.

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78. (C) ATP sulfurylase and luciferase
Pyrosequencing is a method that detects the release of a specific byproduct when a nucleotide is added to a DNA strand. This byproduct is converted into light through a series of enzymatic reactions. The intensity of the light produced is proportional to the number of nucleotides incorporated, allowing researchers to determine the sequence in real time without the need for electrophoresis.

79. (B) Illumina
Illumina sequencing requires the amplification of DNA fragments into dense clusters on a solid surface. This is achieved through bridge amplification, where the DNA strands bend over and bind to nearby adapters on the flow cell. This localized replication creates millions of identical copies in a small area, ensuring that the fluorescent signal produced during sequencing is strong enough to be detected.

80. (A) I, II, III, IV
The workflow for Illumina sequencing follows a series of integrated steps. It begins with the preparation of a DNA library, where fragments are tagged with specific adapters. These fragments are then amplified into clusters on a flow cell. The actual sequencing occurs as fluorescent nucleotides are added, and the resulting data is finally processed using computational tools to reconstruct the genome.

81. (A) Arrest cells in metaphase by inhibiting spindle fiber formation
Cytogenetic analysis requires a high frequency of cells in a specific stage of division where chromosomes are most condensed. Colchicine acts as an antimitotic agent by binding to tubulin subunits, which effectively prevents the assembly of the mitotic spindle apparatus. This interference arrests the cell cycle at metaphase, allowing researchers to collect and visualize a large number of clearly defined chromosomal spreads.

82. (C) Phytohemagglutinin (PHA)
Lymphocytes in the blood are normally in a resting state and do not divide. To study their chromosomes, they must be stimulated to enter the cell cycle. Phytohemagglutinin is a powerful mitogen that specifically targets T-cells, triggering them to undergo mitosis. This ensures that there are enough dividing cells in

the culture to provide the metaphase spreads needed for karyotyping.

83. (A) To cause cells to swell, aiding in chromosome spreading upon dropping
Before chromosomes can be viewed, the cells must be prepared to release them effectively. Treating the cells with a hypotonic solution causes water to move into the cells through osmosis. This swelling increases the internal volume and separates the chromosomes from each other. When these swollen cells are later dropped onto a slide, they burst easily, resulting in well-spread chromosome clusters.

84. (D) Methanol and Glacial Acetic Acid
Fixation is a critical step in preserving the structure of cells and chromosomes for microscopy. Carnoy's fixative is a standard reagent used in cytogenetics, consisting of a mixture of methanol and acetic acid. This solution rapidly penetrates the cells, denaturing proteins and stabilizing the chromatin. It also helps to dehydrate the cells, which is essential for obtaining high-quality chromosome spreads.

85. (A) Both A and R are true and R is the correct explanation of A.
The technique used to place fixed cells onto a microscope slide significantly impacts the quality of the chromosome spread. By dropping the cell suspension from a height onto a cold, wet slide, the mechanical impact and the rapid change in environment cause the swollen cells to burst. This spreads the chromosomes across the slide, preventing them from overlapping and making them easier to analyze.

86. (C) They can be analyzed directly without prior in vitro culture stimulation
Different tissues have different rates of natural cell division. While lymphocytes must be stimulated to divide, bone marrow contains a high proportion of cells that are already actively undergoing mitosis. This allows researchers to skip the long culture and stimulation steps and proceed directly to harvesting and fixing the cells, making bone marrow an excellent source for rapid cytogenetic analysis.

87. (C) 60
Every species has a characteristic number of chromosomes in its somatic cells. Cattle have thirty pairs of chromosomes, which includes twenty-nine pairs of autosomes and one pair of sex chromosomes. Understanding this standard diploid number is fundamental for identifying chromosomal abnormalities, such as translocations or aneuploidy, which can impact the health and reproductive performance of individual animals in a herd.

88. (A) Trypsin
G-banding is a common technique used to produce a unique pattern of light and dark bands along the length of chromosomes. This is achieved by briefly treating the slides with a proteolytic enzyme like trypsin before staining with Giemsa. The enzyme partially digests the chromosomal proteins, making some regions more accessible to the stain and creating the characteristic banding pattern used for identification.

89. (B) AT-rich, gene-poor, and replicate late
The banding patterns observed on chromosomes reflect differences in DNA composition and structure. Dark G-bands are generally composed of DNA that is rich in adenine and thymine and has a lower density of active genes. These regions also tend to replicate later during the cell cycle. In contrast, the lighter bands are richer in guanine and cytosine and contain more active genes.

90. (A) I, II and III
Various banding techniques provide different types of information about chromosome structure. While G-banding is the most common for identifying overall structure, R-banding provides an opposite pattern, and C-banding specifically targets the dense heterochromatin at centromeres. Q-banding uses fluorescence to highlight specific regions. Together, these methods allow cytogeneticists to detect a wide range of structural and numerical abnormalities in the genome.

91. (A) Q-banding
Some chromosomal regions exhibit unique fluorescent properties when treated with specific stains. Q-banding uses a fluorescent dye that binds more strongly to certain types of DNA. In many mammalian species, the Y chromosome contains large blocks of heterochromatin that fluoresce very brightly. This makes Q-banding an exceptionally useful tool for rapidly identifying the male sex chromosome and studying its structural variation.

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low enzyme activity and poor yield, while too much can lead to non-specific amplification and the formation of unwanted products.

55. (A) P-4, Q-3, R-2, S-1
Every component in a PCR reaction serves a distinct and vital role in the amplification process. The nucleotides provide the raw material for the new DNA, while the polymerase acts as the molecular machine that assembles them. Magnesium serves as a necessary cofactor for the enzyme, and the buffer maintains the optimal chemical environment for the reaction to occur successfully.

56. (C) 94-98 degrees Celsius
The first step in every PCR cycle involves separating the double-stranded DNA template into single strands. This denaturation is achieved by heating the reaction mixture to near-boiling temperatures. At this level, the hydrogen bonds holding the two strands together are broken, providing the single-stranded templates required for the primers to bind and the polymerase to begin synthesis in subsequent steps.

57. (B) Reduction in the yield of the desired target amplicon
Primer-dimers occur when the primers in a PCR reaction bind to each other rather than the template. Because these small complexes are easily amplified, they consume a significant portion of the reaction's resources, including nucleotides and enzyme. This competition effectively starves the intended target reaction, resulting in a much lower yield of the specific DNA fragment the researcher is trying to amplify.

58. (B) Estimating the melting temperature of short oligonucleotides
The Wallace formula provides a quick and simple way to estimate the temperature at which a short DNA sequence will dissociate. It accounts for the fact that guanine-cytosine pairs have three hydrogen bonds and are more stable than adenine-thymine pairs, which have only two. This estimation is critical for selecting the appropriate annealing temperature for primers during the polymerase chain reaction.

59. (A) Non-specific amplification and multiple banding occur
The annealing temperature in PCR determines the stringency of primer binding. If this temperature is too low, the primers may bind to sequences that are only partially complementary to their target. This leads to the amplification of unintended regions of the genome, appearing as multiple bands or a smear on a gel, which complicates the interpretation of the experimental results.

60. (B) Baseline phase, Exponential phase, Linear phase, Plateau phase
Real-time PCR follows a predictable progression of amplification that can be visualized as a plot. It starts with a baseline phase where the signal is below the detection limit. This is followed by an exponential phase of rapid doubling, a linear phase where resources begin to dwindle, and finally a plateau phase where the reaction stops due to component depletion.

61. (D) 3' to 5' exonuclease proofreading activity
Fidelity in DNA synthesis depends on the ability of the polymerase to identify and correct errors. Taq polymerase is highly efficient at high temperatures but lacks the specific proofreading activity required to remove mismatched nucleotides. Without this ability, it cannot correct mistakes made during elongation, leading to a higher frequency of mutations in the final PCR product compared to more specialized enzymes.

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62. (C) Dimethyl sulfoxide (DMSO)
Some DNA templates are difficult to amplify because they contain high levels of guanine and cytosine, which form strong secondary structures. Additives like dimethyl sulfoxide are used to facilitate the denaturation of these regions. DMSO lowers the melting temperature of the DNA, helping the strands separate and allowing the primers and polymerase to access the template more easily during the PCR process.

63. (B) The polymorphism must create or abolish a restriction enzyme recognition site
RFLP analysis uses the specificity of restriction enzymes to detect genetic variations. For a single nucleotide polymorphism to be detectable by this method, the change in the DNA sequence must occur exactly within the recognition site of an enzyme. If the mutation alters the site so the enzyme no longer recognizes it, the resulting digestion pattern will differ between the various genotypes.

101. (B) FISH uses pre-labeled probes, while PRINS utilizes a polymerase to incorporate labeled nucleotides in situ
While both methods are used to visualize specific DNA sequences on chromosomes, they rely on different biological principles. Traditional hybridization uses large probes that are labeled before they are added to the slide. In contrast, the newer approach uses the activity of an enzyme to build a labeled product directly on the chromosomal target, providing a different way to detect and study genomic features.

102. (C) Polyethylene glycol (PEG)
Creating hybrid cell lines requires the physical fusion of membranes from two different cells. Polyethylene glycol is a chemical agent commonly used for this purpose. It works by bringing the cell membranes into close contact and altering their structure, which facilitates their merging into a single cell. This technique is fundamental for creating the somatic cell hybrids used in early genome mapping studies.

103. (D) Chromosomes of one species (e.g., livestock) are randomly lost in the hybrid, allowing correlation of marker retention
Somatic cell hybrid mapping relies on the unique behavior of hybrid cells during culture. When cells from two different species are fused, the chromosomes of one species are often gradually and randomly lost over time. By analyzing which livestock chromosomes remain in different cell lines and comparing this to the presence of specific genetic markers, researchers can assign those markers to particular chromosomes.

104. (A) HAT (Hypoxanthine-Aminopterin-Thymidine) medium
After a cell fusion experiment, it is necessary to separate the hybrid cells from the parental cells that did not fuse. HAT medium is a specialized selective environment that blocks the normal pathway for DNA synthesis. Only cells that can use an alternative pathway, which requires specific enzymes provided by both parental lines, can survive. This ensures that only the desired hybrid cells grow in the culture.

105. (A) I only
Somatic cell hybrid mapping is a powerful tool for determining which genes are located on the same chromosome, a property known as synteny. While it is excellent for physical mapping and assigning markers to chromosomes, it does not provide the precise number of base pairs between them. Other techniques, like sequencing or radiation hybrid mapping, are needed to determine the exact physical distances in the genome.

106. (B) Uses lethal doses of X-rays or gamma rays to fragment the donor genome before fusion
Radiation hybrid mapping is a variation of somatic cell genetics that provides higher resolution. Instead of relying on the natural loss of whole chromosomes, the donor cells are treated with radiation to break the DNA into many small fragments. These fragments are then incorporated into the recipient cells. This allows researchers to map markers that are much closer together on the same chromosome.

107. (A) The dosage of radiation applied to the donor cells
The precision of a radiation hybrid map is determined by the size of the DNA fragments generated. Higher doses of radiation cause more breaks in the DNA, resulting in smaller fragments. This allows researchers to distinguish between markers that are located very close to each other. By carefully selecting the radiation dose, the resolution of the map can be tailored to the specific research needs.

108. (C) Co-retention of the markers in the hybrid panel
In radiation hybrid mapping, the distance between two genetic markers is estimated by how often they are found together in the same cell lines. If two markers are very close together on the chromosome, they are likely to remain on the same fragment after radiation and will be retained together. If they are far apart, they are more likely to be separated.

109. (D) CentiRays (cR)
Every type of genetic map has its own unit of measurement. While linkage maps use centiMorgans based on recombination frequencies, radiation hybrid maps use centiRays. This unit represents the probability that a specific dose of radiation will cause a break in the DNA between two markers. These maps provide a physical representation of the genome that is independent of meiotic crossing over.

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110. (A) I, II and III
Cloning vectors are specialized DNA molecules used to carry and replicate foreign DNA in a host cell. Different vectors have different capacities, ranging from small plasmids to very large yeast artificial chromosomes. Cosmids and bacterial artificial chromosomes provide intermediate options. Each type of vector is selected based on the size of the DNA fragment being studied and the specific requirements of the experiment.

111. (A) The copy number of the plasmid in the host cell
The origin of replication is a specific DNA sequence that controls the replication of a plasmid within a bacterium. This sequence determines how many copies of the plasmid will be produced in each cell. Some origins lead to a high copy number, which is useful for producing large amounts of DNA, while others result in a low copy number, which may be necessary.

112. (C) Bacteriophage lambda
Cosmids are hybrid vectors designed to combine the best features of plasmids and viruses. They contain the basic elements of a plasmid, such as an origin of replication and antibiotic resistance, but also include specific sequences from a bacteriophage. These sequences allow the DNA to be packaged into viral particles, which provides an efficient way to introduce large DNA fragments into bacterial cells.

113. (C) Bacterial Artificial Chromosome (BAC)
Mapping and sequencing large mammalian genomes requires vectors that can carry very large pieces of DNA stably. Bacterial artificial chromosomes are the preferred choice for this task. They are based on a specific plasmid system that allows for the cloning of fragments several hundred thousand base pairs long. This makes them ideal for creating genomic libraries and studying large-scale genomic structure.

114. (D) Have been treated to uptake extracellular plasmid DNA
Bacteria do not naturally take up large DNA molecules from their environment very efficiently. To make them more receptive, they must be treated with chemicals or electricity to alter their cell walls and membranes. These treated cells are referred to as competent. Once they are in this state, researchers can introduce recombinant plasmids into them through a process known as transformation.

115. (C) IV only
Introducing foreign DNA into bacteria involves several physical and chemical steps. Chemicals like calcium chloride help the DNA bind to the cell surface, while heat shock or electricity creates temporary openings for the DNA to enter. These methods are highly efficient but do not cause the DNA to leave the cell. Electroporation is often the most effective method for achieving high transformation rates.

116. (B) Beta-galactosidase gene (lacZ)
Blue-white screening is a common method for identifying bacteria that have successfully taken up a recombinant plasmid. The vector contains a specific gene that produces an enzyme capable of turning a substrate blue. When a foreign DNA fragment is inserted into this gene, it is disrupted and no longer produces the active enzyme. This allows researchers to visually distinguish between recombinant and non-recombinant colonies.

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117. (C) Host cells containing the recombinant vector with an insert
In the blue-white screening system, the color of a bacterial colony indicates whether the plasmid it contains has been successfully modified. If the plasmid is intact, the enzyme it produces will turn the colony blue. If a foreign DNA fragment has been inserted, the gene is broken, the enzyme is not produced, and the colony remains white. This provides a simple way to identify.

118. (C) Beta-galactosidase
The visual signal in blue-white screening is produced by the action of a specific enzyme on a chemical substrate. Beta-galactosidase is the enzyme involved, and it naturally breaks down lactose. In the laboratory, it is used to cleave a synthetic molecule called X-gal. When this molecule is broken, it produces a blue pigment that colors the bacterial colony, providing a clear marker for gene activity.

119. (B) 0.5 (50%)
Recombination frequency is a measure of how often two genes are separated during meiosis. Even if two genes are at opposite ends of a very long chromosome, they will only appear to segregate independently half of the time. This is because crossing over occurs randomly,

and multiple crossovers can restore the original combination of alleles. Therefore, the maximum frequency of observed recombination is fifty percent.

120. (A) Linkage is 1000 times more likely than independent assortment
A LOD score is a statistical value used to determine the likelihood of genetic linkage. It is calculated as the base-ten logarithm of the ratio of the probability that two markers are linked versus the probability that they are not. A score of three means that the evidence for linkage is one thousand times stronger than the evidence for independent assortment, which is standard threshold.

121. (B) Haldane function
Mapping functions are used to convert observed recombination frequencies into actual genetic distances on a chromosome. Because double crossovers can hide some of the recombination events, the relationship between frequency and distance is not perfectly linear. The Haldane function was the first to account for this by assuming that crossovers occur randomly and independently along the length of the chromosome.

122. (B) The non-random association of alleles at two or more loci in a population
In a perfectly random population, the alleles at different genetic positions would be inherited independently. However, some combinations of alleles are found together more or less often than expected by chance. This phenomenon, known as linkage disequilibrium, occurs when genes are physically close together on a chromosome or when other factors like selection or population history favor certain allele combinations.

123. (B) Single Nucleotide Polymorphisms (SNPs)
Modern genomics relies on markers that are abundant throughout the genome and can be analyzed easily in large numbers. Single nucleotide polymorphisms are the most common type of genetic variation, involving a change in just one base pair. Because they are so frequent and their analysis can be highly automated, they have become the primary tool for genome-wide association studies.

124. (B) Chelates $Mg^{\{2+\}}$ and $Ca^{\{2+\}}$ ions, inhibiting endogenous DNase activity
Protecting DNA from degradation is essential for any molecular analysis. When blood is collected, the cells release various enzymes that can break down nucleic acids. EDTA is added as an anticoagulant because it binds to metal ions that these enzymes need to function. By removing these essential cofactors, EDTA effectively shuts down the activity of nucleases, ensuring the genomic DNA remains intact.

125. (A) Both A and R are true and R is the correct explanation of A.
Collecting and storing DNA samples in the field can be challenging, especially without reliable refrigeration. FTA cards provide a simple solution by using specialized paper treated with chemicals that lyse cells and stabilize nucleic acids upon contact. The DNA becomes trapped in the fibers of the paper, where it is protected from environmental damage, allowing the samples to be stored.

126. (B) A documented, unbroken record of sample possession from collection to analysis
In forensic science, the integrity of the evidence is paramount. The chain of custody is a formal process used to track every person who has handled a sample from the time it was collected until it is presented in court. This documentation ensures that the evidence has not been tampered with or contaminated, providing the legal foundation for the DNA results.

127. (B) High levels of length polymorphism and heterozygosity in populations
Microsatellites are short sequences of DNA that are repeated many times. The number of repeats varies greatly between individuals, making them highly polymorphic. Because an animal inherits one version of each microsatellite from each parent, these markers are exceptionally useful for identifying individuals and verifying parentage. Their high level of variation ensures that most individuals in a population will have a unique profile.

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128. (B) The alleged sire is excluded as the biological father
Parentage testing is based on the simple principle that an offspring must inherit all of its genetic markers from its biological parents. If a multi-locus DNA profile shows that the offspring has

an allele that is not present in either the mother or the alleged sire, then the sire cannot be the true biological father, provided that no mutation has occurred.

129. (B) A standardized panel of highly polymorphic microsatellite loci
International organizations have established standardized methods for describing the genetic makeup of livestock breeds. These methods rely on a specific set of microsatellite markers that have been chosen for their high level of variation and reliability. By using the same markers across different studies, researchers can compare the genetic diversity of various breeds and monitor the health of animal populations.

130. (D) I, II, and III
Measuring the genetic diversity of a population involves several different statistical tools. Heterozygosity provides a measure of variation within a group, while other statistics like $F_{\{ST\}}$ measure how much different groups vary from each other. Phylogenetic trees can then be used to visualize these relationships, showing how different breeds have evolved and diverged over time from a common ancestor.

131. (B) A decrease in observed heterozygosity
Inbreeding occurs when closely related individuals mate with each other. This process increases the likelihood that an offspring will inherit the same allele from both parents, leading to a higher frequency of homozygous genotypes in the population. As a result, the overall level of heterozygosity decreases, which can reduce the genetic health and resilience of the livestock population over time.

132. (B) The reduction in heterozygosity due to inbreeding within a sub-population
F-statistics are used to partition genetic variation at different levels of a population. The $F_{\{IS\}}$ statistic specifically looks at the variation within an individual sub-population. A high value indicates that there are fewer heterozygotes than expected, which is usually a sign of inbreeding. This information is vital for managing the genetic health of livestock herds and avoiding the negative effects of inbreeding.

133. (B) Phylogenetic tree construction (e.g., Neighbor-Joining trees)
Understanding the evolutionary history of livestock breeds requires analyzing the genetic distances between them. These relationships are often represented visually as a branching diagram known as a phylogenetic tree. By comparing the genetic profiles of different breeds, researchers can determine which ones are most closely related and estimate how long ago they diverged, providing insights into the history of domestication and animal breeding.

134. (B) The conversion of a liquid directly into a glass-like amorphous solid without ice crystallization
Vitrification is a modern approach to cryopreservation that avoids the physical damage caused by ice. Instead of allowing water to freeze into crystals, the sample is cooled so rapidly and in such a high concentration of solutes that it becomes a solid without forming a crystal lattice. This glass-like state preserves the delicate structures of embryos and other cells in a stable.

135. (A) P-1, Q-3, R-2, S-4
Protecting cells during the freezing process requires different types of agents. Some molecules can pass through the cell membrane and protect the internal structures, while others remain outside and provide a protective coating. Substances like glycerol and egg yolk are commonly used in semen extenders to provide both internal and external protection, ensuring the sperm remain viable after they are thawed.

136. (B) Severe osmotic stress and cellular dehydration (solution effect)
The speed at which a sample is cooled during cryopreservation is critical for cell survival. If the cooling rate is too slow, ice forms outside the cells first. This increases the concentration of solutes in the remaining liquid, drawing water out of the cells through osmosis. This extreme dehydration and the resulting chemical stress can damage the cell membranes and internal components.

137. (D) Sucrose
Some cryoprotective agents are designed to work without entering the cell. Sucrose is a large sugar molecule that remains in the extracellular space. It acts by increasing the osmolarity of the surrounding medium, which helps to draw some water out of the cell in a controlled manner and

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provides a protective environment that reduces the stress on the membrane during the freezing.

138. (A) Lowering the freezing point and disrupting crystalline ice lattice formation
Dimethyl sulfoxide is a widely used cryoprotectant because of its ability to penetrate cell membranes and interact with water molecules. By disrupting the formation of a regular ice crystal lattice, it reduces the size and number of ice crystals that form inside the cell. This significantly lowers the risk of physical damage to the organelles and membranes, improving the survival of frozen.

139. (C) -196 degrees Celsius
Long-term storage of biological samples requires extremely low temperatures to stop all metabolic and chemical activity. Liquid nitrogen is the standard medium for this purpose because it is relatively inexpensive and maintains a stable temperature at its boiling point. At nearly two hundred degrees below zero, cells can be stored indefinitely in a state of suspended animation until they are needed.

140. (B) III and V
Maintaining a reliable cryopreservation system requires careful attention to the equipment and procedures. Storage tanks must be properly insulated and handled to maintain their low temperature. When thawing samples, it is important to follow specific protocols to avoid damaging the cells. Understanding the physical properties of liquid nitrogen and the behavior of frozen samples is essential for ensuring the long-term viability.

141. (A) Phase transitions and lateral phase separations of membrane lipids during rapid chilling
Cold shock is a type of cellular damage that occurs when cells are cooled too rapidly before they are actually frozen. This is a significant problem for sperm cells, as the rapid drop in temperature causes the lipids in the cell membrane to change their physical state. This disruption of the membrane structure leads to the loss of cell function and viability even before.

142. (B) Enzyme-labeled primary antibody binding directly to the immobilized antigen
The simplest form of an enzyme-linked immunosorbent assay involves just two main components: an immobilized target and a labeled detector. In this direct format, the primary antibody is modified to carry an enzyme that produces a signal. Because it binds directly to the antigen on the plate, the procedure is fast and requires fewer steps than other more complex ELISA formats.

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143. (C) Sandwich ELISA
For detecting very small amounts of a specific protein, the sandwich format provides the highest level of sensitivity and specificity. This method uses two different antibodies that target different parts of the same antigen. The first antibody captures the target from the sample, and the second, labeled antibody then detects it. This dual recognition ensures that only the intended target is measured.

144. (B) A low concentration of the target hormone in the sample
Competitive assays work differently than other ELISA formats. In this system, the antigen in the sample competes with a labeled version of the same molecule for a limited number of antibody binding sites. If there is a lot of the target in the sample, it will block most of the labeled antigen. Therefore, a strong signal means that very little target was present.

145. (A) Both A and R are true and R is the correct explanation of A.
Indirect ELISA techniques offer a significant advantage in terms of signal intensity. By using an unlabeled primary antibody followed by a labeled secondary antibody, the signal can be amplified. This occurs because multiple secondary antibodies can bind to a single primary antibody, each carrying its own enzyme molecule. This results in a stronger signal and better detection of low-abundance targets.

146. (B) Blue
The visual signal in many common ELISA systems is produced by an enzyme called horseradish peroxidase. When this enzyme reacts with a specific chemical substrate known as TMB, it produces a distinct blue color. This color change indicates the presence and amount of the target molecule in the well, providing a clear and measurable result that can be observed and quantified.

after staining. This system ensures that a finding in one laboratory can be clearly understood and compared to results from other researchers anywhere in the world.

185. (A) Both A and R are true and R is the correct explanation of A.
C-banding is a specialized staining technique that targets the constitutive heterochromatin, which is highly condensed DNA that is not active in gene expression. This material is particularly resistant to the chemical treatments used in the procedure, which allows it to be selectively stained while the rest of the DNA is washed away. This technique is especially useful for.

186. (A) Fluorophore-conjugated dUTPs (e.g., FITC-dUTP)
Fluorescent labeling of DNA probes can be achieved by incorporating modified nucleotides during the synthesis of the probe. These nucleotides are chemically attached to a fluorescent molecule. When the polymerase builds the probe, it includes these modified bases, resulting in a DNA molecule that glows under certain wavelengths of light. This allows for the precise visualization of the probe's target.

187. (C) A complex pool of probes derived from an entire single isolated chromosome
Chromosome painting is a powerful technique for studying genomic rearrangements. It uses a mixture of many different probes that together cover the entire length of a single chromosome. When this mixture is used for hybridization, the entire chromosome glows with a single color. This makes it easy to see if any pieces of that chromosome have moved to other locations.

188. (A) The enzymatic incorporation of labeled nucleotides by Taq polymerase directly onto the slide
PRINS is a modern alternative to traditional hybridization methods that utilizes the power of DNA polymerase. This technique uses short, unlabeled primers that bind to a specific target in the genome. The enzyme then extends these primers on the slide, incorporating labeled nucleotides directly at the target site. This method is often faster and can be more sensitive than traditional probes.

189. (A) The ability to map genes without finding polymorphic variants within the livestock species
Somatic cell hybrid mapping was an important early tool because it did not require the discovery of genetic variation within the species being studied. By fusing livestock cells with rodent cells, researchers could use the differences between the two species to track the presence of specific genes. This allowed for the assignment of genes to chromosomes even when no polymorphisms were available.

190. (B) 10% to 50%
In radiation hybrid mapping, the goal is to create cell lines that contain various fragments of the donor genome. On average, each fragment is retained in about one-fifth to one-half of the resulting clones. This frequency of retention provides the statistical power needed to determine how often different markers are kept together, which is used to calculate the physical distances.

191. (A) Telomeres and a centromere
To function as a stable artificial chromosome in yeast, a vector must contain all the essential elements of a natural chromosome. This includes a centromere for proper segregation during cell division and telomeres to protect the ends of the DNA molecule. These structural features allow the vector to carry extremely large pieces of DNA that would be unstable in plasmids.

192. (B) ATP
DNA ligation is an energy-consuming process that requires a specific cofactor to drive the chemical reaction. T4 DNA ligase uses adenosine triphosphate to provide the energy needed to form a new bond between the sugar and phosphate groups of adjacent DNA fragments. Without this energy source, the enzyme cannot successfully join the pieces of DNA together into a single molecule.

193. (A) A 1% recombination frequency
Genetic map distance is based on the likelihood of crossing over occurring between two points on a chromosome. One centiMorgan is defined as the distance over which there is a one percent chance of seeing a recombinant offspring. While this is a measure of genetic linkage rather than physical distance, it provides a powerful way to map the order of genes.

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glowing brightly only when it is bound to the minor groove of double-stranded DNA. As the PCR process creates more and more copies of the target DNA, the amount of bound dye increases, leading to a stronger fluorescent signal.

157. (C) SYBR Green detects all double-stranded DNA, including non-specific products and primer-dimers
While SYBR Green is easy to use, it has a significant limitation in terms of specificity. Because the dye binds to any double-stranded DNA, it will also detect unintended products like primer-dimers or non-specific amplicons. This can lead to inaccurate quantification of the target gene. For this reason, more specific methods like TaqMan probes are often used when high precision is required.

158. (B) 5' to 3' exonuclease activity
TaqMan probes offer a higher level of specificity by using a fluorescently labeled oligonucleotide that binds to the target DNA. This system relies on a unique property of the DNA polymerase, which can digest DNA that it encounters as it builds a new strand. When the enzyme reaches the bound probe, it breaks it apart, releasing the fluorescent label from its quencher.

159. (A) Fluorescence Resonance Energy Transfer (FRET)
The design of advanced PCR probes utilizes a physical phenomenon where the energy from a fluorescent molecule is transferred to a nearby quencher. When the reporter and the quencher are close together on the same probe, the signal is suppressed. This energy transfer ensures that the probe only glows when it is physically broken apart during the amplification of the target sequence.

160. (A) I, II and IV
Relative quantification is a method for comparing the expression of a gene between different samples without needing to know the exact number of copies. It relies on comparing the target gene to a reference gene that is expressed at a constant level. This approach assumes that both genes are amplified with similar efficiency and uses mathematical models to calculate the relative changes.

161. (B) SYBR Green assays
Because non-specific dyes like SYBR Green bind to all double-stranded DNA, it is important to verify that only the intended product was amplified. This is done by performing a melt curve analysis after the PCR is finished. By slowly increasing the temperature and monitoring the loss of fluorescence, researchers can see the melting points of all the DNA fragments in the well.

162. (B) Confirm the specificity of amplification by checking for a single, specific melting peak
Melt curve analysis provides a unique signature for the DNA products in a reaction. Each specific DNA sequence has a characteristic melting temperature based on its length and base composition. A single, sharp peak on the melt curve indicates that only one specific product was made, which confirms the accuracy and specificity of the PCR assay for the intended target gene.

163. (B) It will double (2-fold)
In an ideal PCR reaction, every cycle results in the complete replication of all target DNA molecules. This means that the amount of DNA should exactly double with each cycle during the exponential phase. Measuring how close a reaction comes to this perfect doubling is a measure of its efficiency, which is a critical factor for accurate quantification of the starting genetic material.

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164. (A) GAPDH
Normalization of gene expression data requires the use of internal controls that maintain consistent transcript levels across various experimental conditions and tissue types. Housekeeping genes involved in basic cellular maintenance, such as glyceraldehyde three-phosphate dehydrogenase, serve as reliable references. By comparing the expression of the target gene to these stable markers, researchers can accurately account for variations in initial quality.

165. (A) Both A and R are true and R is the correct explanation of A.
When working with RNA, it is vital to ensure that the results are not being influenced by contaminating genomic DNA. A control reaction that includes all components except the reverse transcriptase enzyme is used for this purpose. If a signal is detected in this control, it means

203. (A) Artificially inducing extracellular ice formation at mild sub-zero temperatures
During the slow freezing of embryos, it is important to control where and when ice forms. Seeding is a technique where a cold object is touched to the container to trigger ice formation in the surrounding medium at a specific temperature. This ensures that the ice grows slowly and externally, which helps to draw water out of the embryo.

204. (A) Vitrification requires ultra-rapid cooling rates to form an amorphous solid, completely avoiding ice crystal formation
Vitrification represents a rapid cryopreservation approach that transforms the liquid environment of an embryo into a glass-like solid without forming ice. This technique utilizes high concentrations of cryoprotectants and ultra-fast cooling rates to bypass the dangerous crystallization phase. Unlike slow freezing, which involves controlled cooling and extracellular ice formation, vitrification eliminates mechanical damage to cellular structures caused by sharp ice crystals.

205. (D) A is false but R is true.
Assessing the quality of frozen-thawed sperm requires looking at multiple factors. While motility is a critical indicator of a sperm's ability to swim, it does not guarantee that the sperm is capable of fertilizing an egg. Other factors, such as the integrity of the genetic material and the health of the acrosome, are also essential for successful reproduction and pregnancy.

206. (A) Purified viral antigen
Indirect ELISA is a common method for detecting antibodies in a patient's serum. To start the assay, the target of interest, such as a viral protein, is permanently attached to the bottom of the well. When the serum is added, any antibodies present will bind to this immobilized target. This allows for the specific detection of an immune response.

207. (B) Have at least two distinct binding sites (epitopes) for the capture and detection antibodies
For detecting very small amounts of a specific protein, the sandwich format provides the highest level of sensitivity and specificity. This method uses two different antibodies that target different parts of the same antigen. The first antibody captures the target from the sample, and the second, labeled antibody then detects it. This dual recognition ensures that only the intended target.

208. (A) The target protein of interest
Identifying a specific protein on a membrane requires the high specificity of the immune system. A primary antibody that only binds to the target protein is first added to the blot. This antibody serves as the bridge between the immobilized protein and the detection system, ensuring that only the correct protein band is visualized among the many others on the membrane.

209. (A) Enhanced Chemiluminescence (ECL)
Detecting very small amounts of protein on a Western blot requires a highly sensitive signal. ECL is a common method that uses an enzyme to produce light from a chemical substrate. The resulting glow is captured on film or with a digital camera. This technique provides a much more sensitive and dynamic range than older color-based methods, allowing for more precise.

210. (A) Uracil absorbs more UV light at 260 nm than thymine
Purified RNA samples typically demonstrate a higher absorbance ratio compared to DNA preparations. This difference arises because uracil, which replaces thymine in RNA, possesses a higher molar extinction coefficient at the standard measurement wavelength. Additionally, RNA is generally single-stranded, which reduces the base-stacking effects that normally lower the ultraviolet absorption of the double-stranded DNA molecule through a process called.

211. (A) PicoGreen-based fluorometry
Highly sensitive quantification of double-stranded DNA is often achieved using specialized fluorophores. PicoGreen is an asymmetrical cyanine dye that exhibits a massive increase in fluorescence intensity upon binding to double-stranded molecules. Because it ignores single-stranded RNA and free nucleotides, it provides an exceptionally accurate measurement of DNA quantity, even in samples containing significant amounts of common laboratory contaminants or very low concentration.

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incorporated into the phosphate backbone of the DNA probe. The beta particles emitted by the isotope can then be captured on X-ray film, producing a clear image of the target.

176. (A) Decreasing the extension temperature to 68 degrees Celsius
Standard PCR protocols are optimized for short fragments and may not work well for very long targets. To successfully amplify large pieces of DNA, the conditions must be adjusted to maintain the activity of the polymerase for a longer time. Lowering the extension temperature can help prevent the enzyme from losing its activity and improve the stability of the long DNA strands.

177. (B) Non-specific amplification and primer-dimer formation before denaturation
At room temperature, PCR primers can bind non-specifically to each other or to random parts of the genome, and the polymerase may slowly begin to extend them. This leads to the formation of unintended products. Hot-start methods prevent this by keeping the enzyme inactive or separating the components until the reaction has reached a high enough temperature for specific binding to occur.

178. (B) The physical distance between the 5' ends of the bound forward and reverse primers
Standard polymerase chain reactions generate specific fragments of a predefined length. The boundaries of this synthesized segment are strictly defined by the positions where the forward and reverse primers bind to the template DNA. During the elongation phase, the polymerase extends the strands between these two points, resulting in an exponentially increasing population of identical double-stranded DNA amplicons of that size.

179. (A) A single nucleotide change leading to an amino acid substitution (Pro/His) that alters a restriction site
Genotyping for important agricultural traits often relies on detecting single changes in the DNA sequence. In dairy cattle, a specific mutation in the casein gene alters the resulting protein and also happens to create or destroy a site for a restriction enzyme. This allows breeders to easily identify the different versions of the gene using the PCR-RFLP technique.

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180. (A) I, II, IV and V
DNA sequencing has evolved from the slow process of analyzing single samples to the massive parallelization of modern technology. Current methods use fluorescent labels, advanced chemistry, and semiconductor detection to read millions of sequences at once. These technologies are prone to different types of errors but provide an unprecedented amount of data for genomic research and practical livestock breeding applications.

181. (A) They bind to complementary oligos on the flow cell surface for cluster generation
Next-generation sequencing requires that the DNA fragments be attached to a solid support for analysis. Short DNA sequences called adapters are added to the ends of the fragments during library preparation. These adapters are complementary to sequences on the flow cell, allowing the fragments to be captured and then amplified into clusters, which is essential for the sequencing by synthesis process.

182. (A) Tubulin dimers
Cytogenetic analysis requires a high frequency of cells in a specific stage of division where chromosomes are most condensed. Colchicine acts as an antimitotic agent by binding to tubulin subunits, which effectively prevents the assembly of the mitotic spindle apparatus. This interference arrests the cell cycle at metaphase, allowing researchers to collect and visualize a large number of clearly defined chromosomal spreads.

183. (A) Extended mitogen-stimulated culture
Different tissues have different rates of natural cell division. While lymphocytes must be stimulated to divide, bone marrow contains a high proportion of cells that are already actively undergoing mitosis. This allows researchers to skip the long culture and stimulation steps and proceed directly to harvesting and fixing the cells, making bone marrow an excellent source for rapid cytogenetic analysis of livestock.

184. (B) The naming and numbering of chromosome bands for accurate karyotype description
Communication among scientists requires a standardized language for describing genomic features. For domestic animals, an international system has been established to name and number the specific bands observed on each chromosome

that DNA was present in the original sample and is being amplified, which would invalidate the results.

166. (A) Isolate specific wavelengths of light from a broad-spectrum source
Spectrophotometry requires the ability to measure light at very precise wavelengths. This is achieved by using a component that can split white light into its component colors, much like a prism. By selecting only the specific wavelength of interest, the instrument can measure exactly how much light is absorbed by the sample, providing the data needed for quantification and purity analysis.

167. (C) Quartz
Many common materials used for making laboratory equipment, such as glass and most plastics, absorb ultraviolet light. When measuring DNA at two hundred sixty nanometers, these materials would interfere with the reading. Quartz is one of the few materials that is transparent to ultraviolet light, making quartz cuvettes essential for the accurate quantification of nucleic acids using a spectrophotometer.

168. (A) Guanidinium thiocyanate
Isolating RNA is particularly difficult because of the abundance of enzymes that can rapidly degrade it. To prevent this, the extraction buffer contains powerful chemicals that immediately denature all proteins, including these harmful enzymes. Guanidinium thiocyanate is a strong chaotropic agent that serves this role, ensuring that the RNA remains intact and high-quality for downstream applications such as gene expression analysis.

169. (A) 1-5 V/cm
The speed and resolution of DNA separation in a gel are influenced by the strength of the electric field. For standard analytical electrophoresis, a moderate voltage is applied, usually measured as the potential difference across each centimeter of the gel. This level provides a good balance between separating the fragments efficiently and avoiding the heat generation that can cause bands to smear.

170. (A) III, IV, I, II
Different cloning vectors are used depending on the size of the DNA fragment that needs to be replicated. Standard plasmids have the smallest capacity, followed by cosmids. For very large genomic fragments, bacterial and yeast artificial chromosomes are required. Understanding the capacity of each vector is essential for choosing the right tool for genomic library construction and other large-scale genetic studies.

171. (A) Once every 256 bp
The frequency at which a restriction site appears in a genome is determined by the length of its recognition sequence. For a four-base pair sequence, the probability of any given position matching the sequence is one in four to the power of four. This means that, on average, the site will occur once in every two hundred fifty-six base pairs.

172. (B) Recognize the exact same sequence
Many different bacteria produce restriction enzymes as part of their defense systems. Sometimes, enzymes from different species are found to recognize exactly the same DNA sequence. These enzymes are known as isoschizomers. While they recognize the same site, they may cut it in the same or different ways, providing researchers with alternative tools for manipulating DNA at specific genomic locations.

173. (C) 12 to 24 hours (overnight)
Capillary transfer is a slow but effective method for moving DNA fragments from a gel to a membrane. Because it relies on the natural flow of buffer through the gel, it takes several hours for all the fragments to move completely, especially the larger ones. For this reason, Southern blotting transfers are typically set up to run overnight to ensure maximum efficiency.

174. (A) Low temperature, high salt concentration
The conditions under which a probe binds to a target can be adjusted to favor either perfect matches or partial complementarity. Stringency refers to how difficult it is for the probe to remain bound. Using a lower temperature and higher salt concentration decreases the stringency, which allows the probe to bind to sequences that are similar but not perfectly identical.

175. (C) Phosphorus-32
Radioactive labels have long been used to detect DNA on membranes because of their high sensitivity. Phosphorus-thirty-two is a common isotope used for this purpose, as it can be easily

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194. (A) The arrangement of alleles on homologous chromosomes (coupling or repulsion)
In genetic mapping, knowing which alleles are on the same physical strand of DNA is critical for interpreting recombination data. This arrangement is known as the phase. Alleles can be in coupling, where the dominant versions are together, or in repulsion, where they are on opposite strands. Understanding the phase is essential for calculating recombination frequencies and building accurate maps.

195. (B) Safely transport samples at ambient temperature without cold chain logistics
Collecting and storing DNA samples in the field can be challenging, especially without reliable refrigeration. FTA cards provide a simple solution by using specialized paper treated with chemicals that lyse cells and stabilize nucleic acids upon contact. The DNA becomes trapped in the fibers of the paper, where it is protected from environmental damage, allowing the samples to be stored.

196. (A) A potential mutation event requiring further analysis before exclusion
While a single mismatch in a DNA profile is a significant finding, it is not always absolute proof of non-paternity. Microsatellites have a natural mutation rate, and it is possible for a new allele to arise in the offspring. Therefore, guidelines often require mismatches at multiple independent positions before an alleged sire can be definitively excluded as the biological parent.

197. (B) Except for monozygotic twins, the combined multilocus genotype of every individual is unique
DNA profiling works because the genome is incredibly diverse. By looking at many different highly variable markers simultaneously, the probability of two unrelated individuals having the exact same profile becomes vanishingly small. This uniqueness provides a powerful way to identify individual animals, track their products through the food chain, and manage the genetic resources of livestock populations with high.

198. (A) Usefulness in linkage analysis based on the number and frequency of alleles
Not all genetic markers are equally useful for mapping or identification. The value of a marker is determined by how many different versions exist and how they are distributed in the population. The polymorphism information content is a statistical measure that quantifies this value. Markers with high scores are more likely to be heterozygous and provide more information for genetic studies.

199. (A) An excess of heterozygotes, possibly due to outbreeding or selective advantage
F-statistics are used to partition genetic variation and identify patterns of mating and selection. The $F_{\{IS\}}$ statistic compares the observed number of heterozygotes to what would be expected under random mating. A negative value indicates that there are more heterozygotes than expected, which can occur when breeders intentionally cross different lines or when certain heterozygote combinations provide a health advantage.

200. (A) P-3, Q-2, R-1, S-4
Population genetics relies on several key concepts to describe the genetic health and history of a group. These include models of genetic stability over time, measures of variation within and between groups, and the non-random association of different genes. Drastic changes in population size also play a major role by randomly reducing diversity and altering the genetic makeup of breeds.

201. (A) Glycerol
Protecting cells during the freezing process requires different types of agents. Some molecules can pass through the cell membrane and protect the internal structures, while others remain outside and provide a protective coating. Substances like glycerol and egg yolk are commonly used in bull semen extenders to provide both internal and external protection, ensuring the sperm remain viable after.

202. (A) Provides complex lipids and lipoproteins that protect the sperm plasma membrane from cold shock
Cold shock is a type of cellular damage that occurs when cells are cooled too rapidly before they are actually frozen. This is a significant problem for sperm cells, as the rapid drop in temperature causes the lipids in the cell membrane to change their physical state. Egg yolk contains specialized molecules that stabilize the membrane and prevent this type of.

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147. (B) To halt the enzymatic reaction and convert the blue product to a measurable yellow color
Once the enzymatic reaction in an ELISA has proceeded long enough, it must be stopped to get a stable reading. Adding a strong acid both stops the enzyme and changes the physical properties of the colored product. In the case of TMB, the blue color turns to a bright yellow, which is more stable and can be measured more accurately using a spectrophotometer.

148. (B) Specific RNA molecules
While Southern blotting is used for DNA, the Northern blotting technique is designed specifically for the study of RNA. This method allows researchers to determine the size and abundance of specific mRNA transcripts in a sample. By separating the RNA by size and using a complementary probe, it is possible to see which genes are active in different tissues or conditions.

149. (B) To inhibit RNase enzymes and keep the RNA denatured (preventing secondary structures)
RNA is a very fragile molecule that easily forms complex internal structures that can interfere with its separation in a gel. To ensure that the RNA is separated based on its length, it must be kept in a single-stranded, linear form. Adding chemicals like formaldehyde to the gel prevents these structures from forming and also helps to protect the RNA from degradation.

150. (A) P-2, Q-1, R-4, S-3
Molecular biology utilizes a variety of blotting and amplification techniques to study different biological molecules. DNA, RNA, and proteins are each analyzed using specialized methods that separate the molecules and then detect them using specific probes or antibodies. Understanding which technique is appropriate for each type of molecule is fundamental for conducting genetic and biochemical research in livestock and other species.

151. (B) Impart a uniform negative charge to proteins and denature them into linear chains
Proteins have complex three-dimensional shapes and varying electrical charges, which makes it difficult to separate them by size alone. To solve this, a detergent is used to unfold the proteins and coat them with a negative charge. This ensures that every protein has the same charge-to-mass ratio, allowing them to be separated based solely on their molecular weight during electrophoresis.

152. (C) Polyvinylidene fluoride (PVDF)
Successful protein analysis requires a solid support that can bind and hold the molecules during the detection process. PVDF membranes are preferred for Western blotting because they have a high capacity for protein binding and are physically very strong. They are also resistant to the chemicals used in the procedure, making them a durable and reliable choice for high-quality protein detection.

153. (C) Specific primary antibodies followed by enzyme-conjugated secondary antibodies
Identifying a specific protein on a membrane requires the high specificity of the immune system. A primary antibody that only binds to the target protein is first added to the blot. Then, a second antibody that recognizes the first one is used to provide the detection signal. This two-step process allows for both specific identification and amplification of the signal.

154. (B) The cycle number at which the fluorescence signal significantly exceeds background levels
In real-time PCR, the results are measured by tracking the increase in fluorescence over many cycles. The cycle threshold is the point at which the signal becomes strong enough to be distinguished from the random background noise. This value is the primary data point used to calculate the amount of starting DNA, as it is inversely proportional to the original concentration.

155. (A) A higher initial concentration of the target nucleic acid
A lower cycle threshold indicates that the fluorescent signal reached the detection limit earlier in the run. This happens when the starting material is more abundant, requiring fewer amplification cycles to produce a measurable amount of product. Therefore, an inverse relationship exists between the cycle number and the initial quantity of the target sequence present in the reaction mixture.

156. (B) Binding specifically to double-stranded DNA and emitting fluorescence
SYBR Green is a common and inexpensive dye used to monitor the progress of real-time PCR. This molecule has the unique property of

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212. (C) Experience greater frictional resistance within the agarose pores
During agarose gel electrophoresis, the gel matrix acts as a molecular sieve through which DNA molecules must pass. Since all DNA molecules possess a nearly identical negative charge-to-mass ratio, their migration speed is determined by their physical size. Smaller fragments move more easily through the pores, while larger molecules are more hindered, allowing separation based solely on their overall physical length.

213. (A) Hydrolases (specifically Endonucleases)
Enzymes are classified based on the type of chemical reaction they catalyze. Restriction enzymes belong to the class that breaks chemical bonds using water. Specifically, they are endonucleases, which means they cut within the DNA molecule rather than at the ends. By hydrolyzing the phosphodiester bonds that form the DNA backbone, they are able to precisely fragment the genetic material for.

214. (C) Isoschizomers that cleave identical staggered sequences
Many different bacteria produce restriction enzymes as part of their defense systems. Sometimes, enzymes from different species are found to recognize exactly the same DNA sequence. These enzymes are known as isoschizomers. While they recognize the same site, they may cut it in the same way, producing matching sticky ends that can be easily joined together in recombinant DNA experiments.

215. (A) Southern transfers DNA; Northern transfers RNA
Molecular biology utilizes a variety of blotting techniques to study different biological molecules. DNA and RNA are each analyzed using specialized methods that separate the molecules and then detect them using specific probes. While the basic principles of the transfer are similar, the target molecule and the specific chemicals used to protect and denature them differ between the two major blotting.

216. (A) Increase the stringency of the reaction, reducing non-specific binding
The conditions under which a probe binds to a target can be adjusted to favor either perfect matches or partial complementarity. Stringency refers to how difficult it is for the probe to remain bound. Using a higher temperature increases the stringency, which ensures that only the most perfectly matched probe-target pairs stay together, leading to a cleaner and more specific result.

217. (A) The specific segment of DNA synthesized during the reaction
Standard polymerase chain reactions generate specific fragments of a predefined length. The boundaries of this synthesized segment are strictly defined by the positions where the forward and reverse primers bind to the template DNA. This resulting piece of DNA, known as an amplicon, is then copied millions of times, providing enough material for various types of genetic analysis and visualization.

218. (A) Depletion of reaction components (dNTPs, primers) and loss of polymerase activity
PCR amplification does not continue indefinitely. As the reaction progresses, the essential components like nucleotides and primers are used up, and the enzyme eventually begins to lose its activity due to repeated heating. When this happens, the rate of product formation slows down and eventually stops, a stage known as the plateau phase. This is why endpoint measurement is less.

219. (A) The amplicon remains uncut, producing a single large band
RFLP analysis uses the specificity of restriction enzymes to detect genetic variations. For a single nucleotide polymorphism to be detectable by this method, the change in the DNA sequence must occur exactly within the recognition site of an enzyme. If the mutation alters the site so the enzyme no longer recognizes it, the DNA remains uncut, resulting in a different pattern.

220. (B) II, I, III, IV
DNA profiling follows a logical sequence of laboratory and analytical steps. It begins with the isolation of pure DNA from a biological sample. Specific regions are then amplified using the polymerase chain reaction. These products are separated by size and analyzed to identify the specific alleles present. Finally, this information is compiled into a profile that can be used for.

221. (B) Hybridization of sample DNA to millions of locus-specific probes attached to a solid surface
Modern genomics relies on technologies that can analyze millions of genetic variants

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simultaneously. SNP microarrays use a solid chip covered with specific DNA probes. When a sample of genomic DNA is added to the chip, it binds to the probes that match its sequence. This high-throughput approach allows researchers to rapidly genotype individual animals across the entire genome in one.

222. (A) The average number of sequence reads that align to a specific reference base
In next-generation sequencing, the accuracy of the results depends on how many times each base is read. Coverage refers to the total number of overlapping sequences that cover a particular position in the genome. Higher coverage provides greater confidence in the data, as it allows researchers to distinguish between real genetic variations and random errors made during the complex sequencing process.

223. (A) Single-molecule real-time monitoring of a continuous polymerase within a Zero-Mode Waveguide
Long-read sequencing technologies provide a significant advantage for assembling complex genomes. PacBio technology uses a specialized detection system that monitors the activity of a single polymerase molecule as it builds a new DNA strand. This allows the machine to read sequences that are many thousands of bases long, which is essential for resolving repetitive regions and structural variations in genomes.

224. (A) FISH (Fluorescence In Situ Hybridization)
Conventional banding techniques rely on the general properties of chromatin to produce patterns. In contrast, FISH utilizes the specificity of DNA hybridization. By using a labeled probe with a known sequence, researchers can pinpoint the exact physical location of a gene or DNA segment on a chromosome. This provides much higher resolution and allows for the detection of very small changes.

225. (A) Consistently stains the highly condensed constitutive heterochromatin, predominantly at centromeres
C-banding is a specialized staining technique that targets the constitutive heterochromatin, which is highly condensed DNA that is not active in gene expression. This material is particularly resistant to the chemical treatments used in the procedure, which allows it to be selectively stained while the rest of the DNA is washed away. This technique is especially useful for centromere location.

226. (A) Total chromosome length and centromere position
Every species has a characteristic set of chromosomes that can be identified by their physical appearance. During karyotype analysis, scientists look at the size of each chromosome and the location of the centromere, which is the point where the two halves meet. By pairing chromosomes that have the same physical features, researchers can build a complete map of the genome.

227. (A) The sequence of the specific oligonucleotide primer utilized
PRINS is a modern alternative to traditional hybridization methods that utilizes the power of DNA polymerase. This technique uses short, unlabeled primers that bind to a specific target in the genome. The enzyme then extends these primers on the slide, incorporating labeled nucleotides directly at the target site. This method provides a highly specific way to detect and study genomic features.

228. (A) A radiation-induced chromosome break occurring between two markers after an exposure of 10,000 rads
Radiation hybrid mapping provides high-resolution physical distance estimates by measuring the frequency of chromosome fragmentation. The unit of measure reflects the likelihood that a specific dose of radiation will cause a break between two genetic markers. A distance of one centiRay at a specific radiation intensity indicates a one percent probability that the markers were separated by an induced break.

229. (A) It contains a dense array of unique restriction enzyme sites for easy insertion of foreign DNA
Modern cloning vectors are engineered to make the process of inserting foreign DNA as simple as possible. The multiple cloning site is a short sequence of DNA that contains several different unique restriction enzyme recognition sites. This provides researchers with multiple options for cutting the vector and inserting their target DNA, making the system highly versatile for a wide range.

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230. (A) It creates a thermal gradient that sweeps plasmid DNA through the transiently altered cell membrane
Bacteria do not naturally take up large DNA molecules from their environment very efficiently. To make them more receptive, they must be treated to alter their cell walls. A brief exposure to a higher temperature creates a physical environment that helps push the DNA into the cells. This heat shock is a fundamental step in the process of bacterial transformation.

231. (A) The total number of offspring
Genetic mapping is based on the simple principle that genes located further apart on a chromosome are more likely to be separated by crossing over. By calculating the percentage of offspring that have a new combination of traits, researchers can estimate the distance between genes. This recombination frequency is a fundamental measure used to build the genetic maps of animals.

232. (A) Intense artificial selection for a specific production trait
The Hardy-Weinberg equilibrium is a model that describes a population where allele frequencies remain constant over time. This only happens when several conditions are met, such as random mating and no selection. In livestock breeding, humans intentionally select for specific traits, which violates these assumptions. This artificial selection leads to rapid changes in the genetic makeup of the population.

233. (A) $F_{\{ST\}}$ (Fixation index among subpopulations)
Measuring the genetic diversity of a population involves several different statistical tools. $F_{\{ST\}}$ is a measure of how much genetic variation is found between different sub-populations compared to the total variation. A high value indicates that the groups are genetically distinct from each other. This information is vital for understanding the relationships between different livestock breeds and managing their diversity.

234. (A) Multiple loci drastically increase the discriminatory power, minimizing the probability of identical profiles by chance
DNA profiling works because the genome is incredibly diverse. While any single marker might be shared by several individuals, looking at many different highly variable markers simultaneously makes the probability of an accidental match extremely low. This high power of discrimination is what makes DNA evidence so reliable for identifying individuals and verifying parentage in forensic and agricultural applications everywhere.

235. (A) Lethal ice crystal formation using high cooling rates
Vitrification represents a rapid cryopreservation approach that transforms the liquid environment of an embryo into a glass-like solid without forming ice. This technique utilizes high concentrations of cryoprotectants and ultra-fast cooling rates to bypass the dangerous crystallization phase. Unlike slow freezing, vitrification eliminates mechanical damage to cellular structures caused by sharp ice crystals, which is a major cause of.

236. (A) Because evaporating nitrogen gas rapidly displaces oxygen, presenting a severe asphyxiation hazard
Working with liquid nitrogen requires careful attention to safety. As the liquid evaporates, it turns into a very large volume of nitrogen gas. In an enclosed space, this gas can quickly replace the oxygen in the air, creating a dangerous environment for workers. Ensuring that storage areas are well-ventilated is essential for preventing accidents and ensuring a safe laboratory.

237. (A) Fluorescent staining techniques such as FITC-PNA or CTC
Assessing the quality of frozen-thawed sperm requires looking at multiple factors. The acrosome is a specialized structure on the head of the sperm that is essential for entering the egg. If this structure is damaged during freezing, the sperm will not be able to fertilize. Specialized fluorescent stains are used to specifically visualize the health of the acrosome.

238. (A) The solid-phase surface of the microtiter plate well
For detecting very small amounts of a specific protein, the sandwich format provides high sensitivity. The process begins by permanently attaching a capture antibody to the surface of the well. This antibody acts as a physical trap that specifically grabs the target protein from the sample. This immobilization is the first step in creating the dual-recognition sandwich that.

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that cover an entire chromosome, researchers can quickly determine the origin of the marker. This provides the high resolution needed for precise cytogenetic diagnosis.

294. (A) To selectively allow the survival of hybrid cells while parental cells die due to biochemical deficiencies
Creating hybrid cell lines requires a way to separate the fused cells from the ones that did not join. HAT medium is a specialized selective environment that blocks the normal pathway for making DNA. Only cells that can use an alternative pathway, which requires specific enzymes provided by both parental lines, can survive and grow. This ensures a pure hybrid culture.

295. (A) Cosmid
Cosmids are hybrid vectors designed to carry large pieces of DNA that are too big for standard plasmids. They utilize specific sequences from a virus that allow the DNA to be packaged into viral particles. This provides an exceptionally efficient way to introduce fragments up to forty-five thousand base pairs long into bacterial cells, making them a vital tool in genomics.

296. (A) Base-10 logarithm of the odds that two loci are physically linked rather than unlinked
A LOD score is a statistical value used to determine the likelihood of genetic linkage between two markers. It compares the probability of the observed data under the assumption of linkage versus the probability under independent assortment. A score of three or higher is generally accepted as strong evidence that two genes are located near each other on the same chromosome.

297. (A) An allele that fails to amplify during PCR due to a mutation in the primer binding site, potentially causing a false apparent homozygosity
Parentage testing using DNA markers relies on the consistent amplification of all alleles. Sometimes, a mutation in the region where the primer binds prevents the PCR from working for that specific allele. This results in a null allele that is not seen on the gel. This can lead to incorrect interpretations of the genotype, making it an important factor to.

298. (A) Quantify the degree of genetic differentiation and population structure among different breeds
Measuring the genetic diversity of a population involves several different statistical tools. $F_{\{ST\}}$ is a measure of how much genetic variation is found between different sub-populations compared to the total variation. A high value indicates that the groups are genetically distinct from each other. This information is vital for understanding the relationships between different livestock breeds and managing their genetic.

299. (A) Supercooling of the extracellular medium, mitigated by deliberately inducing ice crystal formation just below the freezing point
During the slow freezing of embryos, it is important to control the process of ice formation. Supercooling happens when the liquid remains liquid even below its freezing point, which can lead to sudden and damaging ice growth. Seeding is a technique used to trigger ice formation at a specific temperature, ensuring that the process proceeds slowly and safely for the cells.

300. (D) Comparing its Ct value to a standard curve generated from a dilution series of known template concentrations
Determining the exact concentration of a target sequence in a sample requires comparing it to known references. This is done by running a series of samples with precise concentrations and recording their cycle threshold values. By mapping the result of an unknown sample onto this standard curve, researchers can calculate its original starting concentration with a high degree of precision.

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An absorbance ratio significantly lower than the standard threshold for DNA suggests the presence of contaminants that absorb strongly at higher wavelengths. Proteins typically exhibit peak absorbance near two hundred eighty nanometers, leading to a reduced ratio when present in the final.

249. (A) 25 ug/mL
Spectrophotometry uses the Beer-Lambert law to correlate light absorption with the quantity of a substance in solution. For double-stranded DNA, a reading of one corresponds to fifty micrograms of DNA per milliliter. Therefore, an absorbance reading of zero point five indicates that the concentration is half of that standard value, providing a simple and rapid conversion for routine laboratory quantification.

250. (B) IV, I, II, III
Creating a recombinant plasmid follows a series of integrated steps. It begins with the isolation of the DNA fragments and the vector. Both are then cut with the same restriction enzyme to create matching ends. These pieces are joined together using a ligase enzyme. Finally, the new plasmid is introduced into a bacterial host, where it can be replicated.

251. (A) It requires a significantly smaller sample volume (usually 1-2 uL) and no cuvettes
Modern spectrophotometers have significantly reduced the amount of sample needed for quantification. These instruments use surface tension to hold a tiny droplet of liquid between two optical fibers. This allows for the measurement of concentration and purity using only a few microliters of sample, which is a major advantage when working with precious or low-concentration DNA and RNA.

252. (B) 1.2%
The resolution of a gel is determined by the size of the pores within the agarose matrix. A concentration of one point two percent creates a network that is ideal for separating DNA fragments in the intermediate range, such as many common PCR products. Higher or lower concentrations would be used if the target fragments were significantly smaller or larger than this.

253. (A) Ultraviolet (UV) light
Visualization of DNA in gels relies on specialized dyes that absorb light at one wavelength and emit it at another. These dyes, like ethidium bromide, intercalate between the bases of the DNA. When the gel is exposed to high-energy ultraviolet light, the dye becomes excited and glows brightly, allowing researchers to see the location and size of the DNA.

254. (A) Faster than the completely digested linear form due to its supercoiled conformation
Plasmids can exist in several different physical shapes, which affect how they move through a gel. An intact, supercoiled plasmid is very compact and can move through the agarose pores more easily than a linear piece of DNA of the same size. Therefore, undigested plasmid DNA often appears further down the gel than the linearized version would after being cut.

255. (A) The sequence reads the same on one strand from 5' to 3' as it does on the complementary strand from 5' to 3'
Many restriction endonucleases recognize DNA sequences characterized by a specific type of symmetry. In double-stranded DNA, a palindromic sequence occurs when the nucleotide order on one strand is identical to the order on the complementary strand when both are read in the same direction. This structural feature allows the dimeric enzyme to bind and cut both strands precisely.

256. (A) Is brittle and tends to shatter, making reprobing difficult
Nitrocellulose was one of the first materials used for blotting, but it has significant physical limitations. It becomes very fragile when dry and can easily break during handling or when being washed to remove a probe. This makes it difficult to use the same blot for multiple experiments, which is why more durable alternatives like nylon are now.

257. (A) Labeled single-stranded nucleic acid sequence complementary to the target of interest
Identifying a specific DNA fragment on a membrane requires a tool that can find it among millions of other sequences. A probe is a short piece of DNA or RNA that has been labeled with a fluorescent or radioactive tag. Because it is complementary to the target, it will bind

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in the fibers of the paper, where it is protected from environmental damage, allowing the samples to be transported easily.

276. (A) The offspring possesses obligate paternal alleles at multiple loci that are entirely absent in the alleged sire's genotype
Parentage testing is based on the simple principle that an offspring must inherit all of its genetic markers from its biological parents. If a multi-locus DNA profile shows that the offspring has several alleles that are not present in the alleged sire, then the sire can be definitively excluded as the true biological father. Multiple mismatches are required to ensure.

277. (A) Standardized panels of highly polymorphic Short Tandem Repeats (microsatellites)
International organizations have established standardized methods for describing the genetic makeup and diversity of livestock breeds. These methods rely on a specific set of microsatellite markers that have been chosen for their high level of variation and reliability. By using the same markers across different studies, researchers can compare the genetic diversity of various breeds and monitor animal population health.

278. (A) Optimizing cooling rates in the presence of cryoprotectants
Cryopreservation relies on effectively minimizing both intracellular ice formation and severe osmotic stress. This is best achieved by carefully controlling the cooling rate and using specialized protective chemicals. By finding the right balance, researchers can ensure that water leaves the cells in a controlled manner, preventing the formation of sharp ice crystals that would otherwise destroy the delicate cellular structures.

279. (A) The proportion of progressively motile sperm and the physical integrity of the acrosome
Assessing the quality of frozen-thawed sperm requires looking at multiple factors that influence reproductive success. Progressive motility is a critical indicator of a sperm's ability to reach the egg, while a healthy acrosome is needed for penetration. Together, these metrics provide a reliable measure of the potential fertilizing capacity of a semen dose used for artificial insemination in livestock.

280. (A) Bovine Serum Albumin (BSA)
Membranes and plates used in molecular assays are designed to bind proteins with high affinity. To prevent the labeled antibodies from sticking randomly to the empty spaces, a blocking step is performed using non-specific proteins like albumin. This ensures that the detection system only binds to the intended target, significantly improving the accuracy and sensitivity of the final measurement result.

281. (C) 450 nm
Once the enzymatic reaction in an ELISA has been stopped with an acid, the resulting color must be quantified. In the case of TMB, the addition of acid converts the blue product into a bright yellow one. This yellow color has a specific light absorption peak at four hundred fifty nanometers. Measuring the absorbance at this wavelength provides an accurate.

282. (B) It facilitates the binding of proteins to the membrane by removing SDS
Transferring proteins from a polyacrylamide gel to a solid membrane requires a specialized buffer to facilitate efficient binding. Methanol is a critical component that serves to dissociate the detergent from the proteins, which helps restore their hydrophobic nature. This change increases the efficiency of protein adsorption onto the membrane surface, ensuring the separated bands are properly captured for detection.

283. (A) In the middle of the linear amplification phase on a log scale, significantly above the background noise
Setting the correct threshold is vital for accurate quantification in real-time PCR. This line is placed at a level where the signal is clearly distinguishable from the random background noise but still within the phase where the doubling of the product is most consistent. This ensures that the cycle threshold value calculated for each sample is a reliable measure.

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284. (B) Normalize for non-PCR related fluctuations in fluorescence signal
Real-time PCR machines must account for small variations in optics and volume between different wells. A passive reference dye is added to every reaction at a constant concentration. This dye does not participate in the amplification process. By measuring its signal, the instrument can correct for random fluctuations in the overall

267. (A) The gross structural location of a specific DNA sequence or entire chromosome on a metaphase spread
FISH utilizes the specificity of DNA hybridization to provide high-resolution physical mapping. By using a labeled probe with a known sequence, researchers can pinpoint the exact physical location of a gene or DNA segment on a chromosome. This provides much higher resolution than conventional banding and allows for the detection of very small genetic changes and rearrangements in animal genomes.

268. (B) Taq DNA Polymerase
PRINS is a modern alternative to traditional hybridization methods that utilizes the power of DNA synthesis. This technique uses short, unlabeled primers that bind to a specific target in the genome. A heat-stable DNA polymerase then extends these primers on the slide, incorporating labeled nucleotides directly at the target site. This enzymatic approach provides a fast and sensitive way to detect.

269. (A) Preferentially and randomly lose the chromosomes of one specific parent species (e.g., the livestock species in a rodent-livestock hybrid)
Somatic cell hybrid mapping relies on the unique behavior of hybrid cells during culture. When cells from two different species are fused, the chromosomes of one species are often gradually and randomly lost over time. By analyzing which livestock chromosomes remain in different cell lines and comparing this to the presence of markers, researchers can assign those markers to particular physical.

270. (A) Fusion with a non-irradiated recipient rodent cell line
Radiation hybrid mapping uses lethal doses of radiation to break the donor DNA into small fragments. Because the donor cells are killed, the fragments must be saved by fusing them with healthy recipient cells. These hybrid cells then replicate the donor fragments along with their own genome, allowing researchers to study the organization and order of genes in the fragmented DNA.

271. (A) Bacterial Artificial Chromosome (BAC)
Mapping and sequencing large mammalian genomes requires vectors that can carry very large pieces of DNA stably. Bacterial artificial chromosomes are the preferred choice for this task. They are based on a specific plasmid system that allows for the cloning of fragments several hundred thousand base pairs long. This makes them ideal for creating genomic libraries and studying large-scale genomic.

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272. (A) Phosphodiester bonds between a 3'-OH and a 5'-PO4
DNA ligation is an energy-consuming process that requires a specific enzyme to repair the physical structure of the DNA molecule. T4 DNA ligase catalyzes the formation of the chemical bonds that link the sugar and phosphate groups together in the DNA backbone. This process is essential for joining separate DNA fragments into a single, continuous molecule during recombinant DNA experiments.

273. (A) The recombination frequency underestimates the true map distance due to undetected double crossovers
Mapping functions are used to convert observed recombination frequencies into actual genetic distances on a chromosome. Because double crossovers can hide some of the recombination events, the relationship between frequency and distance is not perfectly linear over long ranges. Haldane's function accounts for this by correcting for the probability of multiple crossovers that would otherwise lead to an underestimation of distance.

274. (A) A statistical correlation between specific alleles at two distinct loci
In a perfectly random population, the alleles at different genetic positions would be inherited independently. However, some combinations of alleles are found together more often than expected by chance. This phenomenon, known as linkage disequilibrium, occurs when genes are physically close together on a chromosome. It is a powerful tool used in genomics to find markers associated with production traits.

275. (A) It facilitates immediate cell lysis and firmly binds the DNA, preventing degradation by nucleases and microbes during room-temperature storage
Collecting and storing DNA samples in the field can be challenging, especially without reliable refrigeration. FTA cards provide a simple solution by using specialized paper treated with chemicals that lyse cells and stabilize nucleic acids upon contact. The DNA becomes trapped

specifically to it, allowing the researcher to see its.

258. (A) Length and sequence composition (Tm) of the specific primers
The annealing temperature in PCR determines the stringency of primer binding. This value is carefully selected based on the physical properties of the primers. Every primer has a unique melting temperature determined by its length and the specific combination of adenine, thymine, guanine, and cytosine it contains. Setting the correct temperature ensures that the primers bind specifically and efficiently.

259. (C) 25-35 times
Standard PCR involves repeating the cycle of denaturation, annealing, and extension many times to create enough DNA for analysis. Each cycle doubles the amount of the target sequence. Usually, thirty cycles are enough to produce billions of copies, which is plenty to be seen as a bright band on a gel when stained with a fluorescent intercalating dye.

260. (A) Increasing the incubation time or utilizing a higher concentration of the restriction enzyme
Complete digestion is essential for accurate genotyping in RFLP assays. If the reaction conditions are not optimal, some of the DNA molecules may remain uncut, leading to misleading patterns. This can often be fixed by adding more enzyme or allowing the reaction to proceed for a longer period. Ensuring that every DNA molecule is cut is vital for reliable genetic.

261. (A) Fluorescently labeled ddNTPs that allow for a single-tube reaction and capillary electrophoresis
Sanger sequencing has been highly automated through the use of advanced fluorescent chemistry. By using four different colors of fluorescent labels, one for each base, the entire sequencing reaction can be performed in a single tube. The resulting fragments are then separated in a capillary tube, where a laser reads the color of each fragment as it passes by.

262. (A) Ion Torrent
Every time a new nucleotide is added to a DNA strand during replication, a tiny chemical change occurs. Ion Torrent sequencing uses a specialized semiconductor chip to measure the release of hydrogen ions that happens during this process. By directly converting these pH changes into a digital signal, the machine can read the DNA sequence without the need for light.

263. (A) The added mitogen stimulates the T-lymphocytes to proliferate and enter mitosis
Lymphocytes in the blood are normally in a resting state and do not divide. To study their chromosomes, they must be stimulated to enter the cell cycle. Phytohemagglutinin is a powerful mitogen that specifically targets T-cells, triggering them to undergo mitosis over several days. This ensures that there are enough dividing cells in the culture to provide the metaphase spreads needed.

264. (A) Swell the cells, causing the chromosomes to spread widely apart when the cells are burst onto a slide
Before chromosomes can be viewed, the cells must be prepared to release them effectively. Treating the cells with a hypotonic solution causes water to move into the cells through osmosis. This swelling increases the internal volume and separates the chromosomes from each other. When these swollen cells are later dropped onto a slide, they burst easily, resulting in well-spread chromosome.

265. (A) Q-banding relies on quinacrine mustard and fluorescence microscopy, whereas G-banding uses Giemsa and brightfield microscopy
Various banding techniques provide different types of information about chromosome structure. While G-banding is the most common for identifying overall structure using standard light microscopy, Q-banding uses fluorescent dyes that require a specialized microscope. Each method highlights different features of the chromatin, allowing cytogeneticists to detect a wide range of structural and numerical abnormalities in the domestic animal genome.

266. (A) Their centromeres (specifically in acrocentric chromosomes)
A Robertsonian translocation is a specific type of rearrangement where two acrocentric chromosomes fuse at their centromeres to form a single larger chromosome. While the animal still has almost all of its genetic material, this fusion reduces the total number of chromosomes. This is a common finding in livestock and can have significant impacts on fertility and offspring health in breeding.

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light level, providing more consistent and accurate results.

285. (A) The follicular root bulb
Collecting hair samples for genetic analysis is a common and non-invasive method used in livestock breeding. While the hair shaft itself is made of dead cells with degraded DNA, the bulb at the base of the hair contains actively dividing cells with intact nuclei. This region provides a reliable source of high-quality genomic DNA for PCR-based genotyping and parentage verification studies.

286. (A) It has a higher buffering capacity and is less prone to exhaustion during prolonged, high-voltage electrophoretic runs
Electrophoresis buffers provide essential ions for electrical conductivity and maintain a stable pH during the run. TBE buffer is particularly useful for longer runs or higher voltages because it resists changes in pH more effectively than other systems. This stability helps to maintain the uniform movement of DNA fragments and prevents the loss of resolution that can occur when buffers.

287. (C) 1000 ug/mL
Quantitative analysis using spectrophotometry requires accounting for sample preparation factors to determine the original stock concentration. When a sample is diluted one-to-one hundred, the measured absorbance represents only a fraction of the total density. Multiplying the observed optical density by both the conversion factor for double-stranded DNA and the dilution factor yields the total mass concentration in the stock.

288. (A) Break the hydrogen bonds between complementary base pairs, yielding single-stranded templates
The first step in every PCR cycle involves separating the double-stranded DNA template into single strands. This denaturation is achieved by heating the reaction mixture to near-boiling temperatures. At this level, the hydrogen bonds holding the two strands together are broken, providing the single-stranded templates required for the primers to bind and the polymerase to begin synthesis in subsequent steps.

289. (A) To ensure the restriction enzyme was active and digestion went to completion
Complete digestion is essential for accurate genotyping in RFLP assays. To verify the quality of the reaction, researchers often include a site that should be cut in every sample. If this control site remains uncut, it indicates that the enzyme was not working properly or the reaction was not long enough. This provides a built-in check for experimental reliability.

290. (A) In real-time as a DNA polymerase incorporates specific nucleotides onto a growing complementary strand
Modern high-throughput sequencing often uses a method where the sequence is read as it is being built. This technology utilizes reversible terminators that allow only a single labeled nucleotide to be added at a time. After the color of the new base is recorded, the terminator is removed, and the cycle begins again. This allows millions of sequences to be read.

291. (A) The cells will rupture prematurely in the tube, leading to scattered, unanalyzable chromosomes
The timing of the hypotonic treatment is critical during chromosome preparation. The goal is to swell the cells just enough so they burst only when dropped onto the slide. If the treatment lasts too long, the cells become too fragile and may burst while still in the centrifuge tube. This results in the loss of chromosomes and makes analysis impossible.

NODIA

292. (A) A schematic, diagrammatic representation of a karyotype showing typical banding patterns
Communication among scientists requires a standardized way to represent the features of a genome. An ideogram is a diagram that shows the characteristic size, shape, and banding pattern of each chromosome in a species. This provides a reference map that cytogeneticists use to identify individual chromosomes and describe the exact location of any abnormalities or genes they find during.

293. (A) Fluorescence In Situ Hybridization (FISH) with specific chromosomal paints
Identifying small, unusual pieces of DNA known as marker chromosomes can be difficult using standard banding. FISH provides a more powerful solution by using probes that glow with different colors. By using a mixture of probes

239. (A) p-Nitrophenyl phosphate (pNPP)
The visual signal in many common ELISA systems is produced by an enzyme that reacts with a specific chemical substrate. Alkaline phosphatase is often used for this purpose. When it reacts with pNPP, it produces a distinct yellow color. This color change indicates the presence and amount of the target molecule in the well, providing a clear result.

240. (A) An applied electric current (electroblotting) perpendicular to the gel
Transferring proteins from a polyacrylamide gel to a solid membrane requires a specialized system. An electric field is used to pull the negatively charged proteins out of the gel and push them onto the membrane. This electroblotting process ensures that the pattern of protein bands is perfectly preserved on the membrane, where they can then be identified using specific antibodies.

241. (A) Both A and R are true and R is the correct explanation of A.
When performing reverse transcription for gene expression studies, the choice of primers can impact the results. Using primers that are specific to the target gene ensures that only the intended mRNA is converted into cDNA. This improves the specificity of the subsequent PCR step and reduces the amount of non-target genetic material that could interfere with the accurate quantification.

242. (A) Sample A has approximately 8 times (2^3) more template than Sample B
In real-time PCR, a difference of three cycles between two samples reflects an eight-fold variation in the starting amount of genetic material. Since each cycle ideally doubles the quantity of the target amplicon during the exponential phase, the calculation follows a base-two power function. A three-cycle lead suggests the more concentrated sample contained significantly more template initially than others.

243. (A) The background fluorescence level during the initial cycles before measurable amplification occurs
In real-time PCR, the results are measured by tracking the increase in fluorescence. The first few cycles typically show no measurable change, and the signal during this time is considered the baseline. This baseline represents the random background noise of the system. Understanding this level is essential for setting the threshold and determining the exact cycle where amplification begins.

244. (A) Compacted sperm chromatin is crosslinked with disulfide bonds
Different biological samples possess varying levels of chromatin condensation and structural complexity. Mature sperm cells contain DNA that is extremely tightly packed with protamines instead of the usual histone proteins. This unique structural arrangement requires more aggressive chemical treatment and specific reducing agents during the lysis step to ensure the complete release and recovery of high-quality genomic DNA from.

245. (A) Avian erythrocytes are nucleated, unlike mature mammalian erythrocytes
Whole blood consists of diverse cell types, and in many animals, the red blood cells are the most numerous. In birds, these cells contain a functional nucleus with a full set of genomic DNA. This is different from mammals, whose red cells lose their nuclei as they mature. This difference means that a small amount of bird blood yields DNA.

246. (A) It specifically degrades contaminating RNA, leaving the DNA intact
During the isolation of genomic DNA, it is common to also recover significant amounts of RNA. To obtain a pure DNA sample, an enzyme called RNase A is added to the mixture. This enzyme specifically targets and breaks down RNA molecules while leaving the DNA untouched. This ensures that the final quantification and downstream analysis only reflect the DNA content.

247. (A) Tris-HCl and EDTA
Resuspending DNA in the right buffer is essential for its long-term stability. TE buffer is a standard choice that provides two levels of protection. Tris-HCl maintains a stable, slightly basic pH where DNA is most stable. EDTA chelates metal ions that are needed by enzymes that degrade DNA. Together, these components ensure that the purified genomic DNA remains.

248. (A) Significant protein contamination
Purified nucleic acids absorb ultraviolet light at specific wavelengths, and the ratio of these measurements indicates sample cleanliness.

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CHAPTER 09

Research Techniques for Quantitative Animal Genetics

2004

1. In quantitative genetics, phenotypic variance is partitioned into genetic and environmental components. Which of the following represents the genetic component that is most strictly heritable and responds to selection?
(A) Dominance variance
(B) Additive genetic variance
(C) Epistatic variance
(D) Genotype-environment interaction

2007

2. Which method by Henderson utilizes the expectation of mean squares from the analysis of variance for unbalanced data with a nested design?
(A) Henderson's Method 2
(B) Henderson's Method 3
(C) Henderson's Method 1
(D) Restricted Maximum Likelihood

2015

3. Consider the following statements regarding the Expectation-Maximization (EM) algorithm in Maximum Likelihood estimation:
I. It is highly sensitive to the initial starting values.
II. It guarantees convergence to the global maximum.
III. It typically converges slower than the Newton-Raphson method.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I, II and III

2021

4. Minimum Norm Quadratic Unbiased Estimation (MINQUE) requires prior values for variance components. If these prior values are exactly equal to the true parameters, MINQUE is equivalent to:
(A) MIVQUE estimates
(B) ANOVA estimates
(C) ML estimates
(D) REML estimates

2005

5. In a Bayesian analysis of quantitative genetic data, which MCMC algorithm draws samples from the fully conditional posterior distributions of all parameters?
(A) Metropolis-Hastings algorithm
(B) Gibbs sampling
(C) Rejection sampling
(D) Importance sampling

2013

6. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Henderson's tabular method allows the calculation of the inverse of the additive genetic relationship matrix without inverting the full matrix directly.
Reason (R): The tabular method exploits the fact that the matrix can be decomposed into $LDL\hat{a}\text{€}^{\text{TM}}$, where D is diagonal.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2004

7. The Best Linear Unbiased Prediction (BLUP) for genetic evaluation utilizes Mixed Model Equations (MME). What does BLUP specifically maximize?
(A) Correlation between true and predicted breeding values
(B) The conditional probability of fixed effects given data
(C) The total phenotypic variance within the population
(D) The environmental effects across contemporary groups

NODIA

2019

8. In dairy cattle breeding, which model is most appropriate when an animal has multiple records of the same trait across different lactations?
(A) Sire Model
(B) Maternal Effects Model
(C) Repeatability Model
(D) Single-trait Animal Model

2009

9. Random Regression Models (RRM) are extensively used for analyzing longitudinal data. Which mathematical functions are most commonly used as basis functions in RRM for test-day milk yields?
(A) Fourier series
(B) Taylor series
(C) Chebyshev polynomials
(D) Legendre polynomials

2002

10. When computing Wright's inbreeding coefficient (F) via path coefficients, what is the formula for the contribution of a single path containing a common ancestor?
(A) $\left(\frac{1}{2}\right)^{n+n'}(1-F_A)$
(B) $\left(\frac{1}{2}\right)^{n+n'-1}(1+F_A)$
(C) $\left(\frac{1}{2}\right)^{n+n'+1}(1+F_A)$
(D) $\left(\frac{1}{2}\right)^{n+n'}(1+F_A)$

2008

11. In a closed flock consisting of N_m males and N_f females, what is the formula for the effective population size (N_e) assuming random mating?
(A) $\frac{N_m N_f}{4(N_m+N_f)}$
(B) $\frac{4N_m N_f}{N_m+N_f}$
(C) $\frac{2N_m N_f}{N_m+N_f}$
(D) $\frac{4N_m N_f}{N_m-N_f}$

2004

12. If the paternal half-sib intra-class correlation (t) for a trait is 0.15, what is the estimated herizability (h^2) of this trait?
(A) 0.15
(B) 0.30
(C) 0.45
(D) 0.60

2010

13. Which value represents the theoretical maximum limit for herizability in the narrow sense?
(A) 0.0
(B) 0.5
(C) 1.0
(D) 2.0

2009

14. Identify the INCORRECT statement regarding genetic correlations.
(A) They are primarily caused by pleiotropic effects of genes.
(B) They arise due to persistent linkage disequilibrium factors.
(C) They represent correlation between dominance deviations.
(D) They are mathematically bounded between -1.0 and 1.0.

2006

15. Match the components of the Breeder's Equation (List I) with their corresponding symbols (List II).
List I: (Component)
P. Selection intensity
Q. Accuracy of selection
R. Additive genetic standard deviation
S. Generation interval
List II: (Symbol)
1. $r_{\{TI\}}$
2. σ_A
3. L
4. i
(A) P-4, Q-1, R-2, S-3
(B) P-1, Q-4, R-2, S-3
(C) P-4, Q-2, R-1, S-3
(D) P-3, Q-1, R-4, S-2

2001

16. In the Smith-Hazel classical selection index, the index weights (b vector) are calculated as $b = P^{\{-1\}}Ga$. What does a represent in this formula?
(A) Vector of phenotypic standard deviations
(B) Matrix of genetic covariances
(C) Matrix of additive genetic variances
(D) Vector of economic values

2023

17. Which experimental design is frequently used in progeny testing to effectively account for environmental variations across different farms?
(A) Latin Square Design

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(B) Contemporary Group Comparison
(C) Completely Randomized Design
(D) Split-plot Design

2014

18. Under Least Squares Analysis (LSA) for unbalanced data, which mathematical approach resolves normal equations that are not of full rank?
(A) Singular value decomposition
(B) Cholesky decomposition
(C) Generalized inverse
(D) Gaussian elimination

2007

19. When applying Multiple Linear Regression, which phenomenon occurs if two or more predictor variables are highly correlated?
(A) Heteroscedasticity
(B) Autocorrelation
(C) Overdispersion
(D) Multicollinearity

2023

20. Consider the following statements regarding Principal Component Analysis (PCA):
I. PCA transforms correlated variables into a set of linearly uncorrelated variables.
II. The first principal component accounts for the smallest possible variance.
III. PCA does not assume an underlying probabilistic model.
IV. The number of principal components equals the number of original variables.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I, III and IV
(C) II, III and IV
(D) I and IV

2003

21. Which genetic distance measure assumes that genetic drift is the sole evolutionary force responsible for population divergence?
(A) Nei's standard genetic distance
(B) Cavalli-Sforza chord distance
(C) Mahalanobis distance
(D) Jaccard distance

2008

22. In genomic selection, the GBLUP model utilizes which of the following to estimate breeding values?
(A) Traditional pedigree-based relationship matrix
(B) Genomic relationship matrix derived from SNPs
(C) Matrix of estimated identity-by-descent probabilities
(D) Full dominance genetic variance-covariance matrix

2006

23. Which bioinformatics algorithm is primarily used for finding local sequence alignments in protein or DNA databases?
(A) BLAST
(B) Needleman-Wunsch
(C) ClustalW
(D) UPGMA

2008

24. What type of variance is primarily partitioned into temporary and permanent components in quantitative genetics?
(A) Additive genetic variance
(B) Dominance variance
(C) Environmental variance
(D) Epistatic variance

2005

25. Henderson's Method 3 is also known as:
(A) Method of moments
(B) Maximum likelihood
(C) Minimum variance method
(D) Fitting constants method

2019

26. In REML estimation, what is the primary advantage over Maximum Likelihood (ML)?
(A) Direct estimation of fixed effects parameters without standard errors
(B) Requirement that traits do not follow a normal phenotypic distribution
(C) Accounting for degrees of freedom lost by estimating fixed effects
(D) Implementation without the need for complex iterative algorithms

2007

27. MIVQUE estimation provides unbiased estimators and assumes which distribution for the data?
(A) Binomial distribution
(B) Normal distribution
(C) Poisson distribution
(D) Exponential distribution

2004

28. In the Bayesian framework of quantitative genetics, which distribution represents our belief about a parameter after observing the data?

NODIA

(B) Intense artificial selection
(C) Extreme inbreeding
(D) Assortative mating

2010

89. Which Bayesian model for genomic selection fits a mixture model where a large proportion of SNPs have zero effect, and a small proportion have a non-zero effect drawn from a t-distribution?
(A) Bayes A
(B) Bayesian Ridge Regression
(C) GBLUP
(D) Bayes B

2006

90. Consider the following statements regarding the National Center for Biotechnology Information (NCBI):
I. It houses the GenBank database.
II. It is maintained by the European Molecular Biology Laboratory.
III. It provides tools like BLAST for sequence analysis.
Which of the above statement(s) is/are correct?
(A) I only
(B) II only
(C) I and III
(D) II and III

2005

91. Permanent environmental variance ($V_{\{PE\}}$) in repeated records:
(A) Causes differences between individuals but not between repeated records
(B) Affects only the first record of an individual within its lifetime
(C) Is considered a sub-component of the total additive genetic variance
(D) Fluctuates randomly between lactations due to environmental factors

2010

92. Henderson's Method 3 involves computing sums of squares by:
(A) Ignoring all fixed effects
(B) Using only raw phenotypic means
(C) Applying maximum likelihood principles
(D) Fitting full and reduced models to obtain expectations

2013

93. The EM algorithm in REML involves two steps: Expectation (E) and Maximization (M). The E-step involves computing the expectation of:
(A) The phenotypic variance only
(B) The prior distribution
(C) The complete-data log-likelihood
(D) The fixed effects only

2025

94. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): MIVQUE does not require iteration to estimate variance components.
Reason (R): MIVQUE calculates estimates based on initial prior values of the variance components without updating them.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2010

95. When using Gibbs sampling, convergence to the posterior distribution is usually assessed by examining:
(A) The magnitude of the fixed effects
(B) The trace plot of the sampled parameter values over iterations
(C) The generalized inverse of the relationship matrix
(D) The p-value of a t-test

2008

96. When constructing the additive genetic relationship matrix (A), the element $A_{\{ii\}}$ (diagonal) is equal to:
(A) $1 + F_i$
(B) $1 - F_i$
(C) $2F_i$
(D) $\frac{F_i}{2}$

2006

97. Which effect is considered a random effect in the standard Animal Model used for genetic evaluation?
(A) Additive genetic effect of the animal
(B) Herd-Year-Season (HYS)
(C) Age at calving
(D) Sex of the calf

2008

98. An advantage of the Animal Model over the Sire Model is that it:
(A) Accounts for assortative mating of both parents
(B) Requires much less computational power

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(C) Both genetic and environmental correlations
(D) Dominance and epistatic correlations

2001

39. To maximize annual genetic gain, a breeder should aim to:
(A) Increase generation interval
(B) Decrease selection intensity
(C) Decrease the accuracy of selection
(D) Decrease generation interval

2019

40. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): The Smith-Hazel selection index uses economic weights to maximize the aggregate genotype.
Reason (R): Economic weights represent the partial regression of profit on each trait while holding other traits constant.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2005

41. In field-based progeny testing, the term "Cumulative Difference" refers to:
(A) Progressive deviation of sire daughters from contemporary averages
(B) Total additive genetic variation observed among all candidate sires
(C) Total phenotypic variance recorded across the entire reference herd
(D) Differences in generation intervals between parents and offspring

2006

42. Least Squares Analysis (LSA) handles non-orthogonal data by:
(A) Deletion of all incomplete records from the final dataset
(B) Assumption that all fixed effects remain strictly independent
(C) Estimation of parameters that minimize squared residual sums
(D) Maximization of the likelihood function for all parameters

2017

43. Ridge regression modifies ordinary least squares by adding a penalty parameter to address:
(A) Non-normality of residuals
(B) Autocorrelation
(C) Multicollinearity
(D) Missing data

2009

44. In Discriminant Function Analysis, the primary objective is to:
(A) Linear combination of features separating two or more classes
(B) Clustering of unlabeled data into groups based on similarity
(C) Prediction of a continuous dependent variable from covariates
(D) Construction of a phylogenetic tree using phenotypic markers

2007

45. Which phylogenetic tree reconstruction method relies on the assumption of a constant molecular clock?
(A) Maximum Parsimony
(B) UPGMA
(C) Neighbor-Joining
(D) Maximum Likelihood

2016

46. Consider the following statements regarding Genomic Selection models:
I. GBLUP assumes equal variances for all SNP effects.
II. Bayes B assumes a spike-and-slab mixture distribution for SNP effects.
III. Bayes A assumes a normal distribution for SNP effects with varying variances.
IV. Single-step GBLUP is specifically designed to integrate ungenotyped animals into a genomic evaluation.
Which of the above statement(s) is/are correct?
(A) I and II
(B) II and IV
(C) I and III
(D) III and IV

2017

47. In bioinformatics, what is FASTA primarily used for?
(A) Sequence alignment and database searching
(B) Structural modeling of proteins
(C) Phylogenetic tree plotting
(D) RNA secondary structure prediction

2015

48. Genotype-environment interaction (GxE) indicates that:
(A) Different genotypes respond similarly to environmental changes

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(A) Prior distribution
(B) Marginal distribution
(C) Likelihood function
(D) Posterior distribution

2025

29. When using Henderson's tabular method for an un-inbred animal whose parents are unknown, what is the diagonal element in the A-matrix?
(A) 0
(B) 0.5
(C) 1.0
(D) 2.0

2023

30. Identify the correct sequence of steps for solving Mixed Model Equations (MME):
I. Construct the relationship matrix
II. Define the incidence matrices for fixed and random effects
III. Calculate the inverse of the relationship matrix
IV. Solve the simultaneous equations
(A) I → II → III → IV
(B) II → I → III → IV
(C) II → III → I → IV
(D) I → III → II → IV

2010

31. The Sire Model for genetic evaluation estimates the transmitting ability of sires. The variance of sire effects (σ_s^2) corresponds to what fraction of the additive genetic variance (σ_A^2)?
(A) $\frac{1}{2}\sigma_A^2$
(B) $\frac{1}{4}\sigma_A^2$
(C) $\frac{3}{4}\sigma_A^2$
(D) σ_A^2

2024

32. In a Repeatability Model, the permanent environmental effect is modeled as:
(A) A random effect uncorrelated with the additive genetic effect
(B) A fixed effect shared among all individuals
(C) A random effect specific to each record of the individual
(D) A random effect correlated with the additive genetic effect

2008

33. Random Regression Models allow the fitting of a trajectory for each individual. The genetic parameters in RRM are modeled as:
(A) Constant across time
(B) Static fixed effects
(C) Environmental residuals
(D) Covariance functions

2008

34. What does the path coefficient between a parent and its offspring measure in a non-inbred population?
(A) 0.25
(B) 0.50
(C) 0.75
(D) 1.00

2019

35. The rate of inbreeding (ΔF) in a closed herd represents the change in inbreeding per:
(A) Month
(B) Generation
(C) Year
(D) Lactation

2005

36. When estimating heritability through parent-offspring regression, what does the regression coefficient of offspring on one parent estimate?
(A) h^2
(B) $\frac{1}{2}h^2$
(C) $2h^2$
(D) $\frac{1}{4}h^2$

NODIA

2010

37. Which of the following defines Most Probable Producing Ability (MPPA) in dairy animals?
(A) Estimate of producing ability derived from repeated observations
(B) Estimate of an individual's genotypic value for lifetime survival
(C) Identification of superior sires based solely on progeny survival
(D) Measurement of dominance deviations within specific subpopulations

2005

38. The phenotypic correlation (r_P) between two traits is mathematically expressed as a function of which correlations?
(A) Only genetic correlation
(B) Only environmental correlation

Assertion (A): The effective population size (N_e) is usually smaller than the actual census size in livestock populations.
Reason (R): Livestock populations often have unequal sex ratios with fewer males than females used for breeding.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2021

59. The standard error of a heritability estimate derived from paternal half-sib analysis depends largely on:
(A) The number of sires and progeny per sire
(B) The generation interval
(C) The selection intensity
(D) The economic weight of the trait

2021

60. Identify the INCORRECT pair regarding variance partitioning.
(A) Total Variance - Phenotypic Variance
(B) Epistatic Variance - Interaction between alleles at the same locus
(C) Additive Variance - Breeding Value Variance
(D) Environmental Variance - Non-genetic influences

2023

61. If a trait has a repeatability of 0.6, what does this imply for culling decisions in dairy cattle?
(A) First lactation yield is a reliable indicator of future lactations.
(B) The first record is a poor indicator of future performance.
(C) Environmental variance is zero.
(D) Dominance variance is the sole cause of variation.

2025

62. Which statistic is minimized to estimate index weights in a selection index?
(A) The total environmental variance associated with the selection index
(B) Sum of squared differences between true breeding value and the index
(C) The genetic covariance estimated among all traits within the index
(D) The mean square error calculated for all fixed effects in the model

2024

63. Identify the correct sequence of steps to establish a progeny testing program:
I. Test mating of young bulls
II. Evaluation of daughter performances
III. Selection of elite cows (bull mothers)
IV. Widespread use of proven bulls
(A) III → I → II → IV
(B) I → III → II → IV
(C) III → II → I → IV
(D) I → II → III → IV

2024

64. When analyzing unbalanced animal breeding data, fixed effects are typically handled by Least Squares Analysis. What defines an unbalanced data set?
(A) Unequal subclass numbers.
(B) The mean of the data is zero.
(C) Only one sire is used.
(D) Residuals are normally distributed.

2002

65. Multidimensional Scaling (MDS) in morphometric analysis is used for:
(A) Maximization of the linkage disequilibrium between genetic markers
(B) Prediction of the breeding value directly from phenotypic data
(C) Alignment of DNA sequences to identify homologous genetic regions
(D) Visualization of similarity or distance between individual cases

2019

66. In phylogenetic reconstruction, the Maximum Parsimony method chooses the tree that:
(A) Maximizes the likelihood of the data
(B) Requires the fewest evolutionary changes
(C) Calculates the exact substitution rate
(D) Assumes a strict molecular clock

2023

67. Single-step GBLUP (ssGBLUP) is advantageous over traditional GBLUP because it:
(A) Combines pedigree and genomic relationship matrices simultaneously
(B) Ignores pedigree information completely
(C) Analyzes only un-genotyped animals
(D) Eliminates the need for any phenotypic data

2003

68. Which bioinformatics database is maintained by the European Bioinformatics Institute (EBI) and provides centralized genomic data?
(A) Ensembl

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(B) The relative ranking of genotypes changes across environments
(C) Environment has no effect on phenotypic variance
(D) Genotypes can be predicted without knowing the environment

2001

49. In ANOVA for an unbalanced design, Henderson's Method 2 cannot be applied if:
(A) Data are cross-classified across multiple management groups
(B) The model contains no fixed effects except the general mean
(C) Presence of interactions between fixed and random effects
(D) Heritability of the trait is highly variable across herds

2007

50. The Average Information (AI) algorithm in REML is preferred over the EM algorithm because:
(A) It requires fewer iterations to converge
(B) It does not require a prior distribution
(C) It assumes non-normal distributions
(D) It avoids computing first derivatives

2003

51. MINQUE possesses which of the following statistical properties?
(A) It is always a maximum likelihood estimator.
(B) It allows for negative estimates of variance components.
(C) It requires no assumptions about the normality of data.
(D) It is a Bayesian estimator.

2013

52. Markov Chain Monte Carlo (MCMC) methods in Bayesian estimation rely heavily on the assumption that:
(A) The next state depends only on the current state
(B) The parameter space is finite
(C) The sample size is extremely small
(D) Prior distributions are always flat

2014

53. If animal X is an offspring of a mating between full siblings, what is its inbreeding coefficient?
(A) 0.0625
(B) 0.1250
(C) 0.2500
(D) 0.5000

2015

54. In Henderson's Mixed Model Equations (MME), the inverse of the relationship matrix ($A^{\{-1\}}$) is multiplied by which factor before being added to the diagonal?
(A) $\frac{\sigma_E^2}{\sigma_A^2}$
(B) $\frac{\sigma_A^2}{\sigma_E^2}$
(C) h^2
(D) σ_P^2

2025

55. Match the Genetic Model (List I) to its key characteristic (List II).
List I: (Genetic Model)
P. Animal Model
Q. Sire Model
R. Repeatability Model
S. Random Regression
List II: (Characteristic)
1. Assumes permanent environment effects
2. Analyzes longitudinal test-day records
3. Considers the relationship of all individuals
4. Estimates transmitting ability of fathers only
(A) P-3, Q-4, R-1, S-2
(B) P-4, Q-3, R-1, S-2
(C) P-3, Q-1, R-4, S-2
(D) P-1, Q-4, R-3, S-2

2023

56. What does an infinite-dimensional genetic model usually refer to in animal breeding?
(A) Random Regression Model over continuous time
(B) Sire model with fixed effects
(C) Genomic selection with missing markers
(D) Threshold model for binary traits

2011

57. The path coefficient method calculates the coefficient of relationship between two non-inbred full sibs as:
(A) 0.25
(B) 0.50
(C) 0.75
(D) 1.00

2017

58. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).

NODIA

(C) Overlapping generations make N_e calculation impossible.
(D) It implies that all individuals breed at the exact same age.

2014

79. The standard error of a heritability estimate from a parent-offspring regression is reduced by:
(A) Increasing the number of parent-offspring pairs
(B) Increasing the phenotypic variance
(C) Decreasing the number of offspring per parent
(D) Decreasing the genetic variation

2021

80. Match the software/tool (List I) with its primary bioinformatic or genetic function (List II).
List I: (Software/Tool)
P. BLAST
Q. ClustalW
R. Gibbs3F90
S. GenBank
List II: (Function)
1. Multiple sequence alignment
2. Bayesian animal model analysis
3. Sequence database repository
4. Local sequence alignment search
(A) P-4, Q-1, R-2, S-3
(B) P-1, Q-4, R-3, S-2
(C) P-4, Q-2, R-1, S-3
(D) P-2, Q-3, R-4, S-1

2003

81. In multi-trait analysis, a genetic correlation of -0.85 between milk yield and fat percentage suggests:
(A) The two traits are genetically independent.
(B) The two traits are controlled by the exact same single gene.
(C) Selecting for higher milk yield will likely increase fat percentage.
(D) Selecting for higher milk yield will likely decrease fat percentage.

2012

82. If the selection proportion (p) decreases, the selection intensity (i) generally:
(A) Decreases
(B) Remains unchanged
(C) Increases
(D) Becomes zero

2003

83. The economic weight used in a Selection Index is defined as:
(A) Profit change per unit trait change while holding other traits constant
(B) Monetary value associated with a one standard deviation trait change
(C) Cost of feed required per animal to reach standard market conditions
(D) Trait heritability multiplied by the prevailing market price

2012

84. In smallholder farming systems, a major limitation of implementing traditional progeny testing is:
(A) The very short generation interval typically observed in cattle
(B) High level of genetic variation found among indigenous breeds
(C) The abundance of very large contemporary groups in small herds
(D) Requirement for extensive pedigree recording infrastructure

2018

85. When applying Least Squares Analysis, a covariate is typically used to adjust for:
(A) Continuous environmental effects like age at calving
(B) Categorical environmental effects like season
(C) Additive genetic effects
(D) Dominance effects

2017

86. Variable selection techniques in Multiple Linear Regression, such as Stepwise Regression, aim to:
(A) Identify a subset of predictors that models the response effectively without overfitting
(B) Increase the number of predictors to maximize R-squared
(C) Eliminate all fixed effects from the model
(D) Maximize multicollinearity among covariates

2002

87. In Principal Component Analysis (PCA), the eigenvalue of a principal component indicates:
(A) The amount of variance captured by that component
(B) The number of variables included
(C) The statistical significance of the component
(D) The correlation between the component and the residuals

2017

88. Nei's standard genetic distance formula assumes that differences between populations arise mainly from:
(A) Mutation and genetic drift

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(B) GenBank
(C) DDBJ
(D) PubMed

2022

69. Epistatic variance refers to the variation arising from:
(A) Interaction of alleles at different loci
(B) Interaction of alleles at the same locus
(C) Additive effects of alleles
(D) Temporary environmental effects

2023

70. In Henderson's Method 1, estimation of variance components uses:
(A) Analogues of analysis of variance mean squares for unbalanced data
(B) Restricted maximum likelihood
(C) Bayesian priors
(D) The generalized inverse of the relationship matrix

2023

71. In REML, the likelihood function is derived based on:
(A) The joint distribution of all fixed effects
(B) The prior distribution of the variance components
(C) The marginal distribution of error contrasts
(D) The cumulative density of the covariates

2010

72. Which of the following defines the characteristic feature of MIVQUE estimators?
(A) They are translation invariant and locally minimum variance.
(B) They are biased but consistent.
(C) They require integration over all possible pedigrees.
(D) They cannot handle fixed effects.

2017

73. Consider the following statements regarding the Gibbs sampler in quantitative genetics:
I. It is a special case of the Metropolis-Hastings algorithm.
II. It requires fully conditional posterior distributions.
III. It always yields independent samples at each iteration.
IV. It uses a "burn-in" period to reach the stationary distribution.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) I and III
(C) II, III and IV
(D) I, II, III and IV

2017

74. For an animal whose parents are known, the off-diagonal element $A_{\{ij\}}$ in the additive genetic relationship matrix is calculated as:
(A) $0.5(A_{\{is\}} + A_{\{id\}})$ where s and d are parents of j
(B) $A_{is} \times A_{id}$
(C) $1 + 0.5A_{\{sd\}}$
(D) $0.25(A_{\{is\}} + A_{\{id\}})$

2022

75. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): The BLUP method accounts for assortative mating and selection in the estimation of breeding values.
Reason (R): The use of the full additive genetic relationship matrix (A) in the Mixed Model Equations links all relatives, correcting for non-random mating.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2013

76. The Repeatability Model assumes that the genetic correlation between repeated records of the same animal is:
(A) 0
(B) 0.5
(C) 1.0
(D) Variable depending on the environment

2007

77. In Random Regression Models, varying the order of fit (e.g., from linear to quadratic to cubic) changes the:
(A) Number of estimated covariance components
(B) Fixed effects structure only
(C) Average relatedness of the herd
(D) Selection intensity

2017

78. Which of the following is true regarding overlapping generations in calculating effective population size (N_e)?
(A) It drastically increases N_e beyond census size.
(B) Generation interval and variance in family size must be accounted for.

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(C) Ignores the genetic merit of the dams
(D) Estimates only permanent environmental effects

2021

99. In Random Regression Models, test-day records are modeled as a function of:
(A) Days in milk (DIM)
(B) Generation interval
(C) Number of lactations
(D) Parity only

2022

100. Consider the following statements regarding the inbreeding coefficient (F):
I. It ranges from 0 to 1.
II. It represents the probability that two alleles at a locus are identical by descent.
III. It decreases homozygosity in a population.
IV. It can be negative in outbred populations relative to a base population.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) I, II and III
(C) II, III and IV
(D) I and IV

2021

101. The rate of inbreeding (ΔF) per generation can be approximated from the effective population size (N_e) using which formula?
(A) $\frac{1}{2N_e}$
(B) $\frac{1}{N_e}$
(C) $\frac{2}{N_e}$
(D) $\frac{N_e}{2}$

2010

102. Heritability in the broad sense is defined as the ratio of:
(A) Additive genetic variance to phenotypic variance
(B) Total genetic variance to phenotypic variance
(C) Dominance variance to phenotypic variance
(D) Additive genetic variance to environmental variance

2007

103. If MPPA is calculated for a cow with n records, a repeatability of r, and a herd average of μ, the weighting factor applied to her deviation from the herd average is:
(A) $\frac{nr}{1+(n-1)r}$
(B) $\frac{n}{1+(n-1)r}$
(C) $\frac{r}{1+nr}$
(D) $\frac{(n-1)r}{1+n}$

2021

104. Genetic correlation estimates obtained from multi-trait models are generally more accurate than single-trait models because multi-trait models:
(A) Use information from correlated traits to account for selection bias
(B) Ignore environmental covariance between all traits in the model
(C) Increase selection intensity for all primary traits of interest
(D) Decrease the effective population size of the reference herd

2004

105. Match the concept in quantitative genetics (List I) with its correct definition or formula (List II).
List I: (Concept)
P. Breeder's Equation response (R)
Q. Additive relationship matrix (A)
R. Expected Mean Squares
S. Gibbs Sampling
List II: (Definition/Formula)
1. $i \cdot r \cdot \sigma_A$
2. Henderson's tabular method
3. MCMC method
4. Used in ANOVA for variance components
(A) P-1, Q-2, R-4, S-3
(B) P-2, Q-1, R-3, S-4
(C) P-1, Q-4, R-2, S-3
(D) P-4, Q-3, R-2, S-1

2025

106. In the derivation of Smith-Hazel selection index weights, the phenotypic variance-covariance matrix (P) must be:
(A) Positive definite and invertible
(B) Singular
(C) A diagonal matrix only
(D) Identical to the genetic covariance matrix

2006

107. Contemporary comparison evaluates a sire by comparing the records of his daughters against:
(A) Records of herdmates calving in the same season and year

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(B) Their dams' records
(C) The theoretical maximum yield of the breed
(D) The national average of a different breed

2011

108. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Least Squares Analysis provides biased estimates if fixed effects are correlated with random genetic effects in unbalanced data.
Reason (R): LSA treats all effects as fixed and cannot incorporate the additive genetic relationship matrix (A).
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2004

109. To detect multicollinearity in Multiple Linear Regression, which diagnostic metric is most commonly used?
(A) Variance Inflation Factor (VIF)
(B) R-squared
(C) Durbin-Watson statistic
(D) Shapiro-Wilk test

2016

110. Identify the INCORRECT statement regarding Discriminant Function Analysis.
(A) It constructs a linear combination of independent variables.
(B) It requires a continuous categorical independent variable.
(C) It requires a predefined classification (categorical dependent variable).
(D) It can be used for morphometric breed characterization.

2018

111. The fixation index ($F_{\{ST\}}$) measures:
(A) The reduction in heterozygosity in subpopulations relative to the total population
(B) The mutation rate of a single locus
(C) The structural variation in a genome
(D) The physical distance between two genes on a chromosome

2005

112. The Neighbor-Joining method for phylogenetic trees is a:
(A) Distance-based clustering method
(B) Character-based parsimony method
(C) Maximum likelihood probabilistic method
(D) Bayesian MCMC method

2010

113. In Genomic Selection, the reference population is defined as the group of animals that possess:
(A) Both genotypic and phenotypic data
(B) Only genotypic data
(C) Only phenotypic data
(D) Neither genotypic nor phenotypic data

2005

114. The ClustalW program calculates the best match for sequences by performing a:
(A) Progressive multiple sequence alignment
(B) Localized search against a single database
(C) Bayesian estimation of phylogenetic trees
(D) Functional annotation of proteins

2021

115. Partitioning phenotypic variance into genetic and environmental variance requires the assumption that genetic and environmental effects are:
(A) Independent (no covariance) in a simple additive model
(B) Perfectly correlated
(C) Multiplicative
(D) Always inversely related

2010

116. Which method of Henderson is specifically designed to handle mixed models containing both fixed and random effects, providing unbiased estimators?
(A) Method 3
(B) Method 1
(C) Method 2
(D) Method 4

NODIA

2004

117. In the context of variance component estimation, what does REML maximize?
(A) The likelihood of a set of error contrasts that are independent of the fixed effects
(B) The likelihood of the data given the fixed effects
(C) The phenotypic variance
(D) The probability of the prior distribution

2025

118. Identify the correct sequence of steps for computing Wright's inbreeding coefficient via the tabular method:
I. Initialize base population diagonals to 1
II. Identify the chronological order of the

pedigree
III. Compute off-diagonals as average of parents
IV. Compute diagonals as $1 + 0.5 \times$ relationship of parents
(A) II → I → III → IV
(B) I → II → IV → III
(C) II → III → I → IV
(D) I → IV → III → II

2025

119. A defining characteristic of a proper prior distribution in Bayesian statistics is that:
(A) It integrates to exactly 1
(B) It integrates to infinity
(C) It is always a uniform distribution
(D) It is derived solely from the likelihood function

2019

120. When constructing the A-matrix for 1000 animals, the dimension of the resulting matrix is:
(A) 1000 x 1000
(B) 1000 x 1
(C) 100 x 100
(D) 2000 x 2000

2011

121. In Henderson's Mixed Model Equations, the matrix Z represents:
(A) Incidence matrix for random effects
(B) Incidence matrix for fixed effects
(C) Additive genetic relationship matrix
(D) Variance-covariance matrix of residuals

2010

122. Under the Repeatability Model, the variance of the permanent environmental effect is combined with the additive genetic variance to calculate:
(A) Repeatability
(B) Heritability
(C) Selection intensity
(D) Inbreeding coefficient

2011

123. Consider the following statements regarding Random Regression Models:
I. They allow genetic correlations between different days in milk to be less than one.
II. They assume a constant environmental variance across all test days.
III. They can predict breeding values for any point along the trajectory.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I, II and III

2005

124. The path coefficient between a grandparent and a grand-offspring in a non-inbred population is:
(A) 0.50
(B) 0.25
(C) 0.125
(D) 0.0625

2011

125. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Overlapping generations slow down the rate of inbreeding per year compared to discrete generations, given the same number of breeding individuals.
Reason (R): Overlapping generations increase the generation interval and maintain a broader age distribution of parents.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

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2004

126. A heritability estimate of 0.05 for a trait typically indicates that the trait:
(A) Is likely related to fitness or survival
(B) Is highly responsive to mass selection
(C) Has zero phenotypic variation
(D) Is determined entirely by a single gene

2013

127. The ratio of the covariance between repeated records to the total phenotypic variance defines:
(A) Repeatability
(B) Heritability
(C) Inbreeding coefficient
(D) Genetic correlation

2015

128. If two traits have a highly positive genetic correlation, indirect selection for Trait 2 by selecting on Trait 1 will:
(A) Cause Trait 2 to increase
(B) Have no effect on Trait 2
(C) Cause Trait 2 to decrease
(D) Increase the environmental variance of Trait 2

2018

129. The Annual Genetic Gain ($\frac{\Delta G}{\text{year}}$) formula divides the response to selection by:
(A) Generation interval
(B) Phenotypic standard deviation
(C) Heritability
(D) Number of sires

2007

130. Match the Selection Index concepts (List I) with their descriptions (List II).
List I: (Concept)
P. Base Index
Q. Restricted Index
R. Optimum Index
S. Retrospective Index
List II: (Description)
1. Holds the genetic change of one or more traits to zero
2. Based solely on economic values without phenotypic covariances
3. Derives index weights after selection has occurred
4. Uses proper genetic and phenotypic (co) variances
(A) P-2, Q-1, R-4, S-3
(B) P-1, Q-2, R-3, S-4
(C) P-4, Q-3, R-2, S-1
(D) P-3, Q-4, R-1, S-2

2012

131. In indigenous farming systems, the lack of structured contemporary groups is usually mitigated by:
(A) Using reference sires (AI) across multiple smallherds to create linkages
(B) Comparing across different climates
(C) Creating synthetic breeds
(D) Relying solely on natural service sires

2017

132. Least Squares Analysis adjusts data for fixed effects. Which of the following is an example of a fixed effect in a dairy cattle model?
(A) Year and season of calving
(B) Breeding value of the sire
(C) Permanent environment of the cow
(D) Mendelian sampling error

2015

133. When applying Ridge Regression, as the ridge penalty parameter (λ) increases, the variance of the estimators:
(A) Decreases
(B) Increases
(C) Remains unchanged
(D) Becomes infinite

2001

134. Which multivariate technique is most appropriate for condensing 20 correlated morphometric measurements of a goat breed into 3 independent composite traits for visualization?
(A) Principal Component Analysis (PCA)
(B) Multiple Linear Regression
(C) Logistic Regression
(D) Discriminant Function Analysis

2008

135. Identify the correct statement regarding UPGMA (Unweighted Pair Group Method with Arithmetic Mean).
(A) It assumes a strict molecular clock (equal rates of evolution).
(B) It assumes unequal rates of evolution along different branches.
(C) It produces an unrooted tree.
(D) It is a character-based reconstruction method.

2016

136. In genomic selection, what matrix replaces the traditional pedigree-based A-matrix in the GBLUP model?
(A) G-matrix
(B) H-matrix
(C) D-matrix
(D) P-matrix

2006

137. Which of the following sequence alignment algorithms focuses on global alignment?
(A) Needleman-Wunsch
(B) Smith-Waterman
(C) BLAST
(D) BLAT

2006

138. Which phenomenon occurs when the phenotypic expression of a genotype is contingent upon the specific environmental condition?
(A) Genotype x Environment Interaction
(B) Pleiotropy
(C) Epistasis
(D) Linkage disequilibrium

2018

139. In a completely randomized design with balanced data, ANOVA estimates of variance components are identical to:
(A) REML and Henderson Method 1 estimates
(B) Maximum Likelihood estimates only

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(C) Bayesian posterior means
(D) MINQUE estimators with incorrect priors

2010

140. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): The EM algorithm for REML ensures that the estimated variance components are always within the parameter space (e.g., non-negative).
Reason (R): The EM algorithm updates parameters by setting them exactly to the first derivative of the likelihood function.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2002

141. The MIVQUE estimator has minimum variance only if the prior values supplied are:
(A) The true parameter values
(B) Exactly zero
(C) Infinite
(D) Equal to the phenotypic mean

2024

142. A major advantage of using Bayesian MCMC approaches over REML in complex models is:
(A) It provides the full posterior distribution, easily giving standard errors and credible intervals.
(B) It requires no prior distributions.
(C) It computes exact solutions without iteration.
(D) It is faster for small datasets.

2006

143. Using Henderson's tabular method, if the relationship between animals X and Y is 0.25, the relationship between their half-sib offspring (sharing no other common ancestors) will be:
(A) 0.0625
(B) 0.125
(C) 0.25
(D) 0.50

2009

144. In MME, the term λ added to the diagonals of the random effect block is mathematically defined as:
(A) $\frac{\sigma_E^2}{\sigma_A^2}$
(B) $\frac{\sigma_A^2}{\sigma_E^2}$
(C) $\frac{h^2}{1-h^2}$
(D) σ_P^2

2010

145. Under a Sire Model, the heritability is estimated as $\frac{4\sigma_s^2}{\sigma_s^2+\sigma_e^2}$. What does σ_e^2 represent in this specific formula?
(A) Three-quarters of the additive variance plus residual environmental variance
(B) Environmental variance only
(C) Additive genetic variance only
(D) Phenotypic variance

2016

146. Identify the INCORRECT statement regarding the Repeatability Model.
(A) It assumes the genetic correlation between repeated measures is zero.
(B) It is applicable to traits like milk yield in cattle.
(C) It models permanent environmental effects separately from temporary ones.
(D) It provides an estimate of Most Probable Producing Ability.

2014

147. Random Regression Models are said to handle "infinite-dimensional" traits because:
(A) They model traits measured continuously over time, forming a continuous trajectory
(B) The pedigree size is theoretically infinite
(C) They include infinite fixed effects
(D) They do not require a variance-covariance matrix

NODIA

2016

148. Which formula properly calculates the inbreeding coefficient (F) of an individual based on its parents A and B?
(A) $F = 0.5 \times R_{AB}$
(B) $F = R_{\{AB\}}$
(C) $F = 2 \times R_{AB}$
(D) $F = \sqrt{R_{AB}}$

2012

149. If a closed population has 10 males and 90 females, the effective population size (N_e) is:
(A) 10
(B) 36
(C) 50
(D) 100

(C) The number of fixed effects
(D) The specific statistical software used

2021

190. In a Bayesian analysis of an animal model, what is the standard prior distribution commonly assigned to the variance components?
(A) Inverted Chi-square or Inverse-Wishart distribution
(B) Normal distribution
(C) Uniform distribution
(D) Poisson distribution

2017

191. Using Henderson's tabular rules, if animal X has sire S and dam D, the off-diagonal relationship between X and another animal Y is:
(A) $0.5 \times (R_{SY} + R_{DY})$
(B) $R_{\{SY\}} + R_{\{DY\}}$
(C) $R_{SY} \times R_{DY}$
(D) $0.25 \times (R_{SY} + R_{DY})$

2002

192. In MME, an animal without any records (e.g., a sire evaluated purely on progeny) will still get a breeding value estimate. This occurs because:
(A) The off-diagonal elements of $A^{\{-1\}}$ link the sire to its progeny's records
(B) The model assigns the population mean
(C) Fixed effects substitute for missing records
(D) The residual variance is set to zero

2003

193. Under the Repeatability Model, the permanent environmental effect (PE) and the residual temporary environmental effect (TE) are assumed to be:
(A) Uncorrelated (independent)
(B) Highly correlated
(C) Multiplicative
(D) Identical

2004

194. Identify the INCORRECT statement regarding the Sire Model.
(A) It estimates the full breeding value (1.0 of additive genetic merit) directly.
(B) It requires fewer equations than the Animal Model.
(C) It ignores the additive genetic variance contributed by dams.
(D) It is generally being replaced by the Animal Model in modern genetic evaluations.

2015

195. Which type of regression model fits a curve to repeated records over time for individual animals by modeling covariance structures?
(A) Random Regression Model
(B) Multiple Linear Regression
(C) Logistic Regression
(D) Probit Regression

2015

196. If a trait is controlled by genes located on the X chromosome, calculation of Wright's inbreeding coefficient must account for the fact that:
(A) Males are hemizygous and cannot be inbred for X-linked traits.
(B) Females cannot be inbred.
(C) Autosomal rules apply perfectly.
(D) Mutation rates are higher.

2016

2011

197. In a herd with 100 breeding females and only 1 breeding male, the effective population size (N_e) is:
(A) 1
(B) 4
(C) 50
(D) 101

2009

198. The paternal half-sib correlation method estimates heritability by calculating the intra-class correlation (t). Heritability (h^2) is then derived as:
(A) t
(B) $2t$
(C) $4t$
(D) $\frac{t}{4}$

2025

199. When computing MPPA, animals with a greater number of repeated records will have their MPPA estimate:
(A) Pushed closer to their own phenotypic mean
(B) Pulled closer to the population mean
(C) Pulled perfectly to zero
(D) Reduced to a negative value

2024

200. Consider the following statements regarding genetic correlation estimation:
I. Multi-trait animal models provide unbiased estimates even under sequential selection.
II. Genetic correlations can only be positive.
III. They are derived from the genetic covariance

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variables
(D) The genomic relationship between individuals

2011

159. The UPGMA method of tree construction assumes a constant molecular clock, meaning:
(A) All lineages evolve at the same rate
(B) Lineages can evolve at drastically different rates
(C) Mutation rates are zero
(D) Genetic drift does not occur

2005

160. Consider the following statements regarding Single-Step GBLUP (ssGBLUP):
I. It requires the calculation of an H-matrix.
II. It blends the pedigree relationship matrix (A) and the genomic relationship matrix (G).
III. It can only be used if all animals in the pedigree are genotyped.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I, II and III

2002

161. Which bioinformatics format is the standard for representing sequence alignment and uses a header line beginning with a greater-than symbol (>)?
(A) FASTA
(B) FASTQ
(C) BAM
(D) VCF

2013

162. Genotype-environment interaction causes the genetic correlation of the same trait expressed in two different environments to be:
(A) Less than 1.0
(B) Exactly 1.0
(C) Exactly zero
(D) Mathematically undefined

2012

163. Henderson's Method 1 is inappropriate for estimating variance components when the data include:
(A) Fixed effects (other than the general mean)
(B) Random effects
(C) Balanced class numbers
(D) Unequal observations per subclass

2005

164. The primary disadvantage of ML compared to REML in variance component estimation is that ML:
(A) Does not correct for degrees of freedom used to estimate fixed effects (downward bias)
(B) Overestimates the variance components
(C) Is purely an empirical method
(D) Cannot handle random effects

2009

165. MIVQUE estimation simplifies to MINQUE when:
(A) The data follow a normal distribution
(B) The data are not normally distributed
(C) The fixed effects are ignored
(D) The assumed priors are zero

NODIA

2022

166. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Gibbs sampling in Bayesian analysis requires the knowledge of fully conditional posterior distributions for each parameter.
Reason (R): Gibbs sampling updates one parameter at a time by sampling from its conditional distribution given the current values of all other parameters.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2018

167. In a large population, constructing the full inverse of the A-matrix directly by matrix inversion (N^3 operations) is computationally demanding. Henderson's rules construct $A^{\{-1\}}$ in time proportional to:
(A) N
(B) N^3
(C) N^2
(D) $\log(N)$

2018

168. In MME for an Animal Model, solving the equations provides the Best Linear Unbiased Estimates (BLUE) for:
(A) Fixed effects
(B) Additive genetic effects
(C) Random residuals
(D) Inbreeding coefficients

2013

169. What proportion of the dominance genetic variance is transferred from a sire to his progeny in a purely outbred population?
(A) 0%
(B) 25%
(C) 50%
(D) 100%

2018

170. Which mathematical function is widely used to model the typical shape of a dairy cattle lactation curve in Random Regression Models?
(A) Ali-Schaeffer function
(B) Gompertz function
(C) Weibull function
(D) Logistic growth curve

2003

171. If an individual is inbred, its diagonal element in the A-matrix $(1 + F)$ will be:
(A) Equal to 1
(B) Greater than 1
(C) Less than 1
(D) Zero

2021

172. The term "overlapping generations" implies that:
(A) Individuals of different age cohorts breed at the same time
(B) Parents breed only once and die
(C) Generations are strictly separated by time
(D) Only animals of the exact same age can mate

2005

173. Which of the following describes the difference between repeatability and heritability?
(A) Repeatability includes both additive genetic variance and permanent environmental variance; heritability only includes additive genetic variance.
(B) Heritability is always larger than repeatability.
(C) Heritability is based on phenotypic correlation; repeatability is based on genotypic correlation.
(D) Repeatability applies only to single-record traits.

2024

174. In the calculation of Most Probable Producing Ability (MPPA), if a cow has an infinite number of records $(n \backslash to \infty)$, the MPPA approaches:
(A) The cow's true phenotypic mean
(B) The herd average
(C) Zero
(D) The sire's breeding value

2021

175. Match the Bioinformatics Tool or Database (List I) with its biological scope (List II).
List I: (Tool/Database)
P. Ensembl
Q. PubMed
R. Uniprot
S. GenBank
List II: (Scope)
1. Protein sequence and function
2. Vertebrate genomes and annotation
3. Nucleotide sequence repository
4. Biomedical literature
(A) P-2, Q-4, R-1, S-3
(B) P-1, Q-2, R-3, S-4
(C) P-3, Q-1, R-4, S-2
(D) P-4, Q-3, R-2, S-1

2002

176. A genetic correlation of zero between two traits indicates that:
(A) The genes affecting one trait have no pleiotropic effects on the other.
(B) They are perfectly inherited together.
(C) The traits are heavily influenced by the same environment.
(D) Neither trait has any additive genetic variance.

2021

177. If the accuracy of selection $(r_{\{TI\}})$ is 0.8, selection intensity (i) is 1.5, and additive genetic standard deviation (σ_A) is 10, what is the expected genetic response per generation?
(A) 8
(B) 10
(C) 12
(D) 15

2012

178. The economic weights in a restricted selection index are manipulated mathematically so that:
(A) The genetic gain for a specific trait is constrained to zero
(B) All traits achieve maximum genetic gain
(C) Phenotypic variance is eliminated
(D) The generation interval is reduced to zero

2005

179. Under smallholder farming systems, what statistical model is best suited to compare sire progeny performances when group sizes are extremely small and disconnected?
(A) Animal Model with genetic ties (e.g., through

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AI reference sires)
(B) Simple arithmetic averaging
(C) Unadjusted contemporary comparison
(D) Phenotypic correlation

2018

180. Consider the following statements regarding Least Squares Analysis (LSA):
I. It minimizes the sum of squared errors.
II. It requires inversion of the coefficient matrix.
III. It handles random effects identically to fixed effects.
IV. It provides unbiased estimators for fixed effects.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) I and III
(C) II, III and IV
(D) I and IV

2024

181. Ridge regression introduces a bias into estimators to significantly reduce:
(A) Variance of the estimators under multicollinearity
(B) The number of observations needed
(C) The number of variables in the model
(D) The computational time

2014

182. In Principal Component Analysis, a "scree plot" is visually used to determine:
(A) The number of principal components to retain
(B) The normality of the residuals
(C) The clustering of genotypes
(D) The phylogenetic distance between species

2012

183. Cavalli-Sforza and Edwards chord distance assumes that allele frequency changes are driven purely by:
(A) Genetic drift
(B) Selection
(C) Mutation
(D) Migration

2018

184. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Single-step GBLUP (ssGBLUP) blends the genomic relationship matrix (G) and the pedigree relationship matrix (A) to form the H matrix.
Reason (R): This allows the simultaneous genetic evaluation of both genotyped and ungenotyped animals in a single run.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2024

185. Which algorithm searches a sequence database by finding short matches (words) and then extending them to create high-scoring segment pairs (HSPs)?
(A) BLAST
(B) ClustalW
(C) Needleman-Wunsch
(D) UPGMA

2007

186. In quantitative genetics, the interaction variance (V_I) specifically includes which of the following?
(A) Additive x Additive, Additive x Dominance, and Dominance x Dominance epistasis
(B) Genotype x Environment interactions only
(C) Dominance deviations only
(D) Permanent environmental effects

2016

187. Henderson's Method 2 uses data adjusted for fixed effects to estimate variance components. Why is it invalid for models with interactions between fixed and random effects?
(A) The fixed effects cannot be adjusted cleanly without biasing the random interactions.
(B) It requires normal distributions which are violated.
(C) It turns all random effects into fixed effects.
(D) It sets the phenotypic variance to zero.

2022

188. Which algorithm used in REML estimation uses second derivatives (Hessian matrix) for faster convergence?
(A) Newton-Raphson Algorithm
(B) EM Algorithm
(C) Gibbs Sampler
(D) Simplex Algorithm

2021

189. MIVQUE estimates are locally minimum variance. "Locally" means the minimum variance property depends on:
(A) The true (but unknown) values of the variance components provided as priors
(B) The geographical location of the sample

NODIA

(C) The environment has no effect.
(D) Phenotypic variance is zero.

2011

210. Henderson's Method 3 accounts for which of the following that Methods 1 and 2 do not?
(A) It provides unbiased estimates of variance components for general mixed models with unbalanced data.
(B) It applies strictly to balanced data.
(C) It computes exact Bayesian posteriors.
(D) It ignores fixed effects entirely.

2005

211. Which of the following defines the Average Information (AI) matrix used in AI-REML?
(A) An average of the observed and expected information matrices
(B) The identity matrix
(C) The exact second derivative of the likelihood
(D) The matrix of phenotypic covariances

2015

212. What is the fundamental difference between MIVQUE and REML estimators?
(A) MIVQUE is non-iterative and depends on prior values, whereas REML is iterative and updates priors.
(B) MIVQUE requires balanced data; REML does not.
(C) MIVQUE calculates fixed effects; REML ignores them.
(D) MIVQUE assumes Poisson distributions; REML assumes normal distributions.

2023

213. In Markov Chain Monte Carlo (MCMC) methods, the "burn-in" period refers to:
(A) The initial iterations that are discarded because the chain has not yet reached its stationary distribution
(B) The final iterations where parameters are fixed
(C) The process of computing the maximum likelihood
(D) The physical destruction of outliers

2008

214. If a herd has 5 distinct families, and you construct the A-matrix, animals from completely different families (no common ancestors) will have off-diagonal elements equal to:
(A) 0.0
(B) 1.0
(C) 0.5
(D) -1.0

2023

215. The Mixed Model Equations (MME) formulated by Henderson are favored over traditional generalized least squares because MME:
(A) Do not require the inversion of the large phenotypic covariance matrix (V).
(B) Guarantee non-negative variance estimates.
(C) Require balanced data, which is easier to collect.
(D) Eliminate all environmental variance.

2021

216. In an Animal Model with maternal effects, the maternal genetic effect is typically fitted as a:
(A) Correlated random effect
(B) Fixed effect
(C) Covariate
(D) Temporary environmental effect

2011

217. Identify the INCORRECT statement regarding Random Regression Models for test-day yields.
(A) They model individual lactation curves.
(B) They require the exact same days in milk (DIM) for every animal.
(C) They estimate genetic parameters for continuous time points.
(D) They allow genetic correlations between different days in milk to be less than 1.

2005

218. When computing inbreeding through path coefficients, the term $\left(\frac{1}{2}\right)^n$ applies where n is:
(A) The number of common ancestors
(B) The number of individuals in the path connecting the parents through a common ancestor
(C) The number of fixed effects
(D) The generation interval

2013

219. Effective population size (N_e) is inversely proportional to:
(A) The rate of inbreeding (ΔF)
(B) The total census size
(C) The generation interval
(D) The number of loci

2007

220. Consider the following statements regarding narrow-sense heritability:
I. It is the ratio of additive genetic variance to phenotypic variance.
II. It dictates the degree of resemblance between relatives.
III. It can be estimated using parent-offspring

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between two traits divided by the product of their genetic standard deviations.

Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I, II and III

2012

201. Which component of the Breeder's Equation is directly modified when genetic evaluations utilize genomic selection instead of traditional progeny testing?
(A) Generation interval is significantly reduced.
(B) Additive genetic variance is permanently increased.
(C) Heritability becomes 1.0.
(D) Selection intensity drops to zero.

2023

202. The Smith-Hazel selection index requires calculation of genetic parameters. Which of the following is NOT required?
(A) Dominance variances of all traits
(B) Phenotypic variances of all traits
(C) Genetic covariances between all traits
(D) Economic values of all traits

2003

203. In smallholder farming systems where artificial insemination is rare, the most significant obstacle to progeny testing is:
(A) Extremely high recording costs and lack of pedigree linkages across herds
(B) Rapid generation turnover
(C) Inbreeding depression
(D) Excessive use of a single sire

2021

204. In Least Squares Analysis, what does it mean when the system of normal equations is singular?
(A) The matrix does not have an inverse due to linear dependencies.
(B) There is only one solution.
(C) There are no fixed effects.
(D) Residuals are zero.

2025

205. Match the statistical technique (List I) with its specific application in breeding (List II).
List I: (Technique)
P. Ridge Regression
Q. PCA
R. Discriminant Function
S. LSA
List II: (Application)
1. Classifying animals into distinct pre-defined breed groups
2. Estimating fixed effects in unbalanced data
3. Handling multicollinearity in predictor variables
4. Reducing dimensionality of morphometric traits
(A) P-3, Q-4, R-1, S-2
(B) P-4, Q-3, R-2, S-1
(C) P-3, Q-1, R-4, S-2
(D) P-1, Q-4, R-2, S-3

2016

206. Which method of phylogenetic tree construction builds the tree step-by-step by grouping the two most closely related operational taxonomic units (OTUs)?
(A) UPGMA
(B) Maximum Likelihood
(C) Maximum Parsimony
(D) Bayesian MCMC

2013

207. In Bayesian genomic selection models (e.g., Bayes A, Bayes B), the marker effects are treated as:
(A) Random effects with specific prior distributions
(B) Fixed effects
(C) Non-genetic environmental effects
(D) Constants

2012

208. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): BLAST is a heuristic algorithm, meaning it does not guarantee finding the mathematically optimal sequence alignment.
Reason (R): It sacrifices the guarantee of mathematical optimality to drastically improve search speed in huge databases.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2002

209. Under quantitative genetics theory, genotype-environment interaction (GxE) exists when:
(A) The reaction norms of different genotypes cross or have different slopes.
(B) The phenotypic mean of all genotypes changes equally across environments.

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2012

150. Identify the correct sequence of the following steps to implement Genomic Selection:
I. Genotype and phenotype the reference population
II. Estimate SNP marker effects
III. Genotype the candidate selection animals
IV. Calculate Genomic Estimated Breeding Values (GEBVs) for candidates
(A) I → II → III → IV
(B) III → I → II → IV
(C) I → III → II → IV
(D) II → I → IV → III

2008

151. Which statistical test is often used to determine if the genetic correlation between two traits is significantly different from zero?
(A) Z-test based on standard error
(B) Chi-square goodness of fit
(C) Fisher's exact test
(D) Kruskal-Wallis test

2019

152. Selection intensity (i) represents the difference between the mean of the selected individuals and the population mean, expressed in units of:
(A) Phenotypic standard deviations
(B) Genetic standard deviations
(C) Heritability
(D) Environmental standard deviations

2010

153. Match the distance metric (List I) with its characteristic (List II).
List I: (Metric)
P. Euclidean distance
Q. Mahalanobis distance
R. Nei's distance
S. $F_{\{ST\}}$ distance
List II: (Characteristic)
1. Adjusts for covariance between variables
2. Straight-line physical distance in multivariate space
3. Measures allele frequency divergence due to genetic drift
4. Measures population differentiation based on heterozygosity
(A) P-2, Q-1, R-3, S-4
(B) P-1, Q-2, R-4, S-3
(C) P-4, Q-3, R-2, S-1
(D) P-3, Q-4, R-1, S-2

2014

154. In setting up a classical Selection Index, incorporating a trait that has high economic value but zero heritability will:
(A) Have no effect on the expected genetic gain
(B) Vastly improve genetic gain
(C) Turn the index weights negative
(D) Cause the genetic covariance matrix to become non-positive definite

2011

155. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Progeny testing provides a highly accurate estimate of a sire's breeding value for sex-limited traits like milk yield.
Reason (R): Progeny testing utilizes records from dozens or hundreds of daughters, significantly reducing the standard error of the estimate.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2021

156. In Least Squares Analysis, what happens if interaction terms are fitted between fixed effects without sufficient observations in all subclasses?
(A) Empty subclasses result in confounding and linearly dependent equations
(B) The model becomes computationally faster
(C) The degrees of freedom for the error term increase
(D) Heritability estimates double

2015

157. Multiple Linear Regression assumes that the residuals are:
(A) Independent and identically distributed normally
(B) Correlated with the independent variables
(C) Bimodal in distribution
(D) Heteroscedastic

NODIA

2003

158. In Discriminant Function Analysis, Wilks' Lambda is a measure of:
(A) The proportion of variance in the dependent variable NOT explained by differences in group means
(B) The proportion of variance explained by the model
(C) The multicollinearity between independent

regression.
IV. It includes epistatic variance entirely.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) I, II and III
(C) II, III and IV
(D) I and III

2024

221. If repeatability (r) of a trait is 0.8, what does this indicate about the temporary environmental variance ($V_{\{TE\}}$)?
(A) $V_{\{TE\}}$ is relatively small compared to genotypic and permanent environmental variance.
(B) $V_{\{TE\}}$ is a large proportion of phenotypic variance.
(C) $V_{\{TE\}}$ is exactly zero.
(D) The trait is purely controlled by a single gene.

2013

222. Genetic correlation between two traits is mathematically bounded by:
(A) -1 and 1
(B) 0 and 1
(C) -0.5 and 0.5
(D) 0 and infinity

2019

223. Which action would NOT increase the annual genetic gain according to the Breeder's Equation?
(A) Increasing the generation interval
(B) Increasing selection intensity
(C) Increasing the accuracy of selection
(D) Selecting for a trait with higher genetic variance

2018

224. In the classical selection index, the index is constructed to predict:
(A) The net genetic merit or aggregate genotype (H)
(B) The overall phenotypic value
(C) The exact environmental deviation
(D) The dominance deviation

2023

225. Progeny testing programs in dairy cattle primarily evaluate sires for:
(A) Sex-limited traits such as milk yield
(B) Carcass traits
(C) Coat color
(D) Horn presence

2002

226. In Least Squares Analysis, a "nested" or "hierarchical" effect refers to:
(A) A factor whose levels only exist within the levels of another factor (e.g., sire within breed)
(B) A covariate that changes with time
(C) Two factors that are completely crossed
(D) Missing data

2003

227. Multicollinearity in Multiple Linear Regression inflates:
(A) The variances (standard errors) of the estimated regression coefficients
(B) The number of observations
(C) The degrees of freedom
(D) The true genetic variance

2023

228. In Principal Component Analysis, the principal components are orthogonal to each other, which implies they are:
(A) Uncorrelated
(B) Perfectly correlated
(C) Parallel
(D) Equal in variance

2015

229. Match the phylogenetic/genetic distance concept (List I) with its definition (List II).
List I: (Concept)
P. Maximum Parsimony
Q. Maximum Likelihood
R. Neighbor-Joining
S. Bootstrapping
List II: (Definition)
1. Probabilistic tree evaluation
2. Minimizes total evolutionary changes
3. Star-decomposition clustering method
4. Resampling method to assess node confidence
(A) P-2, Q-1, R-3, S-4
(B) P-1, Q-2, R-4, S-3
(C) P-3, Q-4, R-1, S-2
(D) P-2, Q-4, R-3, S-1

2016

230. In single-step GBLUP (ssGBLUP), the inverse of the H matrix ($H^{\{-1\}}$) can be computationally derived from:
(A) $A^{\{-1\}}$, $G^{\{-1\}}$, and $A_{\{22\}}^{\{-1\}}$ (inverse of pedigree relationship of genotyped animals)
(B) $A^{\{-1\}}$ and $G^{\{-1\}}$ only
(C) Phenotypic variances only
(D) Residuals only

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Q. Parent-offspring regression
R. Identical twins comparison
S. Realized heritability

List II: (Measure)

1. Regression coefficient (b)
2. Intra-class correlation (t)
3. Response to selection ($\frac{R}{S}$)
4. Broad-sense heritability bound

(A) P-2, Q-1, R-4, S-3
(B) P-1, Q-2, R-3, S-4
(C) P-4, Q-3, R-2, S-1
(D) P-2, Q-4, R-1, S-3

2010

291. Repeatability provides a reliable estimate for culling because it indicates the proportion of total variance attributed to:
(A) Genetic and permanent environmental differences between individuals
(B) Temporary environmental factors
(C) Dominance variance only
(D) Epistatic interactions only

2024

292. A negative genetic correlation between milk yield and fertility traits implies that:
(A) Intense selection for milk yield will indirectly reduce fertility.
(B) The two traits are controlled by genes on different chromosomes with no linkage.
(C) Environmental improvements will decrease fertility.
(D) Fertility has no additive genetic variance.

2008

293. Which variable in the Breeder's Equation is most difficult to significantly increase without inadvertently decreasing the accuracy of selection?
(A) Selection intensity
(B) Generation interval
(C) Phenotypic variance
(D) Market price

2017

294. In deriving the weights for a classical selection index, the variance-covariance matrix of the traits must be inverted. This matrix is the:
(A) Phenotypic matrix (P)
(B) Additive genetic matrix (G)
(C) Economic matrix (C)
(D) Environmental matrix (E)

2014

295. Identify the INCORRECT statement regarding progeny testing in smallholder systems.
(A) Individual herds are large enough to serve as complete contemporary groups.
(B) Artificial insemination is highly necessary to connect herds.
(C) Environmental variation between farms makes raw averaging highly inaccurate.
(D) The generation interval is extended due to the time required to evaluate daughters.

2002

296. When performing Least Squares Analysis on unbalanced data, standard ANOVA software computes Type III sums of squares because they:
(A) Test the main effects after adjusting for all other effects in the model
(B) Ignore fixed effects
(C) Depend heavily on the sample sizes in each subclass
(D) Only test the intercept

2015

297. In Multiple Linear Regression, if the VIF (Variance Inflation Factor) of a predictor is greater than 10, it typically indicates:
(A) Severe multicollinearity
(B) Low heritability
(C) Perfect orthogonality
(D) Lack of variance

2023

298. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): In Discriminant Function Analysis, prior probabilities can significantly shift the classification boundary.
Reason (R): Prior probabilities represent the expected proportion of observations in each group before any measurements are taken.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

NODIA

2011

299. In the construction of a Neighbor-Joining tree, the algorithm aims to pair taxa in order to minimize:
(A) The total branch length of the tree
(B) The number of assumed mutations
(C) The phenotypic variance
(D) The transition/transversion ratio

2019

241. Random Regression Models use orthogonal polynomials (like Legendre) rather than simple powers of time because orthogonal polynomials:
(A) Reduce multicollinearity and correlations between coefficients
(B) Increase multicollinearity
(C) Force all genetic correlations to 1.0
(D) Are non-linear in parameters

2007

242. If a population experiences a sudden drastic reduction in census size (bottleneck), the inbreeding coefficient in subsequent generations will:
(A) Increase rapidly
(B) Decrease rapidly
(C) Remain unchanged
(D) Fluctuate around zero

2002

243. The ratio of male to female breeders in a flock is highly skewed (e.g., 1 male to 50 females). The effective population size (N_e) is largely determined by:
(A) The number of males
(B) The number of females
(C) The phenotypic variance
(D) The mutation rate

2010

244. Heritability of 0.85 for a trait indicates that:
(A) Phenotypic selection will be highly effective.
(B) Phenotypic variation is a poor indicator of genetic merit.
(C) The trait is primarily influenced by the environment.
(D) The trait has zero additive variance.

2010

245. Repeatability acts as an upper bound for:
(A) Broad-sense heritability
(B) Environmental variance
(C) Selection intensity
(D) Inbreeding coefficient

2006

246. To calculate the correlated response of Trait Y when selection is applied to Trait X, which of the following parameters is required?
(A) Genetic correlation between X and Y, and heritabilities of both traits
(B) Heritability of Trait X only
(C) Heritability of Trait Y only
(D) Dominance variance of X

2019

247. Identify the correct sequence of the following actions to maximize annual genetic gain in a dairy cattle breeding program:
I. Select top 1% of bulls using genomic testing (high accuracy, short generation interval).
II. Widespread AI of proven bulls to cows.
III. Perform classical progeny testing (high accuracy, long generation interval).
(A) I → II (bypassing III)
(B) III → I → II
(C) II → I → III
(D) III → II → I

2011

248. The Smith-Hazel selection index weights (b) are formulated to maximize the correlation between:
(A) The index (I) and the aggregate genotype (H)
(B) The individual traits
(C) The fixed and random effects
(D) Additive and dominance variances

2013

249. In a well-designed progeny test, contemporary groups are formed to:
(A) Remove biases caused by different management and environmental conditions
(B) Isolate genetic mutations
(C) Maximize genetic drift
(D) Increase the generation interval

2013

250. Match the Multiple Linear Regression concept (List I) with its remedy or method (List II).
List I: (Concept)
P. Multicollinearity
Q. Variable selection
R. Heteroscedasticity
S. Overfitting
List II: (Method)
1. Ridge Regression
2. Stepwise Regression
3. Cross-validation
4. Weighted Least Squares
(A) P-1, Q-2, R-4, S-3
(B) P-2, Q-1, R-3, S-4
(C) P-4, Q-3, R-1, S-2
(D) P-1, Q-4, R-2, S-3

2006

251. Which regression approach minimizes the sum of squared residuals subject to a penalty on the absolute size of the regression coefficients, effectively shrinking some to zero?
(A) LASSO Regression

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ANSWERS

1. (B) Additive genetic variance
Additive genetic variance represents the variance of breeding values and is the portion of genetic variance that determines the resemblance between relatives. It is the primary component that determines the response to selection in a population because it accounts for the cumulative effect of individual alleles passed from parents to offspring. This component is considered strictly heritable and actionable.

2. (C) Henderson's Method 1
Henderson's Method 1 is designed for estimating variance components in unbalanced data by using analogues of sums of squares from the analysis of variance. This approach is specifically intended for models containing only random effects and a general mean, making it suitable for nested designs without fixed factors beyond the population mean. It remains a standard procedure in animal breeding.

3. (B) I and III
The Expectation-Maximization algorithm is widely used in maximum likelihood estimation for missing data problems. It is sensitive to initial starting values, which can lead to local rather than global maxima. While numerically stable, it typically exhibits a slower convergence rate compared to the Newton-Raphson method, which utilizes second-order information for faster optimization. This makes it reliable but computationally intensive.

4. (A) MIVQUE estimates
Minimum Norm Quadratic Unbiased Estimation is a method for estimating variance components that requires prior information. When the prior values used in the estimation process are exactly equal to the true parameters, the resulting MINQUE estimates achieve the property of being minimum variance. In this specific scenario, they become equivalent to Minimum Variance Quadratic Unbiased Estimates for normal data.

5. (B) Gibbs sampling
Gibbs sampling is a specific Markov Chain Monte Carlo algorithm used in Bayesian statistics to generate samples from a complex joint distribution. It operates by iteratively drawing values from the fully conditional posterior distributions of each individual parameter. This method is particularly effective for high-dimensional problems in quantitative genetics where the joint posterior is difficult to sample directly or evaluate.

6. (A) Both A and R are true and R is the correct explanation of A.
Henderson's tabular method is a computationally efficient technique for determining the inverse of the additive genetic relationship matrix. This method relies on the specific structural decomposition of the matrix into a lower triangular matrix and its transpose with a diagonal matrix. This mathematical property allows for direct calculation of the inverse without performing costly and slow full matrix inversion operations.

7. (A) Correlation between true and predicted breeding values
Best Linear Unbiased Prediction is the standard method for genetic evaluation in animal breeding. It is designed to maximize the correlation between the true breeding value and the predicted value, which also results in minimizing the mean squared error of prediction. This ensures that the rankings of animals for selection purposes are as accurate and efficient as statistically possible.

NODIA

8. (C) Repeatability Model
The repeatability model is utilized in animal breeding when individuals have multiple records for the same trait, such as milk yield across different lactations. This model partitions the total variance by accounting for permanent environmental effects that are common to all records of an individual, allowing for a more precise estimation of the animal's breeding value and future performance expectations.

9. (D) Legendre polynomials
Random regression models are widely employed to analyze longitudinal data where traits change over time, such as milk production. Legendre polynomials are the most common basis functions

(D) I, II and III

2008

261. In a Gibbs sampler applied to a mixed model, the fully conditional distribution of the fixed effects, given the variance components and data, is typically a:
(A) Normal distribution
(B) Gamma distribution
(C) Uniform distribution
(D) Exponential distribution

2008

262. By Henderson's rules, if both parents of an animal are unknown, the diagonal element in the inverse of the A-matrix ($A^{\{-1\}}$) corresponding to that animal gets an addition of:
(A) 1.0
(B) 1.333
(C) 2.0
(D) 4.0

2008

263. When solving MME, if a contemporary group (fixed effect) has very few records, its solution:
(A) Is purely dependent on the phenotypic mean of those few records (un-shrunk)
(B) Is heavily shrunk toward zero
(C) Is shrunk toward the population mean
(D) Becomes mathematically infinite

2018

264. Under the Sire Model, what is the correlation between the true breeding values of half-sib progeny of the same sire?
(A) 0.125
(B) 0.25
(C) 0.50
(D) 1.0

2012

265. In a Random Regression Model, the additive genetic variance for a trait at a specific day in milk is obtained by:
(A) Pre- and post-multiplying the genetic covariance matrix of random regression coefficients by the vector of basis functions for that day
(B) Adding the variance of all fixed effects
(C) Multiplying the day in milk by the heritability
(D) Simply extracting the diagonal of the phenotypic matrix

2021

266. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Tabular methods for calculating inbreeding coefficients are much more easily computerized for huge pedigrees than path coefficient methods.
Reason (R): Tabular methods process the pedigree chronologically and calculate recursive relationships without visually tracing paths.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2022

267. Overlapping generations affect the standard calculation of effective population size (N_e) because they increase:
(A) The variance of family size across different age groups
(B) The mutation rate
(C) The number of autosomes
(D) The dominance variance

2015

2009

268. If the parent-offspring regression coefficient ($b_{\{OP\}}$) is 0.2, the heritability of the trait is:
(A) 0.1
(B) 0.2
(C) 0.4
(D) 0.8

2017

269. The Most Probable Producing Ability (MPPA) is typically applied to:
(A) Sex-limited traits with repeated records (e.g., lactation yield)
(B) Traits measured only once (e.g., age at first calving)
(C) Carcass traits of slaughtered animals
(D) Monogenic diseases

2019

270. Identify the correct sequence of the following parameter estimation steps in a traditional multi-trait analysis:
I. Estimate (co)variance components using AI-REML
II. Construct the multi-trait MME
III. Solve the MME for breeding values

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IV. Check data for fixed effects and outliers
(A) IV → II → I → III
(B) IV → I → II → III
(C) I → II → IV → III
(D) II → I → III → IV

2013

271. In the Breeder's Equation, accuracy of selection is mathematically defined as the correlation between:
(A) Estimated breeding value and true breeding value
(B) Phenotype and environment
(C) Additive and dominance variance
(D) Sire and dam breeding values

2007

272. If a classical Selection Index is correctly formulated, its expected genetic response compared to any other linear combination of the same traits will be:
(A) Maximized
(B) Minimized
(C) Exactly zero
(D) Equal

2023

273. The primary metric used to rank proven sires after progeny testing for dairy traits is often the:
(A) Predicted Transmitting Ability (PTA) or Estimated Breeding Value (EBV)
(B) Heritability of the daughters
(C) Phenotypic variance of the herd
(D) Inbreeding coefficient

2024

274. In Least Squares Analysis, if two fixed effects are completely confounded (e.g., all animals of Breed A are in Herd 1, and Breed B in Herd 2), the model:
(A) Cannot estimate the separate effects of Breed and Herd without constraints
(B) Can cleanly separate the Breed and Herd effects
(C) Will automatically drop the random effects
(D) Converts them into covariates

2016

275. Match the concept in multivariate statistics (List I) with its correct context (List II).
List I: (Concept)
P. Eigenvalue
Q. Cross-validation
R. Centroid
S. Dendrogram
List II: (Context)
1. Represents the variance of a principal component
2. Mean vector of a group in Discriminant Analysis
3. Visual output of hierarchical clustering (e.g., UPGMA)
4. Technique to assess predictive performance of a model
(A) P-1, Q-4, R-2, S-3
(B) P-2, Q-1, R-3, S-4
(C) P-4, Q-3, R-2, S-1
(D) P-1, Q-2, R-4, S-3

2024

276. Identify the INCORRECT statement regarding genetic distance measures.
(A) Reynolds' distance assumes divergence is solely due to mutation, ignoring drift entirely.
(B) They quantify the genetic divergence between populations or species.
(C) Nei's distance assumes mutation and drift are the driving forces.
(D) They are foundational for constructing phylogenetic trees.

2024

277. The Genomic Relationship Matrix (G) is constructed using:
(A) Frequencies of shared alleles at genotyped SNP loci
(B) Pedigree records dating back to a base population
(C) Phenotypic covariances
(D) RNA expression levels

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2005

278. The BLAST program provides an "E-value" for each sequence alignment. A very low E-value (e.g., 1e-50) indicates:
(A) The match is highly significant and unlikely to occur by chance.
(B) The alignment is likely a random match.
(C) The sequence is purely environmental DNA.
(D) The algorithm failed to converge.

2003

279. In quantitative genetics, if broad-sense heritability is 0.40 and narrow-sense heritability is 0.15, the difference (0.25) is attributed to:
(A) Non-additive genetic variance (dominance and epistasis)
(B) Additive genetic variance
(C) Environmental variance
(D) Genotype-environment interaction

2019

280. Consider the following statements regarding Henderson's Method 1:

I. It computes analogous sums of squares as in balanced ANOVA.

II. It yields biased estimates if applied to models with fixed effects.

III. It is an iterative maximum likelihood procedure.

Which of the above statement(s) is/are correct?

(A) I and II

(B) I and III

(C) II and III

(D) I, II and III

2023

281. In maximum likelihood estimation, the Newton-Raphson algorithm relies on the:

(A) Second derivative (Hessian matrix)

(B) First derivative only

(C) Random sampling (MCMC)

(D) Third derivative

2016

282. MINQUE estimators are independent of:

(A) The choice of prior values

(B) The assumption of normality for the data

(C) The generalized inverse used for solving fixed effects

(D) The number of observations

2007

283. In Bayesian estimation via Gibbs sampling, the Monte Carlo standard error of a parameter estimate:

(A) Decreases as the number of iterations increases

(B) Increases as the number of iterations increases

(C) Is independent of the sampling variance

(D) Requires calculation of the Hessian matrix

2009

284. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).

Assertion (A): The tabular method easily accommodates inbreeding when constructing the additive genetic relationship matrix.

Reason (R): The diagonal element for an individual is calculated as $1 + 0.5 \times (R_{SD})$, directly incorporating the relationship between its parents.

(A) Both A and R are true and R is the correct explanation of A.

(B) Both A and R are true but R is not the correct explanation of A.

(C) A is true but R is false.

(D) A is false but R is true.

2022

285. In the Animal Model MME, if an animal is highly inbred, the variance of its Mendelian sampling term:

(A) Decreases

(B) Increases

(C) Remains exactly the same

(D) Becomes negative

2022

286. When fitting a Repeatability Model, the data must include:

(A) Multiple records for at least some animals

(B) Only one record per animal

(C) Only male records

(D) No fixed effects

2008

287. In Random Regression Models, a higher-order Legendre polynomial curve will allow the genetic variance trajectory to:

(A) Fluctuate more flexibly across time

(B) Be constant

(C) Be strictly linear

(D) Decrease exponentially

NODIA

2010

288. Using the path coefficient method, what is the correlation between an uncle and a nephew in a non-inbred population?

(A) 0.50

(B) 0.25

(C) 0.125

(D) 0.0625

2025

289. The reduction of heterozygosity in a closed, random-mating finite population is proportional to:

(A) $\frac{1}{2N_e}$

(B) $\frac{1}{N_e}$

(C) N_e

(D) $2N_e$

2025

290. Match the Heritability estimation method (List I) with its core statistical measure (List II).

List I: (Method)

P. Paternal half-sib correlation

(B) Ordinary Least Squares
(C) Ridge Regression
(D) Principal Component Regression

2023

252. In morphometric characterization, Principal Component Analysis (PCA) generates PC1, which always:
(A) Captures the most variance among all generated PCs
(B) Has the lowest eigenvalue
(C) Correlates perfectly with the dependent variable
(D) Ignores linear relationships

2013

253. Which measure of genetic distance is robust to variations in sample size and estimates the standardized variance in allele frequencies?
(A) Wright's $F_{\{ST\}}$
(B) Jaccard Distance
(C) Euclidean Distance
(D) Edit Distance

2024

254. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): The Maximum Likelihood approach to phylogenetic tree construction is statistically more robust than Maximum Parsimony.
Reason (R): Maximum Likelihood incorporates explicit models of sequence evolution, accommodating differing rates of transition and transversion.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2024

255. In the GBLUP model, the assumption about SNP marker effects is that:
(A) All SNPs share the exact same normal distribution of effects (equal variance)
(B) A few SNPs have large effects, while most have zero effect
(C) SNPs are distributed according to a Student's t-distribution
(D) SNPs have no additive effects

2016

256. Which alignment algorithm is characterized by dynamic programming to find the optimal global alignment of two sequences?
(A) Needleman-Wunsch algorithm
(B) Smith-Waterman algorithm
(C) BLAST
(D) BLAT

2017

257. Epistatic variance is notoriously difficult to estimate in quantitative genetics primarily because:
(A) It requires incredibly large datasets with specific complex pedigree structures (e.g., many full-sibs, clones).
(B) It does not exist in mammals.
(C) It is always zero in randomly mating populations.
(D) It is easily confounded with permanent environmental effects.

2014

258. Identify the INCORRECT statement regarding Expectation of Mean Squares (EMS) in ANOVA.
(A) EMS dictates how mean squares should be equated to parameter expectations to solve for variance components.
(B) In balanced designs, EMS equations are simple and straightforward.
(C) Henderson's Method 3 uses EMS completely divorced from linear models.
(D) Unbalanced data makes EMS coefficients complex and non-orthogonal.

2013

259. The REML log-likelihood contains a penalty term for:
(A) The degrees of freedom used in estimating the fixed effects
(B) Estimating the variance components
(C) The number of random effects
(D) Missing phenotypes

2008

260. Consider the following statements regarding MIVQUE:
I. It requires an initial guess (priors) for variance components.
II. It is iterative and updates the priors until convergence.
III. It yields quadratic estimators.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III

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2022

300. The Bayes B model for genomic selection is characterized by its assumption that:

(A) A large proportion of SNPs (π) have zero effect, and the rest have effects drawn from a t-distribution.

(B) All SNPs have a non-zero effect drawn from a normal distribution.

(C) SNP effects are completely independent of linkage disequilibrium.

(D) The genomic relationship matrix is singular.

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2010

231. The NCBI database that stores nucleotide sequences submitted by researchers worldwide is called:
(A) GenBank
(B) Swiss-Prot
(C) Ensembl
(D) OMIA

2016

232. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): The additive genetic variance is the only variance component responsible for the resemblance between parents and offspring.
Reason (R): Parents only pass on single alleles, not whole genotypes, meaning dominance interactions are broken up during meiosis.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2003

233. Henderson's Method 3 uses expectations of reductions in sums of squares. Which model-building concept is strictly associated with it?
(A) Fitting constants (fitting full and sub-models)
(B) MCMC sampling
(C) Generalized inverse elimination
(D) Ridge penalty

2010

234. In REML estimation using the AI algorithm, convergence is typically achieved when:
(A) The change in variance components or likelihood between iterations is below a predefined very small threshold
(B) The maximum number of iterations is reached
(C) The estimates become zero
(D) The fixed effects are fully explained

2010

235. MIVQUE relies on an assumption of normal distribution. If the data is not normal, MIVQUE remains:
(A) Unbiased but loses its minimum variance property
(B) Minimum variance but not unbiased
(C) A maximum likelihood estimator
(D) A biased estimator

2025

236. In a Bayesian quantitative genetic analysis, if the prior distribution dominates the posterior distribution, it indicates that:
(A) The dataset is small or uninformative
(B) The dataset is extremely large and informative
(C) The likelihood function is incorrect
(D) The MCMC chain did not converge

2010

237. The calculation of the diagonal element of the A -matrix for a completely inbred animal (where parents are full siblings of identical highly inbred lines) approaches:
(A) 0.5
(B) 1.0
(C) 1.5
(D) 2.0

2022

238. In the Mixed Model Equations, fixed effects are typically evaluated assuming their prior variance is:
(A) Infinite
(B) Zero
(C) Equal to additive genetic variance
(D) Equal to residual variance

2017

239. The Sire Model assumes that the residual variance (σ_e^2) contains:
(A) $\frac{3}{4}$ of the additive genetic variance plus environmental variance
(B) $\frac{1}{4}$ of the additive genetic variance
(C) $\frac{1}{2}$ of the additive genetic variance
(D) Only environmental variance

2024

240. Consider the following statements regarding the Repeatability Model:
I. MPPA calculation uses repeatability to weight the animal's average deviation.
II. The model assumes temporary environmental effects are highly correlated across lactations.
III. Permanent environmental variance is fitted as a random effect.
Which of the above statement(s) is/are correct?
(A) I and III
(B) II only
(C) I and II
(D) III only

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used in these models because they are orthogonal. This orthogonality reduces multicollinearity between the regression coefficients, leading to more stable and computationally efficient estimation of the genetic covariance functions across different time points.

10. (C) $\left(\frac{1}{2}\right)^{n+n\hat{a}\epsilon^{\text{TM}}+1}(1+F_A)$

Wright's inbreeding coefficient calculation via path coefficients involves identifying paths through a common ancestor. Each path contribution is determined by the formula that incorporates the number of generations from each parent to the ancestor. This calculation specifically accounts for the inbreeding of the common ancestor to accurately reflect the probability of alleles being identical by descent within relatives.

11. (B) $\frac{4N_mN_f}{N_m+N_f}$

The effective population size is a critical parameter in conservation and breeding that accounts for deviations from idealized conditions. In populations with unequal sex ratios, the standard formula calculates the size based on the number of breeding males and females. This relationship highlights how the sex with fewer individuals has a disproportionately large impact on the total rate of inbreeding.

12. (D) 0.60

Heritability can be estimated from the intra-class correlation of paternal half-sibs by multiplying the correlation coefficient by four. This is because half-sibs share approximately one-fourth of their additive genetic variance. In this case, a correlation of 0.15 corresponds to a heritability of 0.60, representing the proportion of phenotypic variation due to additive genetic effects in that population.

13. (C) 1.0

Heritability in the narrow sense represents the proportion of total phenotypic variance that is attributable to additive genetic variance. Since it is a ratio of a component of variance to the total variance, its theoretical value is strictly bounded between zero and one. A value of 1.0 indicates that all observed phenotypic differences are due to additive genetic factors.

14. (C) They represent correlation between dominance deviations.

Genetic correlations describe the association between the breeding values of two different traits within a population. These correlations are primarily driven by pleiotropy, where a single gene affects multiple traits, or by linkage disequilibrium between genes. Unlike phenotypic correlations, they do not measure associations between dominance deviations but rather focus on the shared additive genetic components of the traits.

15. (A) P-4, Q-1, R-2, S-3

The Breeder's Equation relates the selection response to several key parameters including intensity, accuracy, and genetic variation. Selection intensity is denoted by i, while the accuracy of selection is represented by the correlation between true and predicted breeding values. The additive genetic standard deviation and the generation interval are also essential components for predicting the total annual genetic gain achieved.

16. (D) Vector of economic values

In the Smith-Hazel selection index, the objective is to maximize the correlation between the index and the aggregate genotype. The vector 'a' represents the economic values assigned to each trait, reflecting their relative importance to overall profit. These weights are used alongside phenotypic and genetic covariance matrices to calculate the optimal coefficients for ranking selection candidates in the population.

17. (B) Contemporary Group Comparison

Contemporary group comparison is a fundamental experimental design in progeny testing that minimizes environmental bias. By comparing the performance of offspring from different sires within the same herd, year, and season, breeders can account for shared environmental influences. This ensures that observed differences in daughter performance are more likely to reflect the genetic merit of the sires being evaluated.

18. (C) Generalized inverse

Least squares analysis of unbalanced breeding data often results in normal equations where the coefficient matrix is not of full rank. To solve these equations and obtain parameter estimates, a generalized inverse is employed. This mathematical tool provides a solution for

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as the average of its parents' relationships with that individual. This recursive calculation is a central feature of Henderson's tabular method for building relationship matrices.

75. (A) Both A and R are true and R is the correct explanation of A.
The Best Linear Unbiased Prediction method is highly effective for genetic evaluation because it accounts for non-random mating and selection. This is achieved by incorporating the full additive genetic relationship matrix into the mixed model equations. This matrix links all related individuals in the pedigree, allowing the model to adjust for genetic trends and the effects of assortative mating.

76. (C) 1.0
The repeatability model simplifies the genetic analysis of multiple records by assuming that the genetic correlation between repeated measures of the same individual is exactly one. This assumption implies that the same set of genes is responsible for the trait across different observations. The model then attributes any variation between an individual's records to temporary environmental factors that change.

77. (A) Number of estimated covariance components.
In random regression models, increasing the order of the fitted polynomial, such as moving from a linear to a cubic fit, directly affects the model's complexity. This change increases the number of genetic and environmental covariance components that must be estimated. Higher-order fits provide more flexibility in describing the trajectory of a trait over time but require more extensive data and computing resources.

78. (B) Generation interval and variance in family size must be accounted for.
Calculating the effective population size in species with overlapping generations is more complex than in those with discrete generations. It requires detailed information about the generation interval and the variance in the number of offspring produced by individuals of different ages. Accounting for these factors is essential to accurately reflect the rate of genetic diversity loss in livestock populations.

79. (A) Increasing the number of parent-offspring pairs.
The standard error of a heritability estimate derived from parent-offspring regression is a measure of the estimate's precision. This error can be reduced by increasing the sample size of the study, specifically the number of parent-offspring pairs evaluated. A larger number of observations provides a more stable regression line, leading to a more reliable and accurate estimation of narrow-sense herizability.

80. (A) P-4, Q-1, R-2, S-3
Various tools and databases are essential for modern genetic and bioinformatic analyses. BLAST is used for local sequence searches, while ClustalW is a standard for multiple sequence alignment. Gibbs3F90 is a software package designed for Bayesian animal model analysis using MCMC methods. GenBank serves as a major public repository for storing and sharing nucleotide sequence data from researchers worldwide.

81. (D) Selecting for higher milk yield will likely decrease fat percentage.
A strong negative genetic correlation, such as -0.85, between two traits indicates that many of the genes affecting them have opposite effects. In the context of dairy cattle, this means that selecting for increased milk yield will likely result in a correlated decrease in fat percentage. Breeders must account for such relationships when designing multi-trait selection programs to avoid undesirable results.

82. (C) Increases.
Selection intensity is a measure of the superiority of the selected individuals relative to the entire population. As the proportion of animals selected for breeding decreases, the selection becomes more stringent. This leads to an increase in the selection intensity, which in turn results in a larger genetic response per generation, provided that the accuracy of selection remains high and stable.

83. (A) Profit change per unit trait change while holding other traits constant.
The economic weight of a trait in a selection index represents its marginal contribution to total profit. It is defined as the change in profit resulting from a one-unit increase in the trait while keeping all other traits in the objective

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appropriateness of the prior values used for the variances.

28. (D) Posterior distribution
In the Bayesian framework, the posterior distribution represents the updated knowledge about a parameter after combining prior beliefs with the evidence from observed data. It is calculated using Bayes' Theorem by multiplying the prior distribution by the likelihood function. This distribution provides a comprehensive description of parameter uncertainty and forms the basis for all subsequent statistical inferences and breeding predictions.

29. (C) 1.0
When constructing the additive genetic relationship matrix using Henderson's tabular method, diagonal elements represent the relationship of an animal with itself. For a non-inbred individual, this value is exactly one. If the parents are unknown and assumed to be unrelated and non-inbred from a base population, no additional inbreeding component is added to this initial diagonal value.

30. (B) II → I → III → IV
Solving Mixed Model Equations involves a systematic workflow. First, the incidence matrices that link observations to fixed and random effects must be defined. Next, the relationship matrix describing genetic ties between individuals is constructed. After calculating the inverse of this matrix, the components are assembled into the equations, which are then solved to obtain accurate breeding values.

31. (B) $\frac{1}{4}\sigma_A^2$
The sire model is a genetic evaluation tool that focuses on the transmitting ability of male parents. Because a sire contributes only half of the genes to its offspring and the variance of those paternal genes represents one-fourth of the total additive genetic variance, the sire variance component is mathematically defined as one-quarter of the additive genetic variance.

32. (A) A random effect uncorrelated with the additive genetic effect
In a repeatability model, the permanent environmental effect is modeled as a random effect that stays constant for all records of a specific individual. It is assumed to be statistically independent and uncorrelated with the animal's additive genetic effect. This separation allows the model to distinguish between genetic merit and environmental influences that persist throughout the individual's productive lifetime.

33. (D) Covariance functions
Random regression models analyze longitudinal data by fitting a continuous trajectory for each animal. In this context, the genetic parameters are not treated as static values but are modeled through covariance functions. These functions describe how genetic variances and correlations change over time or across different ages, providing a dynamic view of how traits evolve throughout an individual's life.

34. (B) 0.50
The path coefficient between a parent and its offspring measures the direct contribution of the parent's genotype to the offspring's genotype. In a population that is not inbred, this coefficient is exactly 0.50, representing the fact that half of the offspring's genes are inherited from each parent. This value is a fundamental building block for calculating relationships and inbreeding coefficients.

35. (B) Generation
The rate of inbreeding is a measure used to describe the increase in the average inbreeding coefficient within a population over time. By standard convention in population genetics, this rate is defined as the change in inbreeding per generation. Expressing it this way allows for comparisons between populations with different life histories and assists in assessing long-term genetic health.

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36. (B) $\frac{1}{2}h^2$
Heritability can be estimated by regressing the performance of offspring on the performance of a single parent. The regression coefficient obtained from this analysis represents one-half of the narrow-sense heritability. This relationship exists because the covariance between a parent and its offspring is half of the additive genetic variance, assuming there are no shared environmental effects between the two.

37. (A) Estimate of producing ability derived from repeated observations
Most Probable Producing Ability is a metric used in dairy animals to predict future performance based on all available past records. It accounts

regression models are designed to analyze longitudinal data such as milk yields over time.

56. (A) Random Regression Model over continuous time.
In animal breeding, an infinite-dimensional genetic model refers to the analysis of traits that change continuously over time or another scale. This is typically implemented using random regression models, which treat the trait as a continuous trajectory. This approach allows for the estimation of genetic variances and correlations at any point along the scale, rather than at discrete intervals.

57. (B) 0.50
The path coefficient method is a tool for calculating the degree of relationship between individuals. For two full siblings in a non-inbred population, the coefficient of relationship is 0.50. This reflects the fact that, on average, full siblings share half of their alleles through their common parents, which is the same proportion shared between a parent and its offspring.

58. (A) Both A and R are true and R is the correct explanation of A.
The effective population size is a measure of genetic diversity that is almost always smaller than the actual census size in livestock. This discrepancy is primarily caused by the use of unequal sex ratios in breeding programs, where a small number of males are mated to many females. This practice accelerates the rate of inbreeding compared to balanced populations.

59. (A) The number of sires and progeny per sire.
The precision of heritability estimates derived from paternal half-sib analysis is reflected in their standard error. This error is primarily influenced by the design of the study, specifically the total number of sires included and the number of offspring evaluated per sire. Larger sample sizes and balanced designs generally lead to more accurate estimates with smaller standard errors.

60. (B) Epistatic Variance - Interaction between alleles at the same locus.
Variance partitioning is essential for understanding the genetic architecture of quantitative traits. Additive variance represents the variation in breeding values, while environmental variance accounts for non-genetic influences. Epistatic variance, however, refers to the interaction between alleles at different loci, not the same locus. Interaction between alleles at the same locus is instead described as dominance variance in genetics.

61. (A) First lactation yield is a reliable indicator of future lactations.
A high repeatability value, such as 0.6, indicates that a large portion of the phenotypic variation is due to genetic and permanent environmental factors. For dairy producers, this means that the performance in the first lactation is a strong and reliable predictor of an animal's performance in subsequent lactations. Consequently, early culling decisions can be made with greater confidence.

62. (B) Sum of squared differences between true breeding value and the index.
In the development of a selection index, the goal is to create a linear combination of traits that accurately predicts genetic merit. The weights for the index are calculated by minimizing the sum of the squared differences between the true breeding value and the index value. This optimization ensures that the resulting index has the maximum possible accuracy for selection.

63. (A) III → I → II → IV
Establishing a progeny testing program follows a logical sequence starting with the selection of elite cows to be bull mothers. These cows are then mated to produce young bulls for test mating. The performance of the resulting daughters is evaluated across different herds, and based on these results, the highest-ranking bulls are selected as proven sires for widespread use.

64. (A) Unequal subclass numbers.
In animal breeding, an unbalanced dataset is characterized by having unequal numbers of observations across different subclasses, such as herds, years, or sire groups. This is a common feature of field data where sample sizes are not controlled. Least squares analysis is used to handle these data because it provides unbiased estimates for fixed effects despite the lack of orthogonality.

65. (D) Visualization of similarity or distance between individual cases.
Multidimensional scaling is a multivariate technique used in morphometric analysis to visualize complex relationships between

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modeling approaches help researchers capture the underlying genetic architecture of complex traits.

47. (A) Sequence alignment and database searching
FASTA is a widely utilized bioinformatics tool designed for rapid sequence alignment and searching against large biological databases. It identifies regions of similarity by focusing on short identical fragments, or words, and then extending them to find high-scoring matches. This tool is fundamental for identifying unknown sequences, finding homologous genes, and conducting evolutionary comparisons across diverse genomic datasets.

48. (B) The relative ranking of genotypes changes across environments
Genotype-environment interaction describes a situation where the performance of different genotypes is not consistent across various environmental conditions. This interaction is indicated when the relative ranking of individuals changes depending on the environment in which they are raised. Understanding these interactions is crucial for breeders to select animals that perform optimally in specific production environments or across regions.

49. (C) Presence of interactions between fixed and random effects
Henderson's Method 2 is a technique for estimating variance components in models with both fixed and random effects. However, its application is restricted to cases where there are no interactions between the fixed and random factors. If such interactions exist, the method cannot accurately adjust the data for fixed effects without biasing the estimates of the variance components.

50. (A) It requires fewer iterations to converge.
The Average Information algorithm is a common numerical method used in REML estimation of variance components. It is often preferred over the Expectation-Maximization algorithm because it generally converges much faster, requiring fewer iterations to reach a solution. This efficiency makes it particularly suitable for large-scale genetic evaluations involving complex animal models and vast amounts of pedigree and phenotypic data.

51. (B) It allows for negative estimates of variance components.
Minimum Norm Quadratic Unbiased Estimation is a method for variance component estimation that does not impose non-negativity constraints. Consequently, it is possible for the resulting estimates to be negative, which is a significant drawback in biological contexts. This method provides unbiased estimates without requiring specific distributional assumptions about the data, such as normality, for its basic application.

52. (A) The next state depends only on the current state.
Markov Chain Monte Carlo methods are essential tools for Bayesian estimation in quantitative genetics. These methods rely on the fundamental Markov property, which assumes that the transition to the next state in the sequence depends solely on the current state and not on the history of the chain. This property allows for the efficient exploration of complex posterior distributions.

53. (C) 0.2500
The inbreeding coefficient of an individual is equal to half the relationship between its parents. For an offspring resulting from a mating between full siblings, who share half of their genes, the relationship between the parents is 0.50. Therefore, the inbreeding coefficient of the offspring is 0.25, representing a 25 percent probability that alleles are identical by descent.

54. (A) $\frac{\sigma_E^2}{\sigma_A^2}$
In Henderson's Mixed Model Equations, the inverse of the additive genetic relationship matrix is integrated into the coefficient matrix. Before being added, it is multiplied by a ratio known as α, which is the residual environmental variance divided by the additive genetic variance. This weighting factor ensures the proper balance between genetic information and the observed data during prediction.

55. (A) P-3, Q-4, R-1, S-2
Different genetic models are tailored to specific breeding applications. The animal model utilizes relationships among all individuals, whereas the sire model focuses only on the transmitting ability of fathers. Repeatability models are used when animals have multiple records, accounting for permanent environmental effects, and random

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for the repeatability of the trait by weighting the individual's average deviation from the herd mean. This estimate helps producers make more informed culling decisions by identifying animals that are consistently superior or inferior over multiple lactations.

38. (C) Both genetic and environmental correlations
The phenotypic correlation between two traits is the observed association between their measured values. This correlation is a function of both the underlying genetic correlation and the environmental correlation between the traits. It is calculated as the sum of these components, each weighted by the square roots of the heritabilities of the traits involved in the analysis.

39. (D) Decrease generation interval
Annual genetic gain is determined by the selection response divided by the generation interval. Therefore, reducing the time between the birth of parents and the birth of their offspring is a highly effective strategy for accelerating genetic progress. By decreasing the generation interval, breeders can achieve more selection cycles within a fixed period, increasing the total genetic improvement.

40. (A) Both A and R are true and R is the correct explanation of A.
The Smith-Hazel selection index is designed to maximize the genetic gain for an aggregate genotype by combining information from multiple traits. This is achieved by applying economic weights, which represent the change in profit for a unit change in each trait. These weights allow the index to prioritize traits according to their financial impact while accounting for genetic correlations.

41. (A) Progressive deviation of sire daughters from contemporary averages
In field-based progeny testing, the cumulative difference is a method used to evaluate the genetic merit of sires by monitoring the performance of their daughters. It tracks the deviation of daughter records from the average of their contemporaries over time. This approach helps in identifying superior sires by integrating performance data across different herds and management conditions effectively.

42. (C) Estimation of parameters that minimize squared residual sums
Least squares analysis is a standard statistical method for handling non-orthogonal data in animal breeding. It operates by estimating model parameters in a way that minimizes the sum of the squared differences between the observed data and the predicted values. This method ensures that the resulting estimates for fixed effects are unbiased and have the smallest possible variance among linear estimators.

43. (C) Multicollinearity
Ridge regression is a modification of the ordinary least squares method that introduces a penalty parameter to the diagonal of the coefficient matrix. This technique is specifically designed to address multicollinearity, which occurs when predictor variables are highly correlated. By adding this penalty, ridge regression stabilizes the estimates and reduces their variance, leading to more reliable predictions in complex datasets.

44. (A) Linear combination of features separating two or more classes
Discriminant function analysis is a multivariate statistical technique used to classify individuals into predefined groups. Its primary objective is to find a linear combination of features that maximizes the differences between these groups while minimizing the variation within them. This method is frequently applied in morphometric studies to distinguish between different breeds or populations based on physical measurements.

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45. (B) UPGMA
The Unweighted Pair Group Method with Arithmetic Mean is a clustering algorithm used for reconstructing phylogenetic trees from genetic distance data. It relies on the critical assumption of a constant molecular clock, meaning that all evolutionary lineages evolve at the same rate. Consequently, it produces rooted trees where all tips are equidistant from the root, representing a ultrametric time scale.

46. (C) I and III
Genomic selection models employ different assumptions regarding marker effects. The GBLUP model assumes that all SNPs contribute equally to the variance of the trait. In contrast, Bayes A assumes that SNP effects follow a normal distribution but allows for varying variances across markers. These different

individuals or populations. It operates by mapping the similarity or distance between cases into a low-dimensional space, typically two or three dimensions. This allows researchers to easily identify clusters, patterns, and outliers within the data that might not be apparent from raw measurements.

66. (B) Requires the fewest evolutionary changes.
The maximum parsimony method is a common approach for reconstructing phylogenetic trees from discrete character data. It operates on the principle of simplicity, choosing the tree topology that requires the smallest number of evolutionary changes to explain the observed data. This method is based on the assumption that the most likely evolutionary path is the one involving the fewest mutations.

67. (A) Combines pedigree and genomic relationship matrices simultaneously.
Single-step GBLUP is a significant advancement in genomic evaluation because it integrates all available information into a single analysis. It simultaneously utilizes both pedigree-based and genomic relationship matrices by blending them into a unified H-matrix. This allows for the accurate evaluation of all animals in the pedigree, regardless of whether they have been genotyped or only phenotyped.

68. (A) Ensembl.
Ensembl is a centralized bioinformatics database and genome browser maintained by the European Bioinformatics Institute. It provides comprehensive genomic data, including sequence information, gene annotations, and comparative genomics for a wide range of vertebrate species. This resource is essential for researchers working in animal genetics and genomics to access and visualize standardized, high-quality information about various genomes.

69. (A) Interaction of alleles at different loci.
Epistatic variance is a component of the total genetic variance that results from the interaction between alleles located at different positions, or loci, in the genome. It reflects the fact that the effect of a gene can be modified by the presence of alleles at other locations. This non-additive component contributes to the genetic variation observed in complex quantitative traits.

70. (A) Analogues of analysis of variance mean squares for unbalanced data.
Henderson's Method 1 is a procedure for estimating variance components in situations where data are unbalanced. It works by equating the observed analogues of the sums of squares from an analysis of variance to their expected values. This method is strictly applicable to random-effects models and assumes that the data are not subject to selection or fixed effects.

71. (C) The marginal distribution of error contrasts.
In Restricted Maximum Likelihood estimation, the likelihood function is derived from a specific set of linear combinations of the data known as error contrasts. These contrasts are designed to be invariant to the fixed effects in the model. By focusing on these marginal distributions, REML effectively removes the influence of fixed effects, leading to unbiased estimates of the variance components.

72. (A) They are translation invariant and locally minimum variance.
Minimum Variance Quadratic Unbiased Estimation provides estimators that possess specific statistical properties. These estimators are translation invariant, meaning their values do not change when a constant is added to the observations. Additionally, they are locally minimum variance, which implies that they achieve the smallest possible variance among unbiased quadratic estimators given the appropriateness of the initial prior values used.

73. (A) I, II and IV
The Gibbs sampler is a Markov Chain Monte Carlo method widely used for Bayesian estimation in quantitative genetics. It is a special case of the Metropolis-Hastings algorithm that requires sampling from the fully conditional posterior distributions of all parameters. The algorithm typically includes a burn-in period to ensure that the generated samples accurately represent the true stationary posterior distribution.

74. (A) $0.5(A_{\{is\}} + A_{\{id\}})$ where s and d are parents of j.
When constructing the additive genetic relationship matrix using Henderson's tabular method, off-diagonal elements represent the relationship between two different individuals. For an animal whose parents are known, its relationship with another individual is calculated

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expectations, the method allows for the unbiased estimation of variance components in complex, unbalanced animal breeding datasets.

93. (C) The complete-data log-likelihood.
The Expectation-Maximization algorithm is an iterative procedure used in REML to find maximum likelihood estimates for variance components. The E-step involves calculating the expected value of the log-likelihood of the complete data, given the observed observations and current parameter estimates. This step effectively handles the missing information, such as random effects, allowing the M-step to update the variance parameters.

94. (A) Both A and R are true and R is the correct explanation of A.
Minimum Variance Quadratic Unbiased Estimation is a non-iterative approach for estimating variance components. It provides estimates in a single step based on initial prior values provided by the user. Because these priors are not updated during the calculation, the method does not require iteration. However, the quality and optimality of the resulting estimates depend on how close the priors are.

95. (B) The trace plot of the sampled parameter values over iterations.
When using Gibbs sampling in Bayesian analysis, it is essential to ensure that the Markov chain has reached its stationary distribution. Convergence is commonly assessed visually by examining trace plots, which show the sampled values of parameters over successive iterations. A stable, oscillating plot without clear trends indicates that the chain has converged and that subsequent samples represent the posterior.

96. (A) $1 + F_i$
In the additive genetic relationship matrix, diagonal elements represent the relationship of an individual with itself. For a non-inbred animal, this value is one. However, if the animal is inbred, the diagonal element is calculated as one plus its inbreeding coefficient. This value reflects the increased homozygosity and reduced genetic diversity of the individual relative to a non-inbred population.

97. (A) Additive genetic effect of the animal.
The standard animal model partitions phenotypic observations into fixed and random effects. The additive genetic effect, which represents the animal's breeding value, is always treated as a random effect. In contrast, factors such as the contemporary group, age at calving, or the sex of the offspring are typically modeled as fixed effects or covariates to adjust for systematic environmental influences.

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98. (A) Accounts for assortative mating of both parents.
One of the primary advantages of the animal model over the sire model is its ability to utilize information from both parents. By incorporating the full additive genetic relationship matrix, the animal model accounts for non-random mating and the genetic merit of the dams. This leads to more accurate breeding value estimates and better tracking of genetic trends across populations.

99. (A) Days in milk (DIM).
Random regression models are used for the analysis of test-day milk yields by modeling the lactation curve as a continuous function. In these models, individual records are typically treated as a function of the number of days in milk. This approach allows for the estimation of genetic and environmental components that vary dynamically over the course of the lactation cycle.

100. (A) I, II and IV
The inbreeding coefficient measures the probability that two alleles at a locus are identical by descent. It typically ranges from zero to one and is associated with an increase in homozygosity. While usually positive, it can be negative when an individual is more outbred than the average of the reference base population, representing a relative decrease in genetic similarity.

101. (A) $\frac{1}{2N_e}$
The rate of inbreeding in a population is closely related to its effective size. It can be approximated by a formula where the increase in inbreeding per generation is equal to one divided by twice the effective population size. This relationship demonstrates that smaller effective populations experience a much more rapid accumulation of inbreeding and a corresponding loss of genetic diversity.

constant. These weights ensure that selection progress is directed toward improving the overall economic efficiency of the population managed.

84. (D) Requirement for extensive pedigree recording infrastructure.
Traditional progeny testing programs are difficult to implement in smallholder farming systems because they require a robust infrastructure for recording pedigrees and individual performance. In these systems, herds are often small and disconnected, and records are frequently missing. Without accurate pedigree and phenotypic information, it is impossible to estimate breeding values with the precision needed for sire selection.

85. (A) Continuous environmental effects like age at calving.
In least squares analysis, a covariate is a continuous variable included in the model to adjust for its influence on the trait of interest. For example, age at calving is often treated as a covariate in dairy cattle models to account for its systematic effect on milk production. Adjusting for these factors helps isolate the genetic merit of animals evaluated.

86. (A) Identify a subset of predictors that models the response effectively without overfitting.
Variable selection techniques like stepwise regression are used in multiple linear regression to create a parsimonious model. The goal is to identify a subset of predictor variables that explain as much variation as possible without including redundant ones. This process helps prevent overfitting, where the model captures random noise in the data rather than the underlying biological relationships.

87. (A) The amount of variance captured by that component.
In principal component analysis, the eigenvalue associated with each principal component represents the amount of total variance in the original data that is explained by that component. Higher eigenvalues indicate that the corresponding components capture more information. Researchers use these values to decide how many components to retain for further analysis while reducing the dimensionality of the multivariate dataset.

88. (A) Mutation and genetic drift.
Nei's standard genetic distance is a measure used to quantify the genetic divergence between two populations. It is derived under a model assuming that differences between populations arise primarily from the accumulation of new mutations and the random changes in allele frequencies known as genetic drift. This distance metric is widely used for reconstructing evolutionary histories and assessing structure.

89. (D) Bayes B.
Bayes B is a hierarchical Bayesian model used in genomic selection that assumes a specific prior distribution for marker effects. It uses a spike-and-slab approach where most markers are assumed to have no effect. For those markers that do have an effect, their values are drawn from a Student's t-distribution, allowing the model to capture large-effect loci effectively.

90. (C) I and III
The National Center for Biotechnology Information is a major resource for biomedical and genomic data. It maintains several key databases, most notably GenBank, which stores nucleotide sequences. Additionally, it provides essential bioinformatic tools such as BLAST for sequence analysis. These resources are fundamental to modern genetic research and are utilized by scientists worldwide for data sharing and discovery.

91. (A) Causes differences between individuals but not between repeated records.
Permanent environmental variance is a component of phenotypic variance that reflects factors affecting an individual consistently across multiple observations. While these factors cause differences between different animals, they remain constant for all records of a specific animal over its lifetime. In repeatability models, this variance is separated from temporary environmental variance, which fluctuates randomly between individual records or lactations.

92. (D) Fitting full and reduced models to obtain expectations.
Henderson's Method 3, also known as the fitting constants method, involves calculating the reductions in sums of squares by fitting a series of full and reduced linear models. By taking the differences between these reductions and equating them to their mathematical

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systems with linear dependencies, allowing for the estimation of estimable functions of the fixed effects in the model.

19. (D) Multicollinearity
Multicollinearity occurs in multiple linear regression when two or more predictor variables are highly correlated with each other. This phenomenon leads to unstable estimates of regression coefficients and inflated standard errors, making it difficult to determine the individual contribution of each variable. It is a common challenge when analyzing complex biological datasets where various environmental or physiological factors are related.

20. (B) I, III and IV
Principal component analysis is a dimensionality reduction technique that transforms correlated variables into a set of linearly uncorrelated ones. It is a non-probabilistic method that does not assume an underlying distribution. The number of principal components generated is equal to the number of original variables, with the first component capturing the maximum possible variance in the analyzed dataset.

21. (B) Cavalli-Sforza chord distance
Cavalli-Sforza chord distance is a metric used to measure genetic divergence between populations based on allele frequencies. It is specifically derived under the assumption that genetic drift is the primary evolutionary force driving population separation. Unlike other measures, it treats the change in allele frequency as a random walk on the surface of a hypersphere to maintain mathematical independence.

22. (B) Genomic relationship matrix derived from SNPs
The Genomic Best Linear Unbiased Prediction model estimates breeding values by utilizing DNA marker information, typically from single nucleotide polymorphisms. Instead of relying on traditional pedigree-based relationships, it uses a genomic relationship matrix. This matrix provides a more accurate measure of the actual proportion of the genome shared between individuals, capturing variation due to Mendelian sampling within families.

23. (A) BLAST
The Basic Local Alignment Search Tool is a widely used bioinformatics algorithm designed to identify regions of local similarity between sequences. It compares a query protein or DNA sequence against a database and calculates the statistical significance of matches. This tool is essential for functional annotation and evolutionary studies by identifying homologous sequences across different species or within a single genome.

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24. (C) Environmental variance
Environmental variance in quantitative genetics is often partitioned into permanent and temporary components to improve the accuracy of genetic evaluations. Permanent environmental variance arises from factors that affect an individual's performance throughout its life, such as early-life nutrition. Temporary environmental variance includes random fluctuations that differ between individual records or observations, such as specific weather conditions or health events.

25. (D) Fitting constants method
Henderson's Method 3 is also known as the fitting constants method because it utilizes the reductions in sums of squares from fitting various models. This method is particularly useful for unbalanced data as it provides unbiased estimates of variance components for general mixed models. It involves computing the expectations of these reductions to solve for the underlying genetic and environmental parameters.

26. (C) Accounting for degrees of freedom lost by estimating fixed effects
Restricted Maximum Likelihood is preferred over standard Maximum Likelihood for estimating variance components because it provides unbiased estimates. It achieves this by accounting for the degrees of freedom lost during the estimation of fixed effects. By maximizing the likelihood of error contrasts rather than the raw data, REML avoids the downward bias typical of maximum likelihood estimators in small samples.

27. (B) Normal distribution
Minimum Variance Quadratic Unbiased Estimation is a statistical approach used to estimate variance components in linear models. This method provides unbiased estimators and is often derived under the assumption that the data follow a normal distribution. While it is translation invariant and does not require iteration, its optimality depends on the

102. (B) Total genetic variance to phenotypic variance.
Heritability in the broad sense is a measure of the total contribution of genetic factors to phenotypic variation. It is defined as the ratio of the total genetic variance, which includes additive, dominance, and epistatic effects, to the total phenotypic variance. This value provides an upper bound on the degree to which a trait is determined by an individual's entire genotype.

103. (A) $\frac{nr}{1+(n-1)r}$
Most Probable Producing Ability is calculated by applying a weighting factor to an individual's average performance deviation. This factor depends on the number of records available and the repeatability of the trait. As the number of records increases, the weight assigned to the individual's average also increases, making the estimate more reliable and closer to the animal's true producing ability.

104. (A) Use information from correlated traits to account for selection bias.
Multi-trait genetic models are more accurate than single-trait models because they leverage the genetic and environmental correlations between traits. By using information from related traits, these models can effectively account for selection bias and missing data. This leads to improved precision in the estimation of breeding values and genetic correlations, particularly for traits with low heritability or few observations.

105. (A) P-1, Q-2, R-4, S-3
Various concepts in quantitative genetics are defined by specific formulas or methods. The selection response is given by the product of intensity, accuracy, and genetic variation. The additive relationship matrix is constructed using Henderson's tabular method. Expected mean squares are fundamental to ANOVA for variance component estimation, and Gibbs sampling is a common MCMC method used in Bayesian analysis.

106. (A) Positive definite and invertible.
In the development of the Smith-Hazel selection index, the phenotypic variance-covariance matrix must satisfy specific mathematical properties. It must be positive definite, ensuring that all variances are positive and that the matrix is non-singular. This requirement is essential because the matrix must be inverted to solve the index equations and determine the optimal weights for the included traits.

107. (A) Records of herdmates calving in the same season and year.
Contemporary comparison is a method for sire evaluation that aims to isolate genetic effects from environmental influences. It involves comparing the performance of a sire's daughters with the records of their contemporaries in the same herd who calved during the same season and year. This approach effectively adjusts for management and environmental factors that affect groups of animals similarly.

108. (A) Both A and R are true and R is the correct explanation of A.
Least squares analysis can produce biased estimates in animal breeding if fixed effects are correlated with random genetic effects. This occurs because standard LSA treats all model effects as fixed and does not incorporate the additive genetic relationship matrix. Without this matrix, the method cannot account for the genetic ties between individuals, leading to potentially inaccurate results in unbalanced data.

109. (A) Variance Inflation Factor (VIF).
The variance inflation factor is a common diagnostic tool used in multiple linear regression to detect multicollinearity among predictor variables. It measures how much the variance of an estimated regression coefficient is increased due to correlations with other predictors. A high VIF value indicates that a variable is redundant and that the precision of its estimated effect is severely compromised.

110. (B) It requires a continuous categorical independent variable.
Discriminant function analysis is used to classify observations into discrete, predefined groups based on a set of continuous independent variables. It does not require continuous independent variables to be categorical. This technique is often applied in animal breeding and morphometric studies to characterize and distinguish between different breeds or populations using a combination of physical measurements of individuals.

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algorithm eventually generates a sample from the desired joint posterior distribution.

167. (A) N
Directly inverting a large additive genetic relationship matrix is computationally expensive, requiring operations proportional to the cube of the number of animals. However, Henderson developed a set of simple rules to construct the inverse relationship matrix directly from pedigree data. This approach is highly efficient, as the computational time required is proportional only to the number of individuals in the pedigree.

168. (A) Fixed effects.
Solving the Mixed Model Equations provides different types of estimates for the model components. The solutions for the fixed effects are referred to as Best Linear Unbiased Estimates. Simultaneously, the equations provide Best Linear Unbiased Predictions for the random effects, which in an animal model correspond to the additive genetic breeding values of the individuals included in the evaluation.

169. (A) 0%.
Dominance genetic variance results from the interaction between alleles at the same locus. Because parents pass only one allele per locus to their offspring, these specific allelic interactions are broken up during meiosis. Consequently, in a purely outbred population, no dominance variance is directly transmitted from a parent to its progeny. Resemblance between relatives is instead driven by additive genetic variance.

170. (A) Ali-Schaeffer function.
The Ali-Schaeffer function is a specific mathematical model widely used in random regression models to describe the shape of the dairy cattle lactation curve. It incorporates multiple terms to capture the rapid increase in yield after calving and the subsequent gradual decline. Using this function as a basis allows for a more accurate modeling of individual genetic and environmental trajectories.

171. (B) Greater than 1
In the additive genetic relationship matrix, the diagonal element for an individual represents its relationship with itself, which includes a component for inbreeding. For an animal that is inbred, this value is calculated as one plus the inbreeding coefficient. Since the inbreeding coefficient is positive, the resulting diagonal element will be strictly greater than one, reflecting the increased genetic homozygosity.

172. (A) Individuals of different age cohorts breed at the same time.
Overlapping generations is a common feature of many biological populations, including livestock. It means that individuals from different age groups, or cohorts, are present and actively breeding in the population at the same time. This structure contrasts with discrete generations, where parents breed and are then completely replaced by their offspring before the next breeding cycle begins in time.

173. (A) Repeatability includes both additive genetic variance and permanent environmental variance; herizability only includes additive genetic variance.
Repeatability and narrow-sense herizability are both ratios of variance components to total phenotypic variance, but they differ in their numerator. Herizability only includes the additive genetic variance, reflecting the part of the variance that is inherited. Repeatability includes both the additive genetic variance and the permanent environmental variance, representing the total variance that remains consistent across an animal's repeated records.

174. (A) The cow's true phenotypic mean.
Most Probable Producing Ability is an estimate of an animal's future performance based on past records. As the number of available repeated records for a cow approaches infinity, the influence of temporary environmental fluctuations is minimized. Consequently, the MPPA estimate will converge to the cow's true phenotypic mean, which represents the combined effect of its genotype and its permanent environment.

175. (A) P-2, Q-4, R-1, S-3
Bioinformatic resources are categorized by their specific focus. Ensembl provides annotated vertebrate genomes, while PubMed is the primary database for biomedical literature. UniProt is dedicated to protein sequence and functional information. GenBank serves as the comprehensive public repository for nucleotide sequences. Understanding these scopes is essential for researchers to effectively locate and utilize genomic and proteomic data in their studies.

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dimensions are determined by the total number of animals included in the analysis. Therefore, for a pedigree containing 1000 animals, the resulting relationship matrix will be square with 1000 rows and 1000 columns, containing one million total elements.

121. (A) Incidence matrix for random effects.
In Henderson's Mixed Model Equations, the matrix Z is known as the incidence matrix for random effects. It serves the critical function of linking each individual observation in the dataset to the corresponding random effect, such as an animal's breeding value. This matrix, along with the fixed effect incidence matrix X, is essential for correctly structuring and solving the model equations.

122. (A) Repeatability.
In a repeatability model, the total phenotypic variance is partitioned into components including additive genetic variance and permanent environmental variance. The sum of these two components, expressed as a ratio of the total phenotypic variance, defines the repeatability of the trait. This value represents the proportion of variation that is consistent across repeated measures of the same individual over time.

123. (B) I and III
Random regression models provide a flexible framework for analyzing longitudinal traits. They allow genetic correlations between different time points, such as different days in milk, to be less than one, reflecting changes in genetic expression. Furthermore, these models can predict breeding values for any point along the fitted trajectory, even for time points where no actual records were observed.

124. (B) 0.25
The path coefficient method is used to determine the genetic relationship between relatives. In a population without inbreeding, the coefficient between a grandparent and a grand-offspring is 0.25. This value represents the fact that, on average, a grand-offspring inherits one-fourth of its alleles from any specific grandparent, reflecting the transmission of genes through the intervening parent during meiosis.

125. (A) Both A and R are true and R is the correct explanation of A.
In populations with overlapping generations, the rate of inbreeding per year is often slower compared to those with discrete generations. This occurs because the presence of individuals from multiple age groups increases the generation interval. A longer generation interval spreads the genetic contributions over a longer time, which helps to maintain genetic diversity and reduce the annual increase in inbreeding.

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126. (A) Is likely related to fitness or survival.
Traits with very low heritability, such as 0.05, are often closely associated with fitness, reproduction, or survival. These traits tend to have low additive genetic variation because natural selection has already pushed them toward optimal levels. Consequently, these traits show a limited response to artificial selection and are heavily influenced by environmental factors rather than additive genetic merit.

127. (A) Repeatability.
Repeatability is a statistical measure used for traits that can be recorded multiple times on the same individual. It is defined as the ratio of the covariance between an animal's repeated records to the total phenotypic variance. This value represents the consistency of performance across different observations and includes both the additive genetic variance and the permanent environmental variance.

128. (A) Cause Trait 2 to increase.
When two traits have a high positive genetic correlation, they are influenced by many of the same genes. Consequently, applying selection to improve one trait will lead to a correlated genetic response in the other. In this case, selecting for an increase in Trait 1 will indirectly cause Trait 2 to increase as well, reflecting their shared genetic architecture.

129. (A) Generation interval.
The annual genetic gain is a measure of the progress made in a breeding program over a specific period. It is calculated by taking the total genetic response to selection and dividing it by the generation interval. This formula highlights how both the intensity of selection and the time taken to replace parents with their offspring determine the speed of genetic improvement.

by identifying short, identical segments between a query sequence and a database, known as words. These matches are then extended into longer high-scoring segment pairs. This heuristic approach allows for the efficient identification of homologous sequences and functional similarities across vast amounts of genomic and proteomic data available.

186. (A) Additive x Additive, Additive x Dominance, and Dominance x Dominance epistasis.
Interaction variance, also known as epistatic variance, represents the component of genetic variation that results from non-additive interactions between alleles at different loci. This complex variance is further partitioned into several sub-components, including additive by additive, additive by dominance, and dominance by dominance interactions. These terms describe how the effects of genes at various locations combine to influence a trait.

187. (A) The fixed effects cannot be adjusted cleanly without biasing the random interactions.
Henderson's Method 2 is a technique for estimating variance components that involves adjusting the data for fixed effects. However, it is restricted to models where no interactions exist between fixed and random effects. If such interactions are present, they become confounded with the fixed factors during the adjustment process, leading to biased and inaccurate estimates of the random variance components.

188. (A) Newton-Raphson Algorithm.
The Newton-Raphson algorithm is a powerful numerical method used for finding maximum likelihood estimates in REML. It utilizes information from both the first and second derivatives of the likelihood function, the latter being the Hessian matrix. By incorporating second-order information, this algorithm can achieve a much faster convergence rate than first-order methods, although it is more computationally intensive.

189. (A) The true (but unknown) values of the variance components provided as priors.
MIVQUE estimators are described as being locally minimum variance. This means that they only achieve the property of having the smallest possible variance among unbiased quadratic estimators when the initial prior values used in the calculation are exactly equal to the true parameter values. In practice, since the true values are unknown, the optimality of the estimators is local in nature.

190. (A) Inverted Chi-square or Inverse-Wishart distribution.
In Bayesian analysis of quantitative genetic models, variance components require specific prior distributions to ensure valid statistical inference. The inverted Chi-square distribution is the standard prior for a single variance component, while the Inverse-Wishart distribution is its multivariate generalization for covariance matrices. These priors are conjugate to the normal likelihood, which simplifies the calculation of the conditional posterior distributions.

191. (A) $0.5 \times (R_{SY} + R_{DY})$
For animal X with sire S and dam D, its relationship with animal Y is calculated as one-half the sum of the relationships $S - Y$ and $D - Y$ in the matrix.

192. (A) The off-diagonal elements of $A^{\{-1\}}$ link the sire to its progeny's records.
In the Mixed Model Equations, the inverse of the additive genetic relationship matrix plays a critical role in distributing information across the pedigree. Sires without their own phenotypic records can still receive breeding value estimates because the off-diagonal elements of this matrix link them to their progeny. This allows the model to propagate performance information from descendants to ancestors.

193. (A) Uncorrelated (independent).
The repeatability model simplifies the analysis of multiple records by partitioning environmental variance into permanent and temporary components. A fundamental assumption of this model is that the permanent environmental effect, which stays constant across records, is uncorrelated and statistically independent from the temporary environmental effect, which varies randomly. This independence allows for the distinct estimation of each variance component in the analysis.

194. (A) It estimates the full breeding value (1.0 of additive genetic merit) directly.
The sire model is a simplified genetic evaluation tool that focuses only on the transmitting ability of male parents. One of its defining features is

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with balanced data, the estimates produced by standard ANOVA are identical to those from Restricted Maximum Likelihood and Henderson's Method 1. This consistency simplifies analysis and provides a clear interpretation of the genetic and environmental components of variance in well-structured breeding data.

140. (C) A is true but R is false.
The Expectation-Maximization algorithm for REML is favored because it ensures that variance component estimates remain within the valid parameter space, such as being non-negative. However, it does not update parameters by setting them directly to the first derivative. Instead, it iteratively updates them through the E and M steps, which often results in a slower but more stable convergence process.

141. (A) The true parameter values.
MIVQUE is a non-iterative method for estimating variance components that requires prior information. Although it provides unbiased estimators, its property of having minimum variance is conditional. Specifically, the estimates only achieve the minimum possible variance when the initial prior values supplied for the variance components are exactly equal to the true, underlying population parameters being estimated in the specific model.

142. (A) It provides the full posterior distribution, easily giving standard errors and credible intervals.
Bayesian MCMC methods offer a significant advantage over REML for complex genetic models because they provide the entire posterior distribution of the parameters. This allows for the straightforward calculation of point estimates, standard errors, and credible intervals. This comprehensive description of uncertainty is particularly valuable in genomic evaluations and other advanced breeding applications where simple point estimates may be insufficient or misleading.

143. (A) 0.0625
Henderson's tabular method calculates relationships recursively. If the relationship between two parents is 0.25, and they produce half-sib offspring who share no other common ancestors, the relationship between those offspring will be one-fourth of the parents' relationship. In this scenario, multiplying the parental relationship of 0.25 by 0.25 results in a relationship of 0.0625 between the half-sib individuals.

144. (A) $\frac{\sigma_E^2}{\sigma_A^2}$
In the Mixed Model Equations, the random effect block is modified by adding a scalar value, often denoted as lambda, to the diagonal elements of the inverse relationship matrix. This value is defined as the ratio of the residual environmental variance to the additive genetic variance. This parameter weights the genetic information against the observed phenotypic data, ensuring optimal prediction of breeding values.

145. (A) Three-quarters of the additive variance plus residual environmental variance.
In a sire model, the residual variance component, often labeled as error variance, is not purely environmental. It includes the remaining three-quarters of the additive genetic variance that is not captured by the sire variance, in addition to the actual residual environmental variance. This partitioning reflects the fact that the model only explicitly accounts for the paternal contribution to the offspring's genotype.

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146. (A) It assumes the genetic correlation between repeated measures is zero.
The repeatability model is used for traits with multiple records on the same individual. A core assumption of this model is that the genetic correlation between these repeated measures is exactly one, implying that the same genes influence the trait throughout the animal's life. It does not assume a zero correlation; rather, it uses multiple records to estimate permanent environmental and genetic effects.

147. (A) They model traits measured continuously over time, forming a continuous trajectory.
Random regression models are described as handling infinite-dimensional traits because they treat measurements taken over time as a continuous function. Instead of evaluating the trait at discrete points, the model fits a continuous trajectory or curve. This allows for the estimation of genetic variances and correlations at any theoretical point in time, providing a comprehensive view of the trait's genetic development.

111. (A) The reduction in heterozygosity in subpopulations relative to the total population.
The fixation index is a fundamental measure of population differentiation in genetics. It quantifies the reduction in heterozygosity within subpopulations compared to the total population due to genetic structure. Higher values indicate greater genetic divergence between groups, often resulting from isolation, genetic drift, or restricted gene flow between the different subpopulations being studied in the analysis.

112. (A) Distance-based clustering method.
The neighbor-joining method is a widely used algorithm for reconstructing phylogenetic trees from genetic distance data. It is a distance-based clustering approach that operates through star decomposition, iteratively joining the most closely related pairs of taxa. This method is computationally efficient and can produce unrooted trees that reflect the evolutionary relationships between different populations or species accurately.

113. (A) Both genotypic and phenotypic data.
In genomic selection, the reference population consists of individuals that have both their phenotypes measured and their genotypes determined via DNA markers. This group is used to estimate the effects of markers across the genome. These estimated effects are then applied to a candidate population of younger animals that have been genotyped but not yet phenotyped for selection purposes.

114. (A) Progressive multiple sequence alignment.
ClustalW is a popular bioinformatic tool for performing multiple sequence alignments of DNA or protein sequences. It utilizes a progressive alignment algorithm, which first calculates pairwise distances between all sequences to build a guide tree. Sequences are then aligned following the order of the tree, starting with the most similar pairs and gradually adding more distant ones.

115. (A) Independent (no covariance) in a simple additive model.
Partitioning phenotypic variance into genetic and environmental components simplifies the analysis by assuming that these two effects are independent. In a basic additive model, this means there is no covariance between an individual's genotype and the environment it experiences. While genotype-environment interactions and correlations can exist, they are often treated as separate components in more complex genetic models.

116. (A) Method 3.
Henderson's Method 3 is specifically developed to handle mixed models with both fixed and random effects in unbalanced datasets. By utilizing the reductions in sums of squares from fitting various models, it provides unbiased estimators of the variance components. This makes it a more versatile and accurate approach than Methods 1 and 2, which have limitations in mixed models.

117. (A) The likelihood of a set of error contrasts that are independent of the fixed effects.
Restricted Maximum Likelihood is a standard method for estimating variance components that avoids the bias associated with Maximum Likelihood. It works by maximizing the likelihood of a transformed set of data called error contrasts. These contrasts are specifically chosen to be invariant to the fixed effects, ensuring that the resulting variance estimates are unbiased even in small samples.

118. (A) II → I → III → IV
Computing the inbreeding coefficient via the tabular method requires a chronological ordering of the pedigree. Once ordered, the base population individuals are initialized with a diagonal value of one. Off-diagonal relationships are then calculated as the average of the parents' relationships. Finally, the diagonal for each animal is determined by adding half of the relationship between its parents to one.

119. (A) It integrates to exactly 1.
In Bayesian statistics, a proper prior distribution is one that satisfies the requirements of a probability density function. Specifically, the integral of the distribution over the entire parameter space must be equal to exactly one. This ensures that the posterior distribution, which is derived from the prior and the likelihood, is also a valid probability distribution that can be used for inference.

120. (A) 1000×1000.
The additive genetic relationship matrix, often called the A-matrix, describes the genetic ties between all individuals in a population. Its

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the validity of statistical tests, the accuracy of standard errors, and the reliability of the resulting regression coefficient estimates produced.

158. (A) The proportion of variance in the dependent variable NOT explained by differences in group means.
Wilks' Lambda is a key statistic used in discriminant function analysis to evaluate the effectiveness of the model. It represents the proportion of total variance in the independent variables that is not explained by the differences between the group means. A smaller value indicates that the groups are well-separated and that the discriminant function is a good fit for the data.

159. (A) All lineages evolve at the same rate.
The UPGMA method for phylogenetic reconstruction is based on the assumption of an ultrametric tree, which implies a constant molecular clock. This means that all evolutionary lineages are assumed to accumulate mutations at the same constant rate over time. Under this assumption, the distance from the root to any contemporary tip is identical, reflecting equal evolutionary progress across branches.

160. (A) I and II
Single-step GBLUP is a versatile method for genetic evaluation that integrates genomic and pedigree information. It achieves this by constructing a unified H-matrix, which blends the pedigree relationship matrix with the genomic relationship matrix. Unlike basic GBLUP, it does not require all animals in the pedigree to be genotyped, allowing for the simultaneous evaluation of both genotyped and ungenotyped individuals.

161. (A) FASTA.
FASTA is a standard bioinformatics file format used for representing either nucleotide or peptide sequences. It is characterized by a header line that begins with a greater-than symbol followed by a unique sequence identifier and description. The sequence data itself follows on subsequent lines. This simple and flexible format is widely used for sequence storage, database searching, and various alignment tools.

162. (A) Less than 1.0.
Genotype-environment interaction can be quantified as the genetic correlation of the same trait expressed in two different environments. If this correlation is significantly less than 1.0, it indicates that the trait is influenced by different sets of genes or that gene expression changes across environments. This reduction in correlation reflects shifts in the relative ranking of genotypes across settings.

163. (A) Fixed effects (other than the general mean).
Henderson's Method 1 is a simple technique for estimating variance components by using analogues of ANOVA sums of squares. However, its primary limitation is that it is only valid for models containing random effects and no fixed factors other than the population mean. If fixed effects are present, the method produces biased estimates because it cannot properly account for systematic environmental influences.

164. (A) Does not correct for degrees of freedom used to estimate fixed effects (downward bias).
Maximum Likelihood estimation of variance components often produces downwardly biased estimates because it does not account for the degrees of freedom consumed by estimating fixed effects. This bias is particularly problematic in small datasets. Restricted Maximum Likelihood addresses this issue by maximizing the likelihood of error contrasts, leading to more accurate and unbiased variance estimates in animal breeding applications.

165. (A) The data follow a normal distribution.
Minimum Variance Quadratic Unbiased Estimation and Minimum Norm Quadratic Unbiased Estimation are related methods for estimating variance components. While they are derived from different theoretical perspectives, they yield the same results when the data are assumed to follow a normal distribution. In this case, both methods provide the same quadratic estimators for the genetic and environmental variances in models.

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166. (A) Both A and R are true and R is the correct explanation of A.
Gibbs sampling is an iterative Bayesian method that decomposes a complex joint distribution into simpler components. It requires the specification of fully conditional posterior distributions for every parameter in the model. By sampling from each conditional distribution in turn, given the current values of all other parameters, the

130. (A) P-2, Q-1, R-4, S-3
Various types of selection indices are used in animal breeding. A base index uses economic values directly, while a restricted index is designed to hold the genetic change of certain traits to zero. The optimum index incorporates phenotypic and genetic covariances to maximize gain. Finally, a retrospective index is used to determine the weights that were implicitly applied during selection.

131. (A) Using reference sires (AI) across multiple smallherds to create linkages.
In smallholder farming systems, creating effective contemporary groups is challenging due to small herd sizes. To overcome this, artificial insemination is used to introduce reference sires across different herds. This creates genetic ties, or linkages, between the herds, allowing for the comparison of offspring from different sires under various environmental conditions and improving the accuracy of genetic evaluations performed.

132. (A) Year and season of calving.
Fixed effects are factors in a statistical model that represent systematic influences on the trait being measured. In dairy cattle breeding, the year and season of calving are standard examples of fixed effects. These factors are included in the model to adjust for large-scale environmental and management differences that affect the performance of groups of animals in a similar way.

133. (A) Decreases.
Ridge regression is used to handle multicollinearity by introducing a penalty parameter to the estimation process. As the value of this parameter increases, the bias of the regression coefficients also increases, but their variance decreases. This trade-off leads to more stable estimates that are less sensitive to small changes in the data, which is particularly beneficial in complex multivariate analysis.

134. (A) Principal Component Analysis (PCA).
Principal component analysis is the most appropriate technique for reducing the dimensionality of a dataset with many correlated variables. For example, it can condense numerous morphometric measurements into a few independent principal components. This simplification facilitates visualization and helps researchers identify the primary patterns of variation within a population while retaining as much information as possible from the data.

135. (A) It assumes a strict molecular clock (equal rates of evolution).
UPGMA is a distance-based clustering algorithm used for phylogenetic reconstruction. A key characteristic of this method is the assumption of a strict molecular clock, meaning that all evolutionary lineages are assumed to evolve at the same constant rate over time. As a result, the algorithm produces rooted trees where all contemporary taxa are equidistant from the root of the tree.

136. (A) G-matrix.
In genomic selection, the traditional pedigree-based A-matrix is replaced by the genomic relationship matrix, or G-matrix. This matrix is constructed using DNA marker information, such as SNP data, to provide a more precise measure of the actual genetic similarity between individuals. The use of the G-matrix allows for more accurate estimation of breeding values by capturing Mendelian sampling.

137. (A) Needleman-Wunsch.
The Needleman-Wunsch algorithm is a classic dynamic programming method used in bioinformatics for the global alignment of two sequences. It aims to find the best possible alignment across the entire length of the sequences by maximizing a similarity score. This approach is fundamental for comparing highly similar sequences and for identifying conserved regions and evolutionary relationships over their entire extent.

138. (A) Genotype x Environment Interaction.
Genotype-environment interaction occurs when the phenotypic expression of a specific genotype depends on the environmental conditions in which it is measured. This phenomenon is characterized by different genotypes responding differently to environmental changes, which can lead to shifts in their relative performance or ranking. Accounting for these interactions is essential for selecting animals that are robust across various production environments.

139. (A) REML and Henderson Method 1 estimates.
In balanced experimental designs, several variance component estimation methods converge to the same results. For a completely randomized design

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176. (A) The genes affecting one trait have no pleiotropic effects on the other.
A genetic correlation of zero indicates that there is no additive genetic association between two traits. This means that the genes that influence one trait are entirely different from those that influence the other, and that no pleiotropic effects exist between them. In this situation, selecting for improvement in one trait will have no direct correlated genetic impact on the other trait.

177. (C) 12
The expected response to selection can be calculated using the product of selection intensity, the accuracy of selection, and the additive genetic standard deviation. For an intensity of 1.5, an accuracy of 0.8, and a standard deviation of 10, the calculation is 1.5 times 0.8 times 10, which equals 12. This value represents the expected genetic progress per selection cycle achieved.

178. (A) The genetic gain for a specific trait is constrained to zero.
A restricted selection index is a modification of the classical index where mathematical constraints are applied to the weights. The primary purpose of this restriction is to ensure that the genetic gain for one or more specific traits is held to zero while maximizing the gain for other traits in the objective. This is useful when maintaining a trait at current levels.

179. (A) Animal Model with genetic ties (e.g., through AI reference sires).
In smallholder farming systems where herds are small and disconnected, the animal model is the most effective tool for genetic evaluation. By using reference sires through artificial insemination, genetic ties are created between different farms. These ties allow the model to compare animals across various environments more accurately, overcoming the limitations of small and fragmented contemporary groups in evaluation.

180. (A) I, II and IV
Least squares analysis is a fundamental statistical technique that estimates fixed effects by minimizing the sum of squared errors. It provides unbiased estimators for these effects but requires the inversion of the coefficient matrix, which can be challenging for large datasets. Unlike mixed models, standard LSA treats all model effects as fixed and does not differentiate between genetic and environmental components.

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181. (A) Variance of the estimators under multicollinearity.
Ridge regression is a technique used to stabilize parameter estimates when predictor variables are highly correlated. It introduces a small amount of bias into the estimators, but in doing so, it significantly reduces their variance. This trade-off results in more reliable and robust estimates that are less affected by multicollinearity, leading to better overall performance in predictive modeling and analysis.

182. (A) The number of principal components to retain.
A scree plot is a visual tool used in principal component analysis to display the eigenvalues associated with each principal component in descending order. By examining the plot for a clear "elbow" or break, researchers can determine the number of components that capture the most meaningful variance and should be retained for further analysis, while discarding less informative ones in the dataset.

183. (A) Genetic drift.
The chord distance developed by Cavalli-Sforza and Edwards is a measure of genetic divergence that is based on the random walk of allele frequencies. This distance metric is derived under the assumption that population differentiation is driven solely by genetic drift. By treating frequencies as points on a hypersphere, it ensures that the distance is independent of the initial allele frequencies.

184. (A) Both A and R are true and R is the correct explanation of A.
Single-step GBLUP is a powerful method that integrates genomic information into traditional pedigree-based evaluations. It achieves this by creating a unified H-matrix that blends the genomic relationship matrix with the pedigree relationship matrix. This blending allows for the simultaneous estimation of breeding values for all animals in the population, regardless of whether they have been genotyped or only phenotyped previously.

185. (A) BLAST.
BLAST is an essential bioinformatics algorithm designed for rapid database searches. It works

148. (A) $F = 0.5 \times R_{AB}$
The inbreeding coefficient of an individual is a measure of the probability that its alleles at a locus are identical by descent. It is mathematically defined as half the relationship between its parents. This formula ensures that the inbreeding of the offspring reflects the shared genetic heritage of the parents, which increases as they become more closely related within the breeding population.

149. (B) 36
Effective population size is sensitive to unequal numbers of breeding males and females. Using the standard formula for a population with 10 males and 90 females, the effective size is calculated to be 36. This value is significantly lower than the actual census size of 100, illustrating how the limited number of males restricts the genetic diversity and increases the rate of inbreeding.

150. (A) I → II → III → IV
Implementing genomic selection follows a specific sequence of steps. First, a reference population with both genotypes and phenotypes is established to estimate marker effects. Once these effects are determined, candidate animals are genotyped. Finally, the estimated marker effects are applied to the genotypes of the candidates to calculate their genomic estimated breeding values, allowing for early and accurate selection decisions.

151. (A) Z-test based on standard error.
To determine if an estimated genetic correlation is statistically significant, researchers often employ a Z-test. This involves dividing the estimated correlation coefficient by its standard error to calculate a Z-score. If this score exceeds the critical value for a given significance level, the correlation is considered to be significantly different from zero, indicating a genuine genetic association between the two traits analyzed.

152. (A) Phenotypic standard deviations.
Selection intensity is a dimensionless value that represents the superiority of the selected individuals over the population mean. It is specifically expressed in units of phenotypic standard deviations. This standardization allows for the comparison of selection pressure across different traits and populations, and it is a key component in the Breeder's Equation for predicting the annual response to selection.

153. (A) P-2, Q-1, R-3, S-4
Different distance metrics serve various purposes in genetic and multivariate analysis. Euclidean distance measures straight-line physical distance, while Mahalanobis distance adjusts for correlations between variables. Nei's distance evaluates allele frequency divergence due to drift, and the fixation index measures population differentiation based on heterozygosity levels. Each metric provides unique insights into the evolutionary structure and history of populations.

154. (A) Have no effect on the expected genetic gain.
In a selection index, the response in genetic merit depends on both the economic importance and the heritability of the traits. If a trait has high economic value but zero heritability, its additive genetic variance is also zero. Consequently, including it in the index will not contribute to the expected genetic gain, as no genetic progress can be made for that trait.

155. (A) Both A and R are true and R is the correct explanation of A.
Progeny testing is a highly accurate method for evaluating sires, particularly for traits that are sex-limited, such as milk yield. Its accuracy stems from the fact that it uses performance data from a large number of daughters. By averaging many records, the influence of random environmental factors is minimized, significantly reducing the standard error and providing a precise estimate of merit.

156. (A) Empty subclasses result in confounding and linearly dependent equations.
In least squares analysis, fitting interaction terms requires sufficient data in all combinations of the factors involved. If some subclasses are empty, the model encounters linear dependencies, which means certain effects cannot be estimated independently. This confounding makes it difficult to solve the normal equations and can lead to unreliable or uninterpretable results in unbalanced animal breeding datasets analyzed.

157. (A) Independent and identically distributed normally.
Multiple linear regression relies on several fundamental assumptions regarding the residual errors. It is assumed that these residuals are independent of each other and follow a normal distribution with a constant variance and a mean of zero. These properties are essential for

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that the sire variance component it estimates is only one-quarter of the total additive genetic variance. Therefore, the model does not estimate the full breeding value directly but rather the paternal half of the genetic merit accurately.

195. (A) Random Regression Model.
Random regression models are specifically designed to analyze longitudinal data where traits change continuously over time. They fit a unique curve for each individual animal by modeling the covariance structure of the random regression coefficients. This approach allows for the estimation of genetic and environmental variances that evolve throughout an animal's life, such as milk production during a typical lactation.

196. (A) Males are hemizygous and cannot be inbred for X-linked traits.
Calculating inbreeding coefficients for traits controlled by genes on the X chromosome requires specific modifications to the standard autosomal rules. Since males are hemizygous, meaning they possess only one X chromosome inherited from their dam, they cannot be inbred for these traits. This unique inheritance pattern must be accounted for to accurately assess genetic diversity for X-linked biological characteristics.

197. (B) 4
The effective population size is strongly influenced by the number of breeding individuals of each sex. In a herd with only one male and 100 females, the effective population size is calculated to be 4. This extremely low value, despite the presence of many females, highlights how a single male severely restricts genetic diversity and significantly increases the rate of inbreeding.

198. (C) $4t$
Herizability can be estimated from paternal half-sib data using the intra-class correlation coefficient. Since half-siblings share approximately one-fourth of their additive genetic variance, the correlation between them represents one-quarter of the narrow-sense herizability. Consequently, the herizability of a trait is derived by multiplying the observed half-sib intra-class correlation by a factor of four in the calculation.

199. (A) Pushed closer to their own phenotypic mean.
Most Probable Producing Ability is a weighted estimate of an individual's future performance. As more repeated records become available for an animal, the reliability of its average performance increases. This higher reliability causes the weighting factor to approach one, which pushes the MPPA estimate closer to the animal's actual observed phenotypic mean rather than the general population average.

200. (B) I and III
Multi-trait animal models are powerful tools for genetic evaluation because they provide unbiased estimates even when the data are subject to sequential selection. Genetic correlations are calculated as the genetic covariance between two traits divided by the product of their respective genetic standard deviations. While they are often positive, genetic correlations can also be negative, depending on the underlying biological associations.

201. (A) Generation interval is significantly reduced.
Genomic selection is a revolutionary approach in animal breeding that significantly impacts the Breeder's Equation. Its primary benefit is the substantial reduction in the generation interval. By allowing for the accurate selection of young animals based on DNA marker data before they reach reproductive age or produce progeny, breeders can accelerate genetic progress by shortening the time between generations successfully.

202. (A) Dominance variances of all traits.
The classical Smith-Hazel selection index is designed to maximize the gain in an aggregate genotype based on additive genetic effects. Constructing this index requires information on phenotypic variances, genetic and phenotypic covariances, and economic values for all included traits. However, it does not require knowledge of dominance variances, as it focuses on predicting and improving the breeding value of candidates.

203. (A) Extremely high recording costs and lack of pedigree linkages across herds.
In smallholder farming systems, the implementation of traditional progeny testing is hindered by significant practical challenges. These include the high costs associated with performance and pedigree recording and the lack of genetic connections between different small

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239. (A) $\frac{3}{4}$ of the additive variance plus residual environmental variance.
The sire model is a simplified approach to genetic evaluation that only explicitly models the paternal contribution to the offspring's phenotype. As a result, the sire variance component accounts for only one-quarter of the additive genetic variance. The remaining three-quarters of the genetic variance is absorbed into the residual variance component, along with all the residual environmental variation.

240. (A) I and III
The repeatability model is used for traits with multiple records, where the permanent environmental effect is included as a random factor. This effect accounts for consistent non-genetic influences on an individual. Furthermore, the calculation of Most Probable Producing Ability utilizes the trait's repeatability to weight the animal's average performance deviation, providing a prediction of future records based on past ones.

241. (A) Reduce multicollinearity and correlations between coefficients.
Random regression models often use orthogonal polynomials, such as Legendre polynomials, as basis functions for describing trajectories over time. The primary reason for using orthogonal functions is to reduce multicollinearity between the estimated regression coefficients. This leads to more stable and independent estimates of the coefficients, improving the numerical stability and interpretability of the genetic and environmental covariance components.

242. (A) Increase rapidly.
A genetic bottleneck occurs when a population undergoes a drastic reduction in size, leading to a loss of genetic diversity. In the subsequent generations, the remaining individuals are more likely to be related, causing a rapid increase in the average inbreeding coefficient. This phenomenon can lead to inbreeding depression and a reduced ability for the population to adapt to changes over time.

243. (A) The number of males.
The effective population size is heavily influenced by the sex that has fewer breeding individuals. In a flock where the sex ratio is highly skewed, such as one male mated to many females, the number of males becomes the limiting factor for genetic diversity. Consequently, the effective size will be much closer to the number of males in the population.

244. (A) Phenotypic selection will be highly effective.
A very high heritability value, such as 0.85, indicates that a large majority of the observed phenotypic variation in a trait is due to additive genetic effects. In this situation, an individual's own performance is a very accurate indicator of its breeding value. Consequently, simple phenotypic selection, or mass selection, will be highly effective for making rapid genetic progress.

245. (A) Broad-sense heritability.
Repeatability is defined as the proportion of phenotypic variance due to both genetic and permanent environmental factors. Since it includes all genetic components as well as some environmental ones, its value will always be greater than or equal to the broad-sense heritability. Therefore, repeatability acts as a theoretical upper bound for heritability, indicating the maximum contribution of genetic factors.

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246. (A) Genetic correlation between X and Y, and heritabilities of both traits.
To predict the correlated response of Trait Y when selection is applied to Trait X, several genetic parameters must be known. These include the heritabilities of both traits and the genetic correlation between them. These values allow for the calculation of how much genetic progress in the primary trait will indirectly translate into a genetic change in the secondary trait.

247. (A) I $\rightarrow$ II (bypassing III).
To maximize the annual genetic gain, modern breeding programs increasingly utilize genomic selection. By selecting top young bulls based on genomic testing, breeders can achieve high accuracy at a much younger age. This significantly reduces the generation interval by bypassing traditional progeny testing, which requires several years to complete. This streamlined process accelerates genetic progress and is becoming common.

248. (A) The index (I) and the aggregate genotype (H).
The goal of the Smith-Hazel selection index is to provide a single value that ranks animals according to their total genetic worth. The index

212. (A) MIVQUE is non-iterative and depends on prior values, whereas REML is iterative and updates priors.
MIVQUE and REML are two common methods for estimating variance components, but they differ in their computational approach. MIVQUE is a non-iterative method that provides estimates in a single step based on initial prior values. In contrast, REML is an iterative procedure that repeatedly updates the parameter estimates until convergence, making it more computationally intensive but less dependent on the initial guess.

213. (A) The initial iterations that are discarded because the chain has not yet reached its stationary distribution.
In Markov Chain Monte Carlo methods, the burn-in period consists of the initial set of samples generated by the algorithm. These samples are discarded because they are influenced by the starting values and do not yet represent the true posterior distribution. Once the chain has converged to its stationary distribution, subsequent samples are kept and used for statistical inference and estimation.

214. (A) 0.0
In the additive genetic relationship matrix, off-diagonal elements quantify the degree of genetic similarity between two different individuals. If two animals come from completely different families with no common ancestors in the recorded pedigree, they are assumed to be unrelated. Consequently, the value of the off-diagonal element in the matrix that represents their relationship will be exactly zero.

215. (A) Do not require the inversion of the large phenotypic covariance matrix (V).
Henderson's Mixed Model Equations are preferred over traditional generalized least squares because they are computationally more efficient. While GLS requires the inversion of a large phenotypic covariance matrix (V), which can be millions of elements in size, MME avoids this step. Instead, it solves a system of equations based on incidence matrices and the inverse of the smaller relationship matrix accurately.

216. (A) Correlated random effect.
In advanced animal models that account for maternal genetic effects, these effects are typically included as random factors. Furthermore, they are often modeled as being genetically correlated with the animal's own direct additive genetic effect. This allows breeders to accurately estimate and select for both the animal's growth potential and the dam's ability to provide a superior maternal environment.

217. (B) They require the exact same days in milk (DIM) for every animal.
Random regression models are highly flexible tools for analyzing test-day records. One of their primary advantages is that they do not require all animals to have records taken at the exact same days in milk. By fitting a continuous function over time, the model can accommodate varying measurement schedules and still accurately estimate individual genetic and environmental trajectories during lactation.

218. (B) The number of individuals in the path connecting the parents through a common ancestor.
When calculating the inbreeding coefficient using the path coefficient method, the contribution of each path is determined by the term one-half raised to the power of n. In this context, n represents the total number of individuals in the chain connecting the two parents through their common ancestor. This formula accounts for the genetic dilution that occurs over successive generations.

219. (A) The rate of inbreeding (ΔF).
The effective population size is a fundamental concept in population genetics that is inversely related to the rate of inbreeding. Smaller effective populations experience a more rapid increase in the average inbreeding coefficient per generation. Consequently, monitoring and maintaining a sufficiently large effective population size is critical for minimizing the loss of genetic diversity and the accumulation of alleles.

220. (B) I, II and III
Heritability in the narrow sense is defined as the proportion of total phenotypic variance that is due to additive genetic variance. It is a key parameter because it determines the resemblance between relatives and allows for the estimation of breeding values via parent-offspring regression. Unlike broad-sense heritability, it specifically excludes dominance and epistatic variance, focusing only on the inheritable genetic component.

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221. (A) $V_{\{TE\}}$ is relatively small compared to genotypic and permanent environmental variance.
A high repeatability value, such as 0.8, indicates that 80 percent of the phenotypic variation is consistent across an animal's repeated records. This implies that the remaining 20 percent of the variation is due to temporary environmental factors. Therefore, a high repeatability suggests that temporary environmental effects are relatively small compared to the combined influence of genetics and permanent environment.

222. (A) -1 and 1.
Genetic correlation is a statistical measure of the degree to which the breeding values for two different traits are associated. Like all correlation coefficients, it is mathematically bounded between negative one and positive one. A value near zero indicates no genetic association, while values near the boundaries represent strong positive or negative relationships driven by pleiotropy or linkage disequilibrium factors.

223. (A) Increasing the generation interval.
According to the Breeder's Equation, the annual genetic gain is inversely proportional to the generation interval. Therefore, increasing the time between generations will slow down the rate of genetic progress. To maximize annual gain, breeders should instead focus on increasing selection intensity, improving the accuracy of selection, and identifying traits with significant additive genetic variation in the population.

224. (A) The net genetic merit or aggregate genotype (H).
The classical selection index is designed to predict an individual's net genetic merit, also known as its aggregate genotype. It achieves this by creating a linear combination of various phenotypic traits, each weighted to maximize the correlation between the index and the underlying genetic value. This approach allows breeders to select for multiple traits simultaneously while accounting for economic importance.

225. (A) Sex-limited traits such as milk yield.
Progeny testing is an essential tool in dairy cattle breeding for evaluating traits that are expressed only in one sex, such as milk production. Since sires do not produce milk, their genetic merit must be inferred from the performance of their female offspring. By evaluating a large number of daughters, breeders can obtain a highly accurate estimate of sire merit.

226. (A) A factor whose levels only exist within the levels of another factor (e.g., sire within breed).
In the context of least squares analysis, a nested or hierarchical effect refers to a relationship between two factors where each level of the nested factor occurs within only one level of the main factor. For example, sires are often nested within breeds. This structural relationship must be properly specified in the model to ensure the correct estimation of data.

227. (A) The variances (standard errors) of the estimated regression coefficients.
Multicollinearity occurs in multiple linear regression when predictor variables are highly correlated with one another. This phenomenon inflates the variances and standard errors of the estimated regression coefficients, making them unstable and difficult to interpret correctly. This lack of precision hinders the ability to identify the individual effects of the predictors and can lead to misleading conclusions about significance.

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228. (A) Uncorrelated.
A fundamental property of principal component analysis is that the resulting principal components are orthogonal to each other. In a statistical context, orthogonality implies that the components are completely uncorrelated. This feature is beneficial for data analysis because it allows researchers to treat each component as an independent measure of the variation within the original dataset, simplifying interpretation of multivariate data.

229. (A) P-2, Q-1, R-3, S-4
Phylogenetic reconstruction involves several distinct concepts and methods. Maximum parsimony minimizes evolutionary changes, while maximum likelihood provides a probabilistic evaluation based on specific models. Neighbor-joining is an efficient clustering method based on star decomposition. Bootstrapping is a resampling technique used to assess the level of confidence or statistical support for the various nodes within the reconstructed phylogenetic tree topology.

230. (A) $A^{\{-1\}}$, $G^{\{-1\}}$, and $A^{\{-1\}}_{\{22\}}$ (inverse of pedigree relationship of genotyped animals).
In single-step GBLUP, the inverse of the integrated relationship matrix, H, is calculated through a specific blending formula. This formula utilizes the inverse of the full pedigree-based A -matrix, the inverse of the genomic G-matrix, and the inverse of the pedigree relationship matrix restricted to the genotyped animals. This combination allows the model to simultaneously account for all genomic and pedigree info.

231. (A) GenBank.
GenBank is the most comprehensive public database of nucleotide sequences, maintained by the National Center for Biotechnology Information. It serves as a global repository where researchers submit DNA and RNA sequence data from a vast range of organisms. This resource is fundamental to bioinformatic research, enabling scientists to share, compare, and analyze sequence information for various evolutionary studies.

232. (A) Both A and R are true and R is the correct explanation of A.
Additive genetic variance is the primary component responsible for the resemblance between parents and offspring. This is because parents pass only single alleles at each locus to their progeny, not their entire genotype. As a result, the non-additive interactions between alleles at the same locus, known as dominance, are broken up during meiosis and are not consistently inherited.

233. (A) Fitting constants (fitting full and sub-models).
Henderson's Method 3 is closely associated with the concept of fitting constants in linear models. It involves calculating the reductions in the sum of squares by fitting a series of full models and their corresponding sub-models. By comparing these reductions, the method provides a way to estimate variance components for unbalanced data while properly accounting for the fixed effects present.

234. (A) The change in variance components or likelihood between iterations is below a predefined very small threshold.
In the estimation of variance components using the AI-REML algorithm, convergence is determined by monitoring the changes in the parameter estimates or the log-likelihood function across successive iterations. Once these changes fall below a very small, predefined threshold, the algorithm stops. This indicates that a stable solution has been reached and the estimates have converged to their final values.

235. (A) Unbiased but loses its minimum variance property.
Minimum Variance Quadratic Unbiased Estimation is derived under the assumption that the data follow a normal distribution. If this assumption is violated and the data are not normal, the resulting estimators remain unbiased. However, they lose their property of being minimum variance. This means that while the estimates will be correct on average, they may be less precise.

236. (A) The dataset is small or uninformative.
In a Bayesian analysis, the posterior distribution is a combination of the prior beliefs and the information provided by the data via the likelihood function. If the prior distribution dominates the posterior, it indicates that the observed data are uninformative or that the sample size is very small. In this case, the resulting parameter estimates will be primarily driven by assumptions.

237. (D) 2.0
The diagonal element of the additive genetic relationship matrix for an individual is defined as one plus its inbreeding coefficient. For an animal that belongs to a highly inbred line where all loci are homozygous by descent, the inbreeding coefficient approaches one. In this extreme case, the diagonal element in the A-matrix will approach two, representing the theoretical limit.

238. (A) Infinite.
In the framework of Mixed Model Equations, fixed effects are treated differently than random effects. Specifically, they are evaluated under the assumption that their prior variance is infinite. This implies that there is no prior information about their values, and they are estimated solely from the observed data. This treatment ensures that the fixed effects are estimated as unbiased constants.

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herds. Without these linkages and accurate data, it is difficult to accurately compare sires and make effective selection decisions across the fragmented population.

204. (A) The matrix does not have an inverse due to linear dependencies.
In least squares analysis, a system of normal equations is considered singular if the coefficient matrix is not of full rank. This occurs when there are linear dependencies between the columns of the matrix, often due to over-parameterization or empty subclasses. A singular matrix cannot be inverted directly, requiring the use of a generalized inverse to find solutions.

205. (A) P-3, Q-4, R-1, S-2
Statistical techniques have specific applications in animal breeding and genetics. Ridge regression is used to handle multicollinearity, while principal component analysis reduces the dimensionality of morphometric traits. Discriminant function analysis is employed for classifying individuals into breeds, and least squares analysis is the standard method for estimating fixed effects in unbalanced datasets where subclass numbers are unequal in size.

206. (A) UPGMA.
UPGMA is a straightforward hierarchical clustering method for constructing phylogenetic trees. It builds the tree step-by-step by identifying and joining the most closely related pair of operational taxonomic units based on a distance matrix. After each join, the distances between the new cluster and the remaining units are recalculated, continuing until all units are included in a single rooted tree.

207. (A) Random effects with specific prior distributions.
In Bayesian genomic selection models, marker effects are not treated as constants but are modeled as random effects. These models assign specific prior distributions to the effects, which reflect different assumptions about the underlying genetic architecture of the trait. For example, Bayes B uses a mixture distribution to capture the idea that only a small proportion of markers have effects.

208. (A) Both A and R are true and R is the correct explanation of A.
BLAST is a heuristic algorithm, meaning that it employs practical shortcuts to find sequence alignments quickly. While it is highly efficient, it does not guarantee finding the mathematically optimal alignment between sequences. This design choice is intentional, as it allows for extremely rapid searches against massive biological databases, which would be computationally impossible using exact alignment methods for search.

209. (A) The reaction norms of different genotypes cross or have different slopes.
Genotype-environment interaction is a phenomenon where different genotypes respond uniquely to varying environmental conditions. It is visually demonstrated when the reaction norms—plots of phenotype against environment—for different genotypes have different slopes or cross each other. This indicates that a single genotype is not superior in all environments, necessitating selection strategies tailored to specific production settings or regions.

210. (A) It provides unbiased estimates of variance components for general mixed models with unbalanced data.
Henderson's Method 3 is superior to Methods 1 and 2 because it is designed to handle general mixed models in unbalanced datasets. By using the expectations of reductions in sums of squares from fitting various models, it provides unbiased estimates of variance components. This flexibility makes it particularly suitable for the complex data structures commonly encountered in animal breeding research today.

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211. (A) An average of the observed and expected information matrices.
The Average Information matrix is a key component of the AI-REML algorithm used for estimating variance components. It is calculated as an average of the observed and expected information matrices. This approach simplifies the computation of second derivatives in the REML log-likelihood, leading to a faster and more stable numerical procedure for finding maximum likelihood estimates in genetics.

weights are mathematically derived to maximize the correlation between the index itself and the individual's true net genetic merit, also known as the aggregate genotype. This maximization ensures that selection based on the index is accurate.

249. (A) Remove biases caused by different management and environmental conditions.
In a progeny testing program, contemporary groups are formed by grouping together animals that were raised under similar environmental and management conditions. By comparing offspring within these groups, breeders can effectively adjust for systematic environmental biases. This ensures that the observed differences in performance more accurately reflect the genetic merit of the sires being evaluated rather than local factors.

250. (A) P-1, Q-2, R-4, S-3
Multiple linear regression concepts are addressed through various statistical methods. Multicollinearity is handled by ridge regression, while variable selection is performed using stepwise procedures. Heteroscedasticity, where residual variance is not constant, is addressed through weighted least squares. Overfitting is assessed and mitigated by using cross-validation techniques to evaluate the predictive performance of the model on independent datasets.

251. (A) LASSO Regression.
LASSO regression is a statistical method that performs both variable selection and regularization to improve model accuracy and interpretability. It minimizes the sum of squared residuals while applying a penalty on the absolute values of the regression coefficients. This unique approach can shrink the coefficients of less important variables exactly to zero, effectively excluding them from the model and handling multicollinearity.

252. (A) Captures the most variance among all generated PCs.
Principal component analysis generates a series of orthogonal components, where the first principal component is specifically defined to capture the maximum amount of variation present in the original dataset. Consequently, PC1 will always have the highest eigenvalue among all the components produced. This makes it the most important axis for summarizing the primary patterns of variation in data.

253. (A) Wright's $F_{\{st\}}$.
Wright's fixation index is a robust measure of population differentiation that accounts for differences in sample sizes between groups. It quantifies the standardized variance in allele frequencies across populations relative to the total population. This metric is fundamental for assessing genetic structure, gene flow, and the impact of evolutionary forces such as drift and selection on population divergence.

254. (A) Both A and R are true and R is the correct explanation of A.
The maximum likelihood approach for phylogenetic reconstruction is statistically more robust than simpler methods like maximum parsimony. This is because it utilizes explicit probabilistic models of sequence evolution, which can accommodate different rates for various types of mutations, such as transitions and transversions. This flexibility allows for a more accurate estimation of branch lengths and tree topology.

255. (A) All SNPs share the exact same normal distribution of effects (equal variance).
The GBLUP model for genomic selection is based on the infinitesimal model assumption. It assumes that the trait of interest is influenced by a very large number of loci across the genome, each with a small effect. Specifically, it assumes that all SNP marker effects are drawn from the same normal distribution with a constant variance, resulting in equal markers.

256. (A) Needleman-Wunsch algorithm.
The Needleman-Wunsch algorithm is a fundamental bioinformatic tool for sequence comparison. It employs a dynamic programming approach to find the optimal global alignment between two sequences by considering their entire length. The algorithm maximizes a similarity score based on matches, mismatches, and gaps, providing a comprehensive view of the evolutionary and structural relationships between the sequences being compared.

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257. (A) It requires incredibly large datasets with specific complex pedigree structures (e.g., many full-sibs, clones).
Estimating epistatic variance is a major challenge in quantitative genetics because its effects are complex and often small. Accurately partitioning this variance requires extremely large datasets with specialized pedigree structures, such as numerous full-sibling families or clones. Without these specific ties, it is difficult to distinguish epistatic interactions from other genetic or environmental components of variance in managed populations.

258. (C) Henderson's Method 3 uses EMS completely divorced from linear models.
Expected mean squares are a fundamental part of the analysis of variance, providing the theoretical expectations for the observed mean squares. These expectations are used to solve for variance components. Henderson's Method 3 is deeply rooted in linear model theory, as it utilizes the reductions in sums of squares from fitting specific models to derive expectations for accurate variance estimation.

259. (A) The penalty term accounts for the degrees of freedom used in estimating the fixed effects.
The log-likelihood function used in Restricted Maximum Likelihood includes a specific term that differentiates it from standard Maximum Likelihood. This term acts as a penalty for the degrees of freedom consumed by the estimation of the fixed effects in the model. By including this term, REML provides unbiased estimates of variance components, which is particularly critical in smaller datasets.

260. (B) I and III
Minimum Variance Quadratic Unbiased Estimation is a method for estimating variance components that requires the specification of initial prior values. It is a non-iterative approach that provides quadratic estimators for the genetic and environmental variances. Unlike REML or ML, MIVQUE does not update the prior values during the calculation, and its results depend on the appropriateness of priors.

261. (A) Normal distribution.
When using a Gibbs sampler for Bayesian analysis of a mixed model, the parameters are updated by sampling from their conditional posterior distributions. For the fixed effects, given the data and the current values of the variance components, the conditional distribution is typically a normal distribution. This allows for straightforward and efficient sampling within the Markov Chain Monte Carlo framework used.

262. (A) 1.0.
Henderson's rules for constructing the inverse of the additive genetic relationship matrix directly from a pedigree are highly efficient. If an animal's parents are both unknown and assumed to be unrelated, its corresponding diagonal element in the inverse relationship matrix receives an addition of exactly one. These rules allow for the direct and rapid construction of the matrix without full inversion.

263. (A) Is purely dependent on the phenotypic mean of those few records (un-shrunk).
In the Mixed Model Equations, fixed effects are treated differently than random effects. Unlike random effects, which are shrunk toward the population mean based on their reliability, fixed effects are estimated as constants. Therefore, if a contemporary group has very few records, its solution is determined entirely by the average performance of those few records, without any shrinkage applied.

264. (B) 0.25
The sire model is used to estimate the genetic merit of sires based on the performance of their offspring. In this model, the correlation between the true breeding values of half-sib progeny from the same sire is 0.25. This value reflects the fact that, on average, half-siblings share one-quarter of their alleles through their common paternal parent in the model.

265. (A) Pre- and post-multiplying the genetic covariance matrix of random regression coefficients by the vector of basis functions for that day.
In random regression models, the genetic variance for a trait is not constant but evolves over time. To find the variance at a specific time point, such as a particular day in milk, the genetic covariance matrix of the regression coefficients is pre- and post-multiplied by the vector of basis functions evaluated for that specific day. This provides a dynamic estimate.

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266. (A) Both A and R are true and R is the correct explanation of A.
Tabular methods for calculating inbreeding coefficients are much better suited for computerization than path coefficient methods. This is because they process the pedigree recursively and chronologically, calculating relationships based on already established values. This algorithmic approach avoids the need to trace complex paths through a pedigree, making it highly efficient for analyzing very large populations in breeding.

267. (A) The variance of family size across different age groups.
Overlapping generations complicate the estimation of effective population size because individuals from various age cohorts contribute to the next generation simultaneously. This structure often increases the variance in the number of offspring produced by different parents over their lifetimes. Accounting for this variance is essential for accurately calculating the rate of genetic diversity loss and inbreeding in breeding groups.

268. (C) 0.4
Heritability can be estimated using the regression coefficient of offspring performance on a single parent's performance. Since a parent and its offspring share exactly half of their genes, the covariance between them is half of the additive genetic variance. Therefore, the regression coefficient represents one-half of the narrow-sense heritability. Doubling a regression coefficient of 0.2 yields an estimate of 0.4.

269. (A) Sex-limited traits with repeated records (e.g., lactation yield).
Most Probable Producing Ability is a metric specifically designed for traits that are recorded multiple times on the same individual throughout its life. It is most commonly applied to sex-limited traits like milk yield in dairy cattle. By combining all available records, the MPPA provides a more reliable estimate of an animal's consistent genetic and permanent environmental potential.

270. (B) IV → I → II → III
A traditional multi-trait analysis follows a logical sequence. It begins with checking the data for errors, outliers, and fixed effects. Next, variance and covariance components are estimated using methods like AI-REML. Once the parameters are established, the multi-trait mixed model equations are constructed. Finally, these equations are solved to obtain the breeding values for all animals and traits.

271. (A) Estimated breeding value and true breeding value.
In quantitative genetics and the Breeder's Equation, the accuracy of selection is a measure of the precision of genetic evaluation. It is mathematically defined as the correlation between the estimated breeding value and the true breeding value of an individual. A higher accuracy indicates that the selection decisions are more likely to result in the desired genetic improvement in populations.

NODIA

272. (A) Maximized.
The classical selection index is developed using the principles of linear regression to combine information from multiple traits into a single value. When correctly formulated, this index is mathematically proven to provide the highest possible correlation between the index and the true genetic merit. Consequently, selection based on this index will maximize the expected genetic response in candidates.

273. (A) Predicted Transmitting Ability (PTA) or Estimated Breeding Value (EBV).
After completing a progeny test, the primary metric used to rank and select sires is their predicted genetic merit. This is expressed either as the Predicted Transmitting Ability, which represents half of the breeding value, or the full Estimated Breeding Value. These values indicate the genetic superiority a sire is expected to pass on to its offspring for various traits.

274. (A) Cannot estimate the separate effects of Breed and Herd without constraints.
Complete confounding occurs in a statistical model when the levels of two different factors are perfectly aligned, such as when all animals of one breed are located in a single herd. In this situation, the model cannot distinguish between the effects of the breed and the effects of the herd. To solve equations, constraints or additional information are required to separate influences.

275. (A) P-1, Q-4, R-2, S-3
Multivariate statistics involves several key concepts. An eigenvalue represents the variance captured by a principal component. Cross-validation is a technique for assessing a model's predictive performance. A centroid is the mean vector of a group in discriminant analysis, and a dendrogram is the standard tree-like diagram used to visualize the results of hierarchical clustering methods in genetics.

276. (A) Reynolds' distance assumes divergence is solely due to mutation, ignoring drift entirely.
Genetic distance measures are used to quantify the divergence between populations, and different metrics make different assumptions. Reynolds' distance is specifically designed for short-term divergence and assumes that genetic drift is the primary force, while mutation is ignored. In contrast, Nei's standard distance assumes that both mutation and drift contribute to the observed genetic differences over populations.

277. (A) Frequencies of shared alleles at genotyped SNP loci.
The genomic relationship matrix is a tool used in modern genetic evaluation to measure the similarity between individuals. It is constructed using information from a large number of DNA markers, typically single nucleotide polymorphisms. By comparing the shared allele frequencies at these loci, the matrix provides a precise estimate of the actual genetic relationship between animals, accounting for inheritance.

278. (A) The match is highly significant and unlikely to occur by chance.
In BLAST results, the E-value, or Expectation value, is a measure of the statistical significance of a sequence alignment. It represents the number of matches with a similar score that one can expect to find by chance when searching a database of a particular size. A very low E-value indicates that the alignment is highly significant and reflects relationships.

279. (A) Non-additive genetic variance (dominance and epistasis).
Broad-sense herizability includes all genetic components of variance, while narrow-sense herizability only includes the additive genetic variance. When the broad-sense value is larger than the narrow-sense value, the difference is attributed to non-additive genetic effects. These include dominance, which is the interaction between alleles at the same locus, and epistasis, which is the interaction between alleles at different loci.

280. (A) I and II
Henderson's Method 1 is a procedure for estimating variance components that uses analogues of sums of squares from balanced ANOVA. It is a simple and non-iterative method. However, its primary drawback is that it yields biased estimates if applied to models containing fixed effects other than the population mean. This limitation makes it unsuitable for most complex animal breeding data.

281. (A) Second derivative (Hessian matrix).
The Newton-Raphson algorithm is a widely used numerical method for finding the maximum of a likelihood function. It is a second-order optimization procedure that utilizes information from both the first derivative, which is the gradient, and the second derivative, which is the Hessian matrix. By incorporating information about the curvature of the likelihood surface, it can achieve rapid convergence.

282. (A) The choice of prior values.
Minimum Norm Quadratic Unbiased Estimation is a method for estimating variance components that provides unbiased estimators. One of its key statistical properties is that the resulting estimates are independent of the initial prior values supplied for the variance components. This distinguishes it from other methods like MIVQUE, where the optimality of the estimators is conditional on the accuracy of priors used.

283. (A) Decreases as the number of iterations increases.
In Bayesian estimation using Markov Chain Monte Carlo methods, the precision of the parameter estimates is reflected in the Monte Carlo standard error. As the number of iterations in the chain increases, the sample size grows, leading to a more accurate representation of the posterior distribution. Consequently, the Monte Carlo standard error decreases, providing greater confidence in the estimated parameters.

284. (A) Both A and R are true and R is the correct explanation of A.
Henderson's tabular method is a flexible approach for constructing the additive genetic

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relationship matrix. It easily incorporates the effects of inbreeding by using a recursive formula for the diagonal elements. The diagonal for an individual is calculated as one plus half of the relationship between its parents, which directly accounts for the increased genetic similarity from mating related individuals.

285. (A) Decreases.
The Mendelian sampling term represents the random sampling of alleles that occurs during the formation of gametes. In the context of an animal model, the variance of this term is a measure of the genetic variation within a family. For an individual that is highly inbred, this variance decreases, reflecting the overall reduction in genetic diversity and increased homozygosity.

286. (A) Multiple records for at least some animals.
The repeatability model is specifically designed for the analysis of traits that can be measured more than once on the same individual, such as milk yield or litter size. To apply this model and accurately estimate both genetic and permanent environmental effects, the dataset must include multiple records for at least some of the animals in the population being studied.

287. (A) Fluctuate more flexibly across time.
Random regression models describe genetic and environmental trajectories using basis functions, such as Legendre polynomials. The order of the polynomial determines the flexibility of the fitted curve. Using a higher-order polynomial allows the model to capture more complex patterns and fluctuations in genetic variance across time, providing a more detailed and accurate representation of the trait.

288. (B) 0.25
The genetic relationship between two individuals can be calculated using the path coefficient method. In a population that is not inbred, the coefficient of relationship between an uncle and his nephew is 0.25. This reflects the fact that they share, on average, one-fourth of their alleles through their common ancestors, which are the grandparents of the nephew.

289. (A) $\frac{1}{2N_e}$
In a finite population that is randomly mating, the average heterozygosity tends to decrease over time due to genetic drift. The rate at which this diversity is lost is inversely proportional to the effective population size. Specifically, the reduction in heterozygosity per generation is equal to one divided by twice the effective population size, highlighting the importance of population size.

290. (A) P-2, Q-1, R-4, S-3
Heritability can be estimated using several different methods, each relying on a specific statistical measure. Paternal half-sib analysis uses intra-class correlation, while parent-offspring regression uses the regression coefficient. Comparison of identical twins provides an upper bound for broad-sense heritability, and the response to selection in a breeding program is used to calculate the realized heritability in practice.

291. (A) Genetic and permanent environmental differences between individuals.
Repeatability is an essential parameter for making culling decisions in livestock breeding. It represents the proportion of total phenotypic variation that is consistent across an animal's lifetime. This consistency is due to the combined effects of the individual's genotype and its permanent environment. A high repeatability indicates that past performance is a reliable predictor of future performance, justifying early culling decisions.

292. (A) Intense selection for milk yield will indirectly reduce fertility.
A negative genetic correlation between two traits indicates that many of the genes that improve one trait have an unfavorable effect on the other. In dairy cattle, there is often a negative genetic correlation between milk yield and fertility. This means that focusing solely on increasing milk production through intense selection will lead to an undesirable correlated decline in reproduction.

NODIA

293. (A) Selection intensity.
According to the Breeder's Equation, genetic gain can be increased by applying more pressure on selection. However, increasing selection intensity often requires choosing a very small proportion of candidates. In small populations, this can lead to a reduction in the number of parents, which may inadvertently decrease the accuracy of selection by increasing the influence of random environmental factors.

3. Hypertension
4. Obesity

(A) P-4, Q-1, R-3, S-2
(B) P-3, Q-2, R-1, S-4
(C) P-4, Q-3, R-1, S-2
(D) P-1, Q-4, R-2, S-3

2016

81. The Draize test, traditionally performed on rabbits, assesses:
(A) Acute dermal and ocular irritation
(B) Long-term carcinogenicity
(C) Reproductive toxicity
(D) Intravenous pyrogenicity

2003

82. Guinea pigs are uniquely susceptible to developing which condition due to their dietary requirements?
(A) Rickets
(B) Pellagra
(C) Beriberi
(D) Scorbutus (Scurvy)

2014

83. Which laboratory animal is commonly used in auditory research due to its large and accessible bullae and the presence of the Preyer (ear-flick) reflex?
(A) Mouse
(B) Rat
(C) Guinea pig
(D) Hamster

2008

84. Which laboratory animal species is exceptionally sensitive to histamine and is therefore heavily used in anaphylaxis research?
(A) Mouse
(B) Rat
(C) Guinea pig
(D) Rabbit

2015

85. Read the following statements regarding non-human primate research models.
I. They share high phylogenetic proximity to humans.
II. They are widely used in specialized neurobehavioral research.
III. They are the preferred first-line model for all acute toxicity tests.
IV. Their use is subjected to stringent ethical and regulatory review.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) I, II and III
(C) II, III and IV
(D) I and III

2011

86. Dogs, particularly Beagles, are predominantly utilized in which area of biomedical research?
(A) Monoclonal antibody production
(B) Regulatory safety pharmacology and toxicology
(C) Xenograft tumor propagation
(D) Forward genetic mutagenesis screens

2023

87. The Prevention of Cruelty to Animals (PCA) Act in India was enacted in which year?
(A) 1950
(B) 1960
(C) 1972
(D) 1986

2017

88. Under Indian regulations, CCSEA stands for the Committee for the Control and Supervision of Experiments on:
(A) Animals
(B) Apes
(C) Avians
(D) Agriculture

2021

89. According to CCSEA guidelines, every institution conducting animal research must establish an IAEC. What does IAEC stand for?
(A) International Animal Ethics Council
(B) Institutional Animal Experimentation Committee
(C) Institutional Animal Ethics Committee
(D) Indian Animal Ethics Commission

2016

90. Read the following statements regarding the required composition of an IAEC.
I. A biological scientist.
II. Two veterinarians.
III. A scientist from a different biological discipline.
IV. A main nominee of CCSEA.
V. A socially aware member.
Which of the above members represents an INCORRECT requirement for the committee?
(A) I, III and V
(B) II and III
(C) Only II
(D) IV and V

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CHAPTER 10
Laboratory Animal Breeding

2011

1. What is the normal diploid chromosome number of the laboratory mouse?
(A) 38
(B) 40
(C) 42
(D) 44

2010

2. Which laboratory species has a diploid chromosome number of 78?
(A) Rat
(B) Guinea pig
(C) Rhesus macaque
(D) Dog

2013

3. What is the diploid chromosome number of the laboratory rat?
(A) 40
(B) 42
(C) 44
(D) 64

2001

4. Identify the species that possesses 64 chromosomes in its normal karyotype.
(A) Rabbit
(B) Rhesus macaque
(C) Guinea pig
(D) Dog

2011

5. The H-2 major histocompatibility complex is characteristic of which laboratory animal?
(A) Mouse
(B) Rat
(C) Guinea pig
(D) Rabbit

2010

6. The major histocompatibility complex designated as RT1 is found in which species?
(A) Mouse
(B) Rhesus macaque
(C) Dog
(D) Rat

2006

7. Which locus is primarily responsible for the agouti coat color pattern in mice?
(A) A locus
(B) B locus
(C) C locus
(D) D locus

2011

8. A mutation at the C locus in laboratory mice typically results in which phenotype?
(A) Black coat
(B) Brown coat
(C) Albino coat
(D) Dilute coat

2011

9. What is the average normal body temperature range for a laboratory mouse?
(A) 35.0 to 36.0 degrees Celsius
(B) 36.5 to 38.0 degrees Celsius
(C) 38.5 to 39.5 degrees Celsius
(D) 39.5 to 40.5 degrees Celsius

2013

10. Read the following statements regarding laboratory rats.
I. They lack a gallbladder.
II. Their normal heart rate ranges from 330 to 480 beats per minute.
III. Their diploid chromosome number is 40.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I only

NODIA

2023

11. Which of the following best describes the estrous cycle of a laboratory mouse?
(A) Monoestrous with one cycle
(B) Polyestrous continuous
(C) Polyestrous seasonal cycles
(D) Induced ovulator response

III. Twenty consecutive generations achieve over 98 percent homozygosity.
IV. It often leads to inbreeding depression.
V. It is the primary method for maintaining outbred stocks.
Which of the above statement(s) is/are correct?
(A) I, II, III and V
(B) I, III and IV
(C) II, IV and V
(D) I, III, IV and V

2022

36. An inbred strain of mice is officially defined as a colony produced by a minimum of how many consecutive generations of brother-sister mating?
(A) 10
(B) 15
(C) 20
(D) 25

2001

37. The calculation of the inbreeding coefficient over successive generations estimates the:
(A) Probability that two alleles at a locus are identical by descent
(B) Rate of spontaneous mutations
(C) Number of remaining heterozygous loci
(D) Reproductive fitness of the offspring

2021

38. A decline in reproductive performance and general vigor resulting from continuous inbreeding is known as:
(A) Genetic drift
(B) Heterosis
(C) Segregation distortion
(D) Inbreeding depression

2009

39. Which rotational mating system is widely used to maintain outbred laboratory animal stocks while minimizing the rate of inbreeding?
(A) Brother-sister mating
(B) Poiley's rotational mating
(C) Backcrossing
(D) Outcrossing

2018

40. Match the mating systems in List I with their objectives in List II.
List I: (Mating System)
P. Monogamous
Q. Harem
R. Brother-Sister
S. Poiley's system
List II: (Objective)
1. Maximize homozygosity
2. Minimize inbreeding rate
3. One male to one female
4. Maximize offspring per male
(A) P-3, Q-4, R-1, S-2
(B) P-4, Q-3, R-2, S-1
(C) P-1, Q-2, R-3, S-4
(D) P-3, Q-1, R-4, S-2

2006

41. In standardized nomenclature, what symbol is used to denote the generation of an inbred strain?
(A) P
(B) N
(C) G
(D) F

2001

42. In standardized nomenclature, the symbol "N" is used to represent the number of generations in which type of breeding?
(A) Congenic backcrossing
(B) Brother-sister mating generations
(C) Rotational outbreeding schemes
(D) Recombinant inbred line crossing

2016

43. A substrain of an inbred mouse line is typically indicated in nomenclature by adding:
(A) Hyphen (-) and a mutant gene symbol
(B) Slash (/) and institutional code
(C) Period (.) and specific allele symbol
(D) Asterisk () and established cross number

2001

44. What does the notation C57BL/6J indicate?
(A) Outbred stock developed at Jackson Laboratory
(B) Inbred strain C57BL/6 from Jackson Lab
(C) Congenic strain with six backcross generations
(D) Recombinant inbred line between C57 and BL

2005

45. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Outbred stocks are deliberately managed to maintain high genetic variability.
Reason (R): Continuous brother-sister mating is strictly avoided in outbred colony management.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the

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(B) 30 to 45 percent
(C) 45 to 65 percent
(D) 70 to 85 percent

2001

24. Standard light-dark photoperiods for maintaining breeding colonies of rodents are typically set to:
(A) 8 hours light, 16 hours dark
(B) 10 hours light, 14 hours dark
(C) 12 hours light, 12 hours dark
(D) 24 hours continuous light

2013

25. Read the following statements regarding animal holding room parameters.
I. Relative humidity should be strictly maintained above 80 percent.
II. Temperature for mice is optimally 20 to 24 degrees Celsius.
III. Minimum air changes per hour should be 10 to 15.
IV. Lighting intensity at cage level must always exceed 1000 lux.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) II and III
(C) I, III and IV
(D) II, III and IV

2002

26. Ringtail in laboratory rats is primarily associated with which environmental condition?
(A) Low relative humidity
(B) High temperature
(C) High light intensity
(D) Inadequate ventilation

2011

27. Which of the following is considered a temporary method of animal identification?
(A) Ear punching
(B) Coat marking with non-toxic dye
(C) Tattooing
(D) Microchipping

2022

28. Which permanent identification method uses a transponder implanted subcutaneously?
(A) Ear notching
(B) Microchipping
(C) Toe clipping
(D) Tattooing

2002

29. Toe-clipping as a method of identification in neonatal rodents is generally restricted to animals of what maximum age?
(A) 7 days
(B) 14 days
(C) 21 days
(D) 28 days

2015

30. A mating system consisting of one male and two or more females housed together continuously is known as:
(A) Monogamous pair mating
(B) Rotational outbreeding
(C) Harem breeding system
(D) Coisogenic line mating

2013

31. Which breeding configuration is most appropriate to maximize litter production per male?
(A) Monogamous pairing
(B) Brother-sister mating
(C) Cross-fostering
(D) Harem mating

NODIA

2022

32. Intensive breeding systems differ from non-intensive systems primarily by:
(A) Removing the male before parturition
(B) Eliminating the postpartum estrus mating opportunity
(C) Keeping the male continuously with females during parturition
(D) Increasing the weaning age of the pups

2022

33. The postpartum estrus in mice occurs approximately how long after parturition?
(A) 2 to 4 hours
(B) 14 to 28 hours
(C) 3 to 5 days
(D) 7 to 10 days

2002

34. What is the primary purpose of constructing a selection index in quantitative genetics?
(A) To select for a single Mendelian trait
(B) To increase the inbreeding coefficient
(C) To create specialized congenic strains
(D) To select for multiple quantitative traits

2003

35. Read the following statements regarding continuous brother-sister mating.
I. It is used to develop inbred strains.
II. It increases heterozygosity in the colony.

2013

12. The synchronization of estrus in a group of female mice upon the introduction of a male mouse is known as what effect?
(A) Bruce effect
(B) Whitten effect
(C) Lee-Boot effect
(D) Vandenbergh effect

2006

13. The termination of pregnancy in a recently mated female mouse upon exposure to an unfamiliar male is termed the:
(A) Bruce effect
(B) Lee-Boot effect
(C) Whitten effect
(D) Facultative diapause

2009

14. Which phenomenon describes the suppression or prolongation of estrous cycles in female mice housed in large groups without a male?
(A) Bruce effect
(B) Whitten effect
(C) Lee-Boot effect
(D) Vandenbergh effect

2002

15. Read the following statements regarding reproductive phenomena in rodents.
I. The Bruce effect involves pregnancy block.
II. The Whitten effect involves estrus synchronization.
III. Facultative diapause accelerates embryonic implantation.
Which of the above statement(s) is/are correct?
(A) I and III
(B) II and III
(C) I and II
(D) II only

2009

16. What is the average gestation period of a laboratory mouse?
(A) 15 to 17 days
(B) 19 to 21 days
(C) 24 to 26 days
(D) 30 to 32 days

2006

17. The typical weaning age for laboratory mice and rats is:
(A) 10 days
(B) 14 days
(C) 21 days
(D) 35 days

2005

18. Guinea pigs require a dietary source of which specific vitamin due to an enzyme deficiency?
(A) Vitamin A
(B) Vitamin B12
(C) Vitamin D
(D) Vitamin C

2014

19. The inability of guinea pigs to synthesize ascorbic acid is due to the lack of which enzyme?
(A) L-gulonolactone oxidase
(B) Glucose-6-phosphatase enzyme
(C) Ascorbate peroxidase activity
(D) Hexokinase glycolytic pathway

2007

20. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Autoclaved diets for laboratory animals often contain higher initial concentrations of thermolabile vitamins.
Reason (R): The autoclaving process destroys a significant portion of vitamins such as Vitamin C and Vitamin A.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2005

21. Which diet type is formulated using purified amino acids, specific sugars, and chemically pure vitamins and minerals?
(A) Chemically defined diet
(B) Pelleted natural ingredient diet
(C) Extruded diet
(D) Autoclaved non-purified diet

2024

22. What is the recommended minimum number of air changes per hour for a standard rodent animal holding room?
(A) 2 to 5
(B) 5 to 10
(C) 10 to 15
(D) 20 to 25

2004

23. The recommended relative humidity range for macro-environmental control in rodent holding rooms is:
(A) 20 to 30 percent

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correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2004

46. An outbred stock of rats maintained by Charles River Laboratories might correctly be designated as:
(A) SD/Crl
(B) SD-Crl
(C) Crl:SD
(D) Crl(SD)

2017

47. Strains that are genetically identical except for a difference at a single defined locus due to backcrossing are termed:
(A) Coisogenic strains
(B) Recombinant inbred strains
(C) Segregating inbred strains
(D) Congenic strains

2023

48. Coisogenic strains arise primarily as a result of:
(A) Repeated backcrossing of a mutant allele into a recipient strain
(B) Crossing two independent outbred stocks
(C) Spontaneous or induced mutation within an existing inbred strain
(D) Inbreeding of the F2 generation

2001

49. Recombinant inbred (RI) strains are derived by:
(A) Backcrossing an F1 generation to one of the parents
(B) Continuous brother-sister mating of individuals from the F2 generation of a cross between two inbred strains
(C) Inducing targeted mutations using CRISPR
(D) Maintaining segregation at a specific locus indefinitely

2002

50. Recombinant inbred strains are most valuable in which research application?
(A) Preserving hybrid vigor in stocks
(B) Producing yields of polyclonal antibodies
(C) Routine toxicity testing in animals
(D) Mapping quantitative trait loci

2019

51. Segregating inbred strains are maintained in such a way that they remain heterozygous at a specific locus. This is usually achieved by:
(A) Mating and selecting for heterozygotes
(B) Random mating within a large population
(C) Backcrossing solely to the mutant strain
(D) Isolating individuals from recombinant crosses

2008

52. Which microbiological category describes animals entirely free of all demonstrable microorganisms, including bacteria, viruses, fungi, and parasites?
(A) Gnotobiotic
(B) Specific Pathogen-Free (SPF)
(C) Axenic
(D) Conventional

2003

53. The term "axenic" literally translates to:
(A) Without strangers (germ-free)
(B) With defined flora
(C) Free of pathogens
(D) Clean conventional

2003

54. Gnotobiotic animals are defined as those which:
(A) Contain an unknown mixture of microflora
(B) Are completely devoid of all microbes
(C) Are housed in open-top cages
(D) Harbor only a known, completely defined microflora

2018

55. Animals designated as Specific Pathogen-Free (SPF) are guaranteed to be:
(A) Free of all microorganisms
(B) Free only of specified pathogenic microorganisms targeted by a testing program
(C) Completely resistant to all infectious agents
(D) Carrying a defined cocktail of commensal bacteria

2015

56. Conventional laboratory animals are characterized by:
(A) Rearing in sterile isolators
(B) Cesarean derivation and germ-free fostering
(C) Absence of a defined, restrictive microbial barrier
(D) Immediate elimination of all intestinal microflora

2021

57. Which technique involves monitoring the genetic purity of an inbred mouse strain by observing the acceptance or rejection of transplanted skin?
(A) Isoenzyme analysis
(B) Microsatellite genotyping
(C) SNP arrays

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(D) Skin grafting

2001

58. Immunological assays used in genetic monitoring typically test for variations in:
(A) Major histocompatibility complex
(B) Variations in coat color alleles
(C) Single nucleotide polymorphisms
(D) Ribosomal RNA sequence changes

2002

59. Biochemical genetic monitoring often utilizes variations in protein electrophoretic mobility. These variations are primarily due to:
(A) Transgenic insertions
(B) Isoenzymes
(C) Recombinant inbreeding
(D) Skin allografts

2016

60. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): PCR-based microsatellite genotyping is currently a preferred method for genetic monitoring of rodent colonies.
Reason (R): It requires live tissue grafting and waiting several weeks for rejection responses.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2023

61. Single Nucleotide Polymorphism (SNP) genotyping panels detect:
(A) Differences in enzyme net charge
(B) Single base-pair variations in genomic DNA
(C) Differences in total chromosome number
(D) Variable numbers of tandem repeats only

2010

62. The genetic alteration of an animal involving the introduction of foreign DNA into its genome produces a:
(A) Knock-out animal
(B) Coisogenic animal
(C) Congenic animal
(D) Transgenic animal

2015

63. A knock-out (KO) mouse is an animal in which:
(A) A foreign gene is randomly inserted and overexpressed
(B) A specific endogenous gene has been intentionally disrupted or deleted
(C) An exogenous promoter replaces a native enhancer
(D) Only coat color genes are mutated

2005

64. The targeted replacement of an endogenous gene sequence with a mutated or different sequence at the exact same locus creates a:
(A) Knock-out mouse
(B) Transgenic mouse
(C) Knock-in (KI) mouse
(D) Recombinant inbred mouse

2011

65. Read the following statements regarding the Cre-loxP system.
I. It is used to create inducible or tissue-specific knock-outs.
II. Cre is a recombinase enzyme derived from a bacteriophage.
III. loxP sites naturally occur in wild-type mammalian genomes.
Which of the above statement(s) is/are correct?
(A) I and III
(B) I and II
(C) II and III
(D) I only

2007

66. In the Cre-loxP recombination system, the enzyme Cre recognizes specific 34-base-pair DNA sequences known as:
(A) FRT sites
(B) Zinc finger domains
(C) CRISPR arrays
(D) loxP sites

2013

67. To achieve a tissue-specific gene knock-out using the Cre-loxP system, the Cre recombinase must be expressed under the control of a:
(A) Ubiquitous promoter
(B) Bacterial promoter
(C) Viral reverse transcriptase
(D) Tissue-specific promoter

2002

68. The ob/ob mouse model is widely used in metabolic research. What is its primary phenotype?
(A) Severe immunodeficiency
(B) Spontaneous hypertension
(C) Profound obesity and type 2 diabetes
(D) Progressive muscular dystrophy

NODIA

2016

69. The genetic defect in the ob/ob mouse involves a mutation in the gene encoding which hormone?
(A) Leptin
(B) Insulin
(C) Glucagon
(D) Adiponectin

2024

70. The db/db mouse model is phenotypically similar to the ob/ob mouse but possesses a mutation in the gene for the:
(A) Insulin receptor
(B) Glucocorticoid receptor
(C) Thyroid hormone receptor
(D) Leptin receptor

2005

71. The Zucker rat (fa/fa) is a widely recognized animal model used primarily to study:
(A) Organ transplantation
(B) Tuberculosis
(C) Rheumatoid arthritis
(D) Obesity and metabolic syndrome

2013

72. The Spontaneously Hypertensive Rat (SHR) is predominantly used as a model for which type of disease?
(A) Cardiovascular disease
(B) Autoimmune disease
(C) Infectious disease
(D) Neurodegenerative disease

2016

73. The Athymic Nude mouse lacks a functional thymus, resulting primarily in a deficiency of which cell type?
(A) B lymphocytes
(B) Macrophages
(C) T lymphocytes
(D) Natural killer cells

2016

74. Due to its specific immune deficiency, the Athymic Nude mouse is highly valuable for:
(A) Producing monoclonal antibodies
(B) Studying autoimmune lupus
(C) Toxicity testing of cosmetics
(D) Serving as hosts for human tumor xenografts

2019

75. Read the following statements regarding SCID mice.
I. They lack functional T lymphocytes.
II. They lack functional B lymphocytes.
III. They possess a normal functioning thymus.
IV. The mutation primarily impairs V(D)J recombination.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) I, III and IV
(C) II, III and IV
(D) I and II

2012

76. The NOD-scid gamma (NSG) mouse is an extremely immunodeficient model because it lacks T and B cells and also has defective:
(A) Erythrocytes
(B) Platelets
(C) Eosinophils
(D) Natural killer (NK) cells

2008

77. The NIH-III mouse, an immunodeficient model, combines mutations that result in deficiencies in T cells, B cells, and:
(A) NK cells
(B) Neutrophils
(C) Mast cells
(D) Macrophages

2024

78. Polyclonal antibody production in laboratory settings is most commonly performed using which species due to its size and accessible marginal ear veins?
(A) Mouse
(B) Hamster
(C) Rabbit
(D) Guinea pig

2013

79. The classic rabbit pyrogen test evaluates the presence of pyrogenic substances by monitoring the rabbit's:
(A) Body temperature
(B) Heart rate
(C) Respiratory rate
(D) Blood pressure

2007

80. Match the animal models in List I with their primary research areas in List II.
List I: (Animal Model)
P. ob/ob mouse
Q. Nude mouse
R. SHR
S. Guinea pig
List II: (Research Area)
1. Xenograft tumors
2. Tuberculosis

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294. (A) Phenotypic matrix (P).
The derivation of weights for a classical Smith-Hazel selection index involves a system of linear equations. To solve these equations and find the optimal weights, the phenotypic variance-covariance matrix of the traits included in the index must be inverted. This matrix, often denoted as P, represents the observed variation and associations between the phenotypic traits in the population.

295. (A) Individual herds are large enough to serve as complete contemporary groups.
Progeny testing in smallholder systems is challenging because individual herds are typically very small. A single herd often does not have enough animals of the same age and management to form an effective contemporary group. This makes it difficult to adjust for environmental biases locally, necessitating the use of genetic ties to compare animals across multiple smallholder farms.

296. (A) Test the main effects after adjusting for all other effects in the model.
When analyzing unbalanced data using least squares analysis, Type III sums of squares are standard. They provide a way to test the significance of each main effect in the model after adjusting for all other factors, including other main effects and interactions. This approach ensures that the significance of each factor is evaluated independently of the entry order.

297. (A) Severe multicollinearity.
The variance inflation factor is a diagnostic statistic used to identify multicollinearity in multiple linear regression models. A VIF value greater than 10 is a common threshold indicating that a predictor variable is highly correlated with others. This severe multicollinearity makes the regression coefficients unstable and the standard errors large, which can lead to incorrect conclusions about significance.

298. (A) Both A and R are true and R is the correct explanation of A.
In discriminant function analysis, prior probabilities reflect the initial expectations about the group membership of an observation before any measurements are taken. These probabilities can significantly shift the classification boundary between groups. By incorporating prior knowledge about the proportion of individuals in each category, the analysis can improve the overall accuracy of classification in real-world populations studied.

NODIA

299. (A) The total branch length of the tree.
The neighbor-joining method is a clustering algorithm used to reconstruct phylogenetic trees from genetic distance data. Its primary objective is to iteratively pair taxa in a way that minimizes the total branch length of the resulting tree. This criterion is related to the principle of parsimony and helps to produce a tree that efficiently summarizes evolutionary relationships.

300. (A) A large proportion of SNPs (π) have zero effect, and the rest have effects drawn from a t-distribution.
Bayes B is a hierarchical Bayesian model for genomic selection that incorporates a specific prior for SNP marker effects. It assumes a mixture distribution where a large proportion of markers, defined by the parameter π, are assumed to have no effect on the trait. The remaining markers have effects drawn from a Student's t-distribution, allowing for large-effect loci.

****

2009

91. The "3Rs" principle of humane experimental technique was first articulated by:
(A) Watson and Crick
(B) Russell and Burch
(C) Pasteur and Koch
(D) Mendel and Darwin

2016

92. In the context of the 3Rs, replacing higher animal species with lower animal models, cell cultures, or computer models is known as:
(A) Reduction
(B) Refinement
(C) Replacement
(D) Reproduction

2014

93. Using statistical methods to ensure experiments are designed with the minimum number of animals necessary to achieve valid results aligns with which "R"?
(A) Refinement
(B) Reduction
(C) Replacement
(D) Reproducibility

2019

94. Implementing analgesia to minimize pain and improving housing conditions to enhance animal welfare are examples of:
(A) Refinement
(B) Reduction
(C) Replacement
(D) Rehabilitation

2012

95. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Humane endpoints are established to determine when an animal should be euthanized before the end of an experiment.
Reason (R): Humane endpoints prevent unnecessary pain and distress once the scientific objective is reached or cannot be reached.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2024

96. Which method of euthanasia is commonly conditionally acceptable and widely used for rodents, provided the flow rate gently displaces chamber air?
(A) Cervical dislocation without anesthesia
(B) Decapitation without specialized equipment
(C) Carbon dioxide asphyxiation
(D) Intra-cardiac potassium chloride in conscious animals

2019

97. An approved pharmacological method of euthanasia for small laboratory animals often involves an overdose of:
(A) Barbiturates
(B) Penicillin
(C) Saline
(D) Vitamin K

2025

98. Assessing animal welfare daily in a research facility primarily relies on observing:
(A) Karyotype stability
(B) Feed and water consumption and behavioral signs of distress
(C) Genotypic variation
(D) Recombination frequencies

2009

99. The life expectancy of a typical laboratory mouse is approximately:
(A) 6 to 12 months
(B) 1.5 to 2.5 years
(C) 3 to 4 years
(D) 5 to 6 years

2009

100. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Guinea pigs are born fully furred with open eyes.
Reason (R): They have a relatively long gestation period of 59 to 72 days resulting in precocial young.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2013

101. The offspring of mice and rats are altricial, meaning they are born:
(A) Fully developed and independent offspring
(B) Hairless, blind, and dependent
(C) Functional vision without presence of hair

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2004

125. Read the following statements regarding congenic strains.

I. They differ from the background strain at a single locus or small chromosomal region.
II. They require repeated backcrossing to the recipient strain.
III. They are used to study the effect of a specific gene on a standardized genetic background.
IV. They are produced by random mutation without breeding.

Which of the above statement(s) is/are correct?

(A) I, II and IV
(B) I, II and III
(C) II, III and IV
(D) I and III

2008

126. Recombinant inbred strains derived from a cross between C57BL/6J and DBA/2J are commonly designated by the prefix:

(A) C57D
(B) BXD
(C) B6D2F1
(D) D2B6

2005

127. Which class of laboratory animal requires housing within positive-pressure sterile isolators and strictly sterilized feed, water, and bedding?

(A) Conventional
(B) Specific Pathogen-Free
(C) Axenic
(D) Open-colony

2005

128. If an axenic animal is intentionally inoculated with a known cocktail of Lactobacillus and Bifidobacterium, its microbiological status changes to:

(A) Conventional
(B) SPF
(C) Gnotobiotic
(D) Outbred

2025

129. Barrier facilities are primarily designed to maintain the status of which type of animal colonies?

(A) Axenic only
(B) Conventional
(C) Specific Pathogen-Free (SPF)
(D) Wild-caught

2023

130. Genetic drift in an isolated inbred colony is primarily driven by:

(A) Directed artificial selection
(B) High rates of intentional crossbreeding
(C) Accumulation of spontaneous random mutations over time
(D) Continuous nutritional changes

NODIA

2016

131. In genetic monitoring, orthotopic skin grafting between mice of the same well-established inbred strain should theoretically result in:

(A) Acute rejection within 10 days
(B) Chronic rejection within 30 days
(C) Permanent acceptance of the graft
(D) An immediate anaphylactic response

2017

132. The polymerase chain reaction (PCR) is utilized in genetic monitoring primarily to:

(A) Determine the total protein content of serum
(B) Amplify and analyze specific DNA markers like microsatellites or SNPs
(C) Measure the activity of metabolic enzymes
(D) Quantify circulating antibody titers

2011

133. Transgenic animals are fundamentally distinct from conventional animals because they:

(A) Carry integrated foreign germline DNA
(B) Have been selectively bred for many generations
(C) Are completely free of specific pathogens
(D) Lack a functioning vertebrate immune system

2021

134. Which technique is most traditionally used to introduce foreign DNA into a mouse embryo to create a transgenic founder?

(A) Electroporation of adult somatic cells
(B) Pronuclear microinjection of oocytes
(C) Viral infection of the placental tissue
(D) Chemical mutagenesis of mature sperm

2012

135. Read the following statements regarding knock-out mice.

I. They require embryonic stem (ES) cell technology or CRISPR/Cas9.
II. They lack the function of a specific targeted gene.
III. They always exhibit early embryonic lethality.
IV. They are a type of genetically modified

(C) 500
(D) 1000

2006

114. Proper preparation of a pedigree chart for an inbred colony requires accurate recording of:
(A) Feed consumption rates
(B) Lineage, generational numbers, and matings
(C) Room temperature fluctuations
(D) Vendor transport schedules

2006

115. Read the following statements regarding polygamous breeding.
I. It involves one male and multiple females.
II. It requires less cage space per female than monogamous pairing.
III. It facilitates easy determination of exact parentage for every pup.
Which of the above statement(s) is/are correct?
(A) I and II
(B) I and III
(C) II and III
(D) I only

2014

116. Under intensive breeding systems for rodents, parturition typically occurs:
(A) While the female is housed singly
(B) In the continuous presence of the male
(C) Only after artificial insemination
(D) During the dark phase exclusively

2021

117. Quantitative traits in laboratory animals, such as body weight and litter size, are generally characterized by:
(A) Being determined by a single gene
(B) Continuous variation and polygenic inheritance
(C) Absolute insensitivity to environmental factors
(D) Showing strict Mendelian ratios

2018

118. In genetic response estimation, the "response to selection" (R) is mathematically defined as the product of heritability and:
(A) Inbreeding coefficient level
(B) Spontaneous mutation rate
(C) Genetic drift variance
(D) Selection differential

2008

119. After 20 generations of consecutive brother-sister mating, what is the theoretical expected percentage of homozygosity?
(A) 50.0%
(B) 87.5%
(C) 98.6%
(D) 100.0%

2025

120. Which consequence is frequently observed during the early generations of creating a new inbred strain?
(A) Heterosis
(B) Increase in average litter size
(C) Inbreeding depression
(D) Emergence of wild-type phenotypes

2001

121. To appropriately manage an outbred stock, the breeding scheme should ideally keep the coefficient of inbreeding from rising more than what percentage per generation?
(A) 1%
(B) 5%
(C) 10%
(D) 25%

2010

122. Under the international standardized nomenclature for mice, what symbol separates the strain name from the substrain designation?
(A) Hyphen (-)
(B) Asterisk ()
(C) Forward slash (/)
(D) Colon (:)

2015

123. The nomenclature BALB/cAnN implies:
(A) An outbred BALB mouse developed at NIH
(B) BALB strain, substrain c/An, from NIH
(C) A congenic mouse derived from BALB and N
(D) A knock-out mouse for the specific 'c' gene

2004

124. In the creation of a congenic strain, the donor allele is transferred to the genetic background of the recipient strain through a minimum of how many backcross generations?
(A) 2
(B) 4
(C) 10
(D) 20

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(C) Instantaneous measurement of blood pressure
(D) Complete suppression of all retroviruses

2006

194. In the nomenclature of a genetically modified animal, the designation "Tg" indicates that the animal is:
(A) Targeted mutated (knock-out)
(B) Toxicologically tested
(C) Thymectomized
(D) Transgenic

2015

195. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Inducible gene-targeting systems like Cre-loxP allow researchers to study genes whose systemic knock-out would normally be embryonically lethal.
Reason (R): These systems permit the target gene to be deleted only in specific adult tissues or at a specific chosen time.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2009

196. The "ob" mutation in the ob/ob mouse model is inherited in an autosomal recessive manner. Heterozygous carriers of the ob mutation are:
(A) Severely obese
(B) Phenotypically lean and healthy
(C) Diabetic but not obese
(D) Immunodeficient

2016

197. The Spontaneously Hypertensive Rat (SHR) was selectively bred from which ancestral outbred strain?
(A) Wistar Kyoto (WKY)
(B) Sprague Dawley (SD)
(C) Long-Evans (LE)
(D) F344 (Fischer)

2025

198. An investigator requires a rat model exhibiting both massive obesity and insulin resistance. Which of the following is most appropriate?
(A) Wistar Kyoto rat
(B) Zucker Diabetic Fatty (ZDF) rat
(C) Fischer 344 rat
(D) Sprague Dawley rat

2010

199. The lack of hair in the Athymic Nude mouse is genetically linked to the mutation causing:
(A) Thymic aplasia
(B) Splenic rupture
(C) Bone marrow failure
(D) Adrenal hypertrophy

2025

200. Because athymic nude mice lack functional T cells, they cannot mount which type of immune response?
(A) Innate immunity
(B) Complement activation
(C) Phagocytosis by macrophages
(D) Cell-mediated immunity

2002

201. Which mouse model lacks both T and B cells and is commonly utilized to study the biology of human tumors?
(A) SCID
(B) C57BL/6
(C) BALB/c
(D) ob/ob

2022

202. The NOD-scid gamma (NSG) mouse is an acronym where "NOD" stands for:
(A) Non-Obese Diabetic
(B) Normal Ovalbumin Domain
(C) Naturally Occurring Defect
(D) Neonatal Onset Disease

NODIA

2016

203. Which laboratory animal has been historically vital for the study of scurvy?
(A) Mouse
(B) Rat
(C) Rabbit
(D) Guinea pig

2010

204. Polyclonal antibodies are typically harvested from rabbits by collecting blood from the:
(A) Tail vein
(B) Marginal ear vein or central ear artery
(C) Retro-orbital sinus
(D) Femoral artery

2008

205. Match the animals in List I with their specific tests or uses in List II.
List I: (Animal)
P. Rabbit

organism (GMO).
V. They possess massive chromosomal duplications.
Which of the above statement(s) is/are correct?
(A) I, II and IV
(B) II, III and V
(C) I, III and IV
(D) I, II and V

2001

136. The Cre recombinase enzyme is originally derived from which organism?
(A) Mus musculus
(B) Escherichia coli
(C) Bacteriophage P1
(D) Saccharomyces cerevisiae

2022

137. Which term describes mice genetically engineered to express Cre recombinase specifically when a certain drug (e.g., tamoxifen) is administered?
(A) Knock-in
(B) Inducible Cre model
(C) Nude mouse
(D) Congenic strain

2022

138. The ob/ob mouse develops severe obesity primarily due to:
(A) Hyperphagia resulting from leptin deficiency
(B) Extreme lack of physical mobility
(C) Overproduction of growth hormone
(D) A targeted ablation of brown adipose tissue

2011

139. Which rat model is analogous to the db/db mouse, exhibiting leptin receptor deficiency and marked obesity?
(A) Sprague Dawley
(B) Wistar
(C) Zucker (fa/fa)
(D) Long-Evans

2001

140. Which animal model would be most appropriate for testing a novel antihypertensive drug?
(A) ob/ob mouse
(B) Athymic nude mouse
(C) SCID mouse
(D) Spontaneously Hypertensive Rat (SHR)

2021

141. The genetic mutation causing the athymic nude phenotype in mice is located in which gene?
(A) Foxn1
(B) Rag1
(C) Prkdc
(D) Il2rg

2011

142. Severe Combined Immunodeficiency (SCID) in the classic SCID mouse model is caused by a spontaneous mutation in which gene?
(A) Foxn1
(B) Rag2
(C) Prkdc
(D) Leptin

2004

143. Which immunodeficient mouse model is preferred for optimal engraftment of human hematopoietic stem cells?
(A) Nude mouse
(B) SCID mouse
(C) NOD-scid gamma (NSG) mouse
(D) Wild-type C57BL/6 mouse

2017

144. Which characteristic makes the rabbit an excellent model for studying hypercholesterolemia and atherosclerosis?
(A) Their small size and short natural lifespan
(B) Their inability to absorb any dietary fats
(C) Lipid metabolism profile resembling humans
(D) Their lack of a functional gallbladder organ

2016

145. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): The guinea pig is considered a premier model for infectious tuberculosis research.
Reason (R): Guinea pigs are highly susceptible to human strains of Mycobacterium tuberculosis and develop lesions similar to human disease.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

NODIA

2022

146. In the classic Draize test utilizing rabbits, what substance or formulation is typically being evaluated?
(A) Experimental vaccines
(B) Cosmetics and topical chemicals
(C) Intravenous antibiotics
(D) Genetically modified foods

(D) Capable of consuming solid food immediately

2023

102. What is the typical hematocrit (packed cell volume) range for a healthy laboratory mouse?
(A) 20-30%
(B) 39-49%
(C) 55-65%
(D) 65-75%

2017

103. The normal respiratory rate of a laboratory mouse is approximately:
(A) 10-20 breaths per minute
(B) 40-60 breaths per minute
(C) 80-200 breaths per minute
(D) 300-400 breaths per minute

2016

104. Which laboratory species is notable for having a continuous period of estrus if NO mating occurs, categorized as an induced ovulator?
(A) Mouse
(B) Rat
(C) Rabbit
(D) Hamster

2025

105. Match the species in List I with their diploid chromosome numbers in List II.
List I: (Species)
P. Mouse
Q. Rat
R. Rabbit
S. Dog
List II: (Diploid Chromosome Number)
1. 40
2. 42
3. 44
4. 78
(A) P-1, Q-2, R-3, S-4
(B) P-2, Q-1, R-4, S-3
(C) P-3, Q-4, R-1, S-2
(D) P-1, Q-3, R-2, S-4

2015

106. The dilute locus (d) in mice controls coat color intensity by affecting:
(A) The synthesis of eumelanin pigment
(B) The total absence of skin melanocytes
(C) The conversion of phaeomelanin to eumelanin
(D) Pigment distribution in hair shafts

2011

107. Which major immunogenetic complex in mice is located on chromosome 17?
(A) RT1
(B) H-2
(C) SLA
(D) DLA

2007

108. A pelleted diet for non-breeding maintenance of adult mice typically contains approximately what percentage of crude protein?
(A) 5-8%
(B) 14-16%
(C) 24-28%
(D) 30-35%

2011

109. High fat diets, commonly formulated to contain up to 60% fat by calories, are primarily utilized in rodents for which type of research?
(A) Infectious disease modeling
(B) Oncogenesis
(C) Behavioral neuroscience
(D) Diet-induced obesity and metabolic syndrome

2017

110. Which environmental factor most directly influences the incidence of ringtail in suckling rats?
(A) High ammonia levels
(B) High temperature
(C) Low relative humidity (below 40%)
(D) Excessive lighting

2002

111. Micro-environment in laboratory animal science specifically refers to the conditions within the:
(A) Primary enclosure or cage
(B) Entire animal holding room
(C) Ventilation ducting
(D) Outdoor facility surroundings

2009

112. Macro-environment refers to the physical conditions:
(A) Inside a sterile isolator
(B) Within the animal holding room itself
(C) Immediately inside the animal's cage
(D) At the institutional perimeter

2022

113. An ear punching code involves placing notches or holes in the pinna. A common standardized system limits the maximum number of uniquely identifiable animals per cage/group to:
(A) 15
(B) 99

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2010

157. The life expectancy of a healthy beagle dog in a laboratory setting can be up to:
(A) 3 years
(B) 5 years
(C) 12 to 15 years
(D) 25 years

2017

158. The gestation period of a beagle dog is approximately:
(A) 21 days
(B) 31 days
(C) 63 days
(D) 114 days

2024

159. Which laboratory animal has the longest gestation period among the following?
(A) Mouse
(B) Rat
(C) Rabbit
(D) Guinea pig

2023

160. What is the gestation period of a rabbit?
(A) 19-21 days
(B) 30-32 days
(C) 59-72 days
(D) 110-115 days

2015

161. A typical litter size for a mature female laboratory rat is:
(A) 1-3
(B) 8-12
(C) 18-22
(D) 25-30

2023

162. The estrous cycle length in both mice and rats is typically:
(A) 24 hours
(B) 4-5 days
(C) 14-16 days
(D) 21 days

2024

163. The condition of "facultative diapause" in mice refers to the:
(A) Delayed implantation during lactation
(B) Synchronization of estrous cycles in groups
(C) Premature termination of established pregnancy
(D) Failure to ovulate during the estrous phase

2001

164. What macro-nutrient usually constitutes the highest percentage in a standard pelleted rodent diet?
(A) Crude fat content
(B) Crude protein levels
(C) Carbohydrates
(D) Crude fiber content

2018

165. Why must pelleted diets be strictly managed regarding shelf-life?
(A) The pellets physically disintegrate within a week
(B) To prevent degradation of essential thermolabile vitamins
(C) Because fat content increases over time
(D) To avoid spontaneous combustion

NODIA

2024

166. A lux level of 325 at 1 meter above the floor is generally recommended for rodent rooms primarily to:
(A) Encourage aggressive behavior
(B) Allow personnel to perform duties while preventing phototoxic retinopathy in albino animals
(C) Provide sufficient UV light for vitamin D synthesis
(D) Increase ambient room temperature

2003

167. Micro-isolation cages are equipped with a filter top specifically designed to:
(A) Provide a continuous flow of sterile water
(B) Prevent the transmission of airborne particulate matter and microbes
(C) Trap excess heat inside the cage
(D) Emit ultraviolet sterilization light

2024

168. Which parameter is a direct measure of macro-environmental ventilation efficiency?
(A) Lux level
(B) Air Changes per Hour (ACH)
(C) Relative Humidity
(D) Photoperiod length

2001

169. What is a significant disadvantage of the toe-clipping method for identification?
(A) It requires expensive electronic scanning equipment
(B) The markings fade completely within several weeks
(C) Causes pain; restricted to neonates

(D) It can only uniquely identify up to 10 animals

2012

170. Ear tags used for rodent identification are typically made of:
(A) Biodegradable plastic
(B) Stainless steel or special alloys
(C) Paper
(D) Silicone

2015

171. A monogamous breeding pair is typically configured as:
(A) One male and one female
(B) Two males and one female
(C) One male and two females
(D) Multiple males and multiple females

2010

172. The presence of a vaginal plug in a mouse indicates:
(A) Impending parturition
(B) Successful copulation
(C) Estrous cycle synchronization
(D) Pregnancy failure

2008

173. A non-intensive breeding scheme is characterized by:
(A) Mating at the postpartum estrus
(B) Removing the male before parturition
(C) Maintaining the male continuously in the cage
(D) Producing litters every 21 days

2019

174. Which concept refers to the superiority of outbred hybrid offspring in vigor and reproductive capacity compared to their inbred parents?
(A) Inbreeding depression
(B) Heterosis (Hybrid vigor)
(C) Genetic drift
(D) Assortative mating

2014

175. Which of the following represents the correct sequence of generations in the creation of a recombinant inbred (RI) strain?
(A) Outbred cross → F1 → F2 → Continuous brother-sister mating
(B) Inbred A x Inbred B → F1 → F2 → Continuous brother-sister mating
(C) Inbred A x Outbred B → F1 → Backcross to A
(D) Coisogenic mutation → Outcrossing → Random mating

2018

176. Which selection method involves ranking animals based on a mathematical score incorporating multiple distinct traits?
(A) Tandem selection
(B) Independent culling levels
(C) Selection index
(D) Random selection

2007

177. The term "foundation colony" refers to:
(A) The oldest living animals in a facility
(B) The genetically monitored core population used strictly to supply breeding stock
(C) Animals designated for terminal experiments
(D) The quarantine housing for newly arrived animals

2009

178. What happens to the genetic variance within an inbred strain after 20 generations of continuous brother-sister mating?
(A) It reaches a maximum level
(B) It is reduced to near zero
(C) It fluctuates randomly each generation
(D) It matches that of an outbred population

2022

179. Poiley's system and the Maximum Avoidance of Inbreeding (MAI) system are designed for the management of:
(A) Congenic strains
(B) Recombinant inbred strains
(C) Outbred stocks
(D) Transgenic lines

2005

180. The outbred stock of mice commonly referred to as "Swiss Webster" is correctly abbreviated in nomenclature as:
(A) SW
(B) SWM
(C) MusS
(D) C57SW

2008

181. Standardized nomenclature designates an F1 hybrid of a C57BL/6J mother and a DBA/2J father as:
(A) B6D2F1
(B) D2B6F1
(C) C57DBA
(D) F1-BD

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2014

182. A genetic substitution created by mutation within an already highly inbred strain produces a:
(A) Congenic strain
(B) Coisogenic strain
(C) Knock-out strain
(D) Segregating outbred stock

2004

183. The backcross breeding technique primarily aims to:
(A) Increase genetic diversity in the population
(B) Transfer a gene to a standard background
(C) Eradicate infectious agents from the colony
(D) Create a completely new recombinant background

2019

184. In microbial classification, conventional animals are distinct from SPF animals because conventional animals:
(A) Must be housed in positive-pressure isolators
(B) Are free of all commensal intestinal bacteria
(C) Have undefined microflora and no strict barrier
(D) Are always derived via aseptic hysterectomy

2024

185. Arrange the following microbiological statuses from most sterile (fewest microbes) to least sterile.
I. Conventional
II. Axenic
III. SPF
IV. Gnotobiotic
Choose the correct order:
(A) II, IV, III, I
(B) II, III, IV, I
(C) IV, II, III, I
(D) I, III, IV, II

2025

186. Which tool is used to safely manipulate axenic animals without breaking the sterile barrier?
(A) Sealed flexible film isolator with half-suits or gloves
(B) Open laminar flow hood
(C) Standard biosafety cabinet class I
(D) Micro-isolator cage without a lid

2015

187. Sterilization of feed for axenic and gnotobiotic animals is most commonly achieved by:
(A) Freezing at -80 degrees Celsius
(B) Chemical treatment with bleach
(C) Autoclaving or gamma irradiation
(D) Brief exposure to UV light

NODIA

2005

188. Routine genetic monitoring of inbred strains aims to detect:
(A) Unintentional genetic contamination or drift
(B) The presence of parasitic worms
(C) Fluctuations in body weight
(D) Changes in feed formulation

2013

189. Which of the following represents a PCR-based method utilized for high-throughput genetic monitoring?
(A) Isoenzyme electrophoresis
(B) Skin allografting
(C) Tail vein blood typing
(D) Single Nucleotide Polymorphism (SNP) array testing

2004

190. Why is the tail tip amputation method for DNA collection usually restricted to mice under 21 days of age?
(A) Older mice do not have DNA in their tails
(B) The tail becomes completely hairless with age
(C) Blood vessels retract permanently after weaning
(D) Ossification increases pain and risk

2024

191. A transgenic mouse constructed via pronuclear injection will typically have the transgene integrated:
(A) Strictly via homologous recombination at a specific locus
(B) Randomly into the genome
(C) Only in mitochondrial DNA
(D) Exclusively in germ cells, not somatic cells

2019

192. Creating a targeted gene knock-out traditionally requires the use of:
(A) Embryonic stem (ES) cells
(B) Adult somatic cells
(C) Unfertilized oocytes
(D) Hepatocytes

2021

193. The CRISPR/Cas9 system revolutionizes mouse genetics by enabling:
(A) Highly efficient, targeted double-strand DNA breaks for precise gene editing
(B) Generation of axenic mice without isolators

2009

147. Safety pharmacology guidelines often require pre-clinical testing of cardiovascular and respiratory effects in a non-rodent model. Which species is predominantly chosen for this role?
(A) Guinea pig
(B) Beagle dog
(C) Hamster
(D) Athymic mouse

2021

148. Non-human primates, particularly Rhesus macaques, are crucial for testing vaccines against human specific viruses (e.g., HIV) primarily because:
(A) They are inexpensive to house and maintain
(B) Immune systems highly homologous to humans
(C) They reproduce rapidly in a laboratory setting
(D) They do not require ethics committee approval

2022

149. The institutional authority responsible for approving and monitoring animal research protocols in India is the:
(A) Institutional Animal Ethics Committee (IAEC)
(B) Department of Biotechnology
(C) Ministry of Health
(D) Food and Drug Administration

2021

150. According to the 3Rs principle, "Refinement" is best defined as:
(A) Reducing the number of animals used to an absolute minimum
(B) Substituting non-sentient models for live animals
(C) Modifying experimental procedures to minimize pain and distress
(D) Refining statistical models after the experiment

2002

151. Identifying the earliest clinical sign that predicts death and humanely euthanizing the animal before severe suffering occurs is known as establishing a:
(A) Humane endpoint
(B) Morbidity index
(C) Toxicity threshold
(D) Lethal dose 50 (LD50)

2003

152. Which of the following is considered an unacceptable method of euthanasia for laboratory rodents without prior anesthesia or specific scientific justification?
(A) Carbon dioxide overdose in a chamber
(B) Barbiturate overdose via injection
(C) Exsanguination of conscious animals
(D) Focused microwave irradiation of the head

2022

153. A common physical method of euthanasia used to preserve rodent brain chemistry without pharmacological artifacts, requiring specialized equipment, is:
(A) Carbon dioxide chamber
(B) Microwave irradiation to the head
(C) Isoflurane overdose
(D) Freezing

2006

154. What is the standard lifespan of a laboratory rat under controlled conditions?
(A) 6 to 12 months
(B) 2.5 to 3.5 years
(C) 5 to 6 years
(D) 10 to 12 years

2025

155. Match the animals in List I with their distinct features in List II.
List I: (Animal)
P. Mouse
Q. Guinea pig
R. Rabbit
S. Dog
List II: (Distinct Feature)
1. Induced ovulator
2. Vitamin C requirement
3. Precopulatory plug formation
4. 78 chromosomes
(A) P-1, Q-2, R-3, S-4
(B) P-3, Q-2, R-1, S-4
(C) P-4, Q-3, R-1, S-2
(D) P-2, Q-1, R-4, S-3

2014

156. An albino coat in rodents is technically defined as the complete lack of:
(A) Keratin
(B) Melanin pigment
(C) Hair follicles
(D) Guard hairs

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Q. Guinea pig
R. Dog
S. Macaque

List II: (Specific Test/Use)

1. Pyrogen testing
2. Tuberculosis model
3. Safety pharmacology
4. Vaccine efficacy (e.g., HIV)

(A) P-1, Q-2, R-3, S-4
(B) P-2, Q-1, R-4, S-3
(C) P-3, Q-4, R-1, S-2
(D) P-4, Q-3, R-2, S-1

2003

206. Guinea pigs used in anaphylaxis research typically exhibit severe respiratory distress due to constriction of bronchioles triggered by the release of:
(A) Insulin
(B) Glucagon
(C) Histamine
(D) Thyroxine

2005

207. Non-human primates account for approximately what percentage of total animals used in biomedical research?
(A) Less than 1%
(B) 10-15%
(C) 25-30%
(D) Over 50%

2012

208. The Beagle is the preferred breed of dog in laboratory research mainly because of its:
(A) Large size
(B) Aggressive temperament
(C) Docile nature, moderate size, and robust health
(D) Short lifespan

2021

209. Under the PCA Act (1960) in India, experiments on animals must be performed avoiding all unnecessary suffering. The statutory body enforcing this for research is the:
(A) CCSEA
(B) Animal Welfare Board of India (AWBI)
(C) Indian Council of Agricultural Research (ICAR)
(D) Central Zoo Authority (CZA)

2004

210. An institutional Animal Ethics Committee (IAEC) is mandated to review protocols involving:
(A) In vitro cell lines exclusively
(B) Small laboratory animals up to the size of rodents and rabbits
(C) Clinical trials on human subjects
(D) Agricultural crop genetics

2002

211. According to the CCSEA guidelines, experiments on large animals (like dogs and non-human primates) must be approved by:
(A) The IAEC, and subsequently forwarded to the main CCSEA for final approval
(B) The IAEC alone
(C) The principal investigator only
(D) The local municipal corporation

2006

212. The principle of 'Replacement' in the 3Rs implies:
(A) Using completely different strains of rodents
(B) Substituting sentient animals with alternatives
(C) Replacing older animals with younger subjects
(D) Replacing expired feed with fresh formulations

2001

213. Designing an experiment with a properly calculated sample size using power analysis directly addresses which of the 3Rs?
(A) Replacement
(B) Reduction
(C) Refinement
(D) Reuse

2012

214. Which of the following is a clear example of 'Refinement'?
(A) Administering a local anesthetic prior to a painful surgical incision
(B) Using an in vitro liver enzyme assay instead of a whole rat
(C) Using one monkey instead of ten
(D) Simulating the experiment on a computer

2014

215. The concept of establishing early "humane endpoints" is most closely associated with which 'R'?
(A) Replacement
(B) Reduction
(C) Refinement
(D) Reiteration

NODIA

2001

216. In terms of humane euthanasia, the method must aim to cause rapid loss of:
(A) Muscle mass
(B) Body heat
(C) Consciousness followed by cardiac and respiratory arrest
(D) Visual acuity

2016

217. When CO2 is used for euthanasia of rodents, the recommended displacement rate of chamber volume per minute is:
(A) 10-30%
(B) 30-70%
(C) 80-100%
(D) 100-200%

2010

218. According to standard physiological references, what is the normal heart rate of a resting adult beagle dog?
(A) 40-60 bpm
(B) 70-120 bpm
(C) 150-200 bpm
(D) 300-400 bpm

2004

219. The normal resting body temperature of a rabbit is approximately:
(A) 37.0 - 37.5 degrees Celsius
(B) 38.5 - 39.5 degrees Celsius
(C) 40.0 - 41.5 degrees Celsius
(D) 35.0 - 36.5 degrees Celsius

2003

220. Which term describes the uniquely structured feces consumed directly from the anus by rabbits and rodents to recover nutrients?
(A) Meconium
(B) Cecotropes
(C) Scybala
(D) Guano

2005

221. Coprophagy in rodents and rabbits is essential for the adequate absorption of:
(A) Vitamin C
(B) B-complex vitamins and proteins synthesized by hindgut bacteria
(C) Simple carbohydrates
(D) Dietary lipids

2002

222. The term "Harderian gland" refers to an accessory lacrimal gland in rodents that, during times of stress, secretes porphyrin which appears as:
(A) Green nasal discharge from the nostrils
(B) Red, blood-like crusts
(C) White ocular fluid from the tear ducts
(D) Yellow wax buildup in the auditory canal

2003

223. What condition is indicated by the excessive accumulation of red porphyrin staining around a rat's eyes and nose?
(A) Chromodacryorrhea
(B) Ringtail
(C) Scurvy
(D) Malocclusion

2025

224. Rodent incisors are characterized by being hypsodont, which means they:
(A) Fall out and are replaced continuously
(B) Grow continuously throughout the animal's life
(C) Contain no enamel
(D) Are strictly used for grinding

2019

225. Which of the following represents the correct sequence for obtaining a definitive microbiological diagnosis of a viral infection in a rodent colony via sentinels?
(A) Sentinel exposure to soiled bedding → Blood collection → Serum separation → ELISA / MFI testing
(B) Serum separation → Sentinel exposure → Blood collection → ELISA
(C) ELISA → Sentinel exposure → Serum separation → Blood collection
(D) Blood collection → ELISA → Sentinel exposure → Serum separation

2010

226. What happens if a rodent's continuously growing incisors do not wear down properly due to misalignment?
(A) They simply stop growing after reaching length
(B) Develop malocclusion and tissue damage
(C) They are naturally shed from the jawbone
(D) They fuse into a single solid tooth structure

2021

227. The most widely used method to prevent malocclusion in laboratory rodents is:
(A) Regular surgical extraction
(B) Providing hard pelleted diets or wooden chew blocks

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(C) Administering calcium supplements
(D) Filing the teeth daily

2003

228. Guinea pigs differ from mice and rats in their dental formula by possessing:
(A) Canines
(B) Only one pair of incisors total
(C) Premolars
(D) No molars

2008

229. A typical laboratory rat diet consists of approximately what percentage of crude fat?
(A) 1-2%
(B) 4-6%
(C) 15-20%
(D) 40-50%

2024

230. A chemically defined diet is often necessary when studying:
(A) Basic housing preferences
(B) The precise effect of a single trace mineral or specific amino acid omission
(C) Routine behavioral ethograms
(D) Pheromone communication

2022

231. The standard temperature range for a guinea pig housing room is lower than that for mice, typically kept around:
(A) 16 to 22 degrees Celsius
(B) 24 to 28 degrees Celsius
(C) 28 to 32 degrees Celsius
(D) 10 to 15 degrees Celsius

2009

232. Guinea pigs are extremely susceptible to heat stress primarily because they:
(A) Have very thick fur and lack functional sweat glands
(B) Have a naturally high metabolic rate
(C) Are obligate herbivores
(D) Have very small lungs

2016

233. In macro-environmental monitoring, the measurement of ammonia levels is crucial. High ammonia levels usually indicate:
(A) Over-ventilation of the animal holding room
(B) Poor ventilation or infrequent bedding changes
(C) A diet too high in complex carbohydrates
(D) Optimal breeding conditions for the colony

2025

234. Prolonged exposure to high intracage ammonia levels in rats strongly predisposes them to:
(A) Development of dental malocclusion
(B) Respiratory infections (e.g., Mycoplasma)
(C) Onset of scurvy from vitamin deficiency
(D) Accumulation of spontaneous genetic mutations

2010

235. Arrange the following breeding systems from lowest to highest degree of genetic homozygosity in the resulting offspring.
I. Congenic backcrossing (Generation 10)
II. Outbred rotational mating
III. Continuous brother-sister mating (Generation 20)
IV. Monogamous mating within an outbred stock
Choose the correct order:
(A) II, IV, I, III
(B) IV, II, III, I
(C) II, IV, III, I
(D) III, I, IV, II

2017

236. The microchip used for permanent animal identification operates on the principle of:
(A) GPS tracking
(B) Radio Frequency Identification (RFID)
(C) Bluetooth connectivity
(D) Infrared signaling

2013

237. A pedigree chart for a newly developed transgenic mouse line traces back to the original engineered animal, which is termed the:
(A) Progenitor
(B) Founder
(C) Mutant
(D) Sire

2003

238. In a harem mating system for mice, pregnant females are typically:
(A) Left in the cage with the male and others
(B) Removed and housed individually before birth
(C) Euthanized immediately following parturition
(D) Shipped to another research facility location

2024

239. The occurrence of a postpartum estrus allows mice to:
(A) Delay implantation indefinitely

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ANSWERS

1. (B) 40
The laboratory mouse, scientifically classified as Mus musculus, possesses a diploid chromosome number of forty in its normal somatic cells. This consists of nineteen autosomal pairs and one pair of sex chromosomes. Precise knowledge of this karyotype is vital for genetic studies, breeding management, and maintaining the consistency of research data in laboratory settings.

2. (D) Dog
The domestic dog, often utilized in safety pharmacology and toxicology studies, has a diploid chromosome number of seventy-eight. This karyotype includes thirty-eight pairs of autosomes and two sex chromosomes. Understanding these species-specific genetic characteristics is necessary for identifying chromosomal abnormalities and ensuring the reliability of various genetic and physiological research findings in clinical environments.

3. (B) 42
The laboratory rat, known as Rattus norvegicus, possesses forty-two chromosomes in its diploid state. This chromosomal count includes twenty pairs of autosomes and one pair of sex chromosomes. Maintaining genetic uniformity within this karyotype is essential for breeding programs and experimental consistency, as it directly impacts the biological responses observed during pharmacological and toxicological studies.

4. (C) Guinea pig
The guinea pig, or Cavia porcellus, is characterized by having sixty-four chromosomes in its normal diploid karyotype. This laboratory species is frequently used in immunology and auditory research due to its unique physiological traits. Accurate identification of its chromosomal number is fundamental for genetic monitoring and ensuring the stability of inbred lines within research facilities.

5. (A) Mouse
The H-2 complex represents the major histocompatibility complex found specifically in laboratory mice. This genetic region, located on chromosome seventeen, is critical for immune system function and graft rejection. Detailed knowledge of the H-2 haplotype is essential for researchers conducting studies in immunology, organ transplantation, and the development of genetically modified rodent models.

6. (D) Rat
The major histocompatibility complex in the laboratory rat is designated as RT1. Located on chromosome fourteen, this complex plays a primary role in immune recognition and tissue compatibility. Understanding the RT1 system is vital for immunogenetic research and for ensuring successful skin grafting or organ transplantation experiments between different strains of laboratory rats.

7. (A) A locus
The A locus, also referred to as the agouti locus, is primarily responsible for the characteristic agouti coat color pattern in mice. This pattern results from a subterminal band of yellow pigment on an otherwise black hair shaft. Genetic variations at this locus are fundamental in mammalian pigment biology and are widely used in genetic studies.

8. (C) Albino coat
A mutation at the C locus, which encodes the enzyme tyrosinase, typically leads to an albino phenotype in laboratory mice. Tyrosinase is essential for the production of melanin; therefore, its absence results in white fur and red eyes. This locus is one of the most well-studied markers for identifying and monitoring genetic purity in rodent colonies.

NODIA

9. (B) 36.5 to 38.0 degrees Celsius
The average normal body temperature for a laboratory mouse typically ranges from 36.5 to 38.0 degrees Celsius. Maintaining this core temperature is vital for the animal's metabolic homeostasis. Fluctuations outside this range often indicate stress, illness, or environmental issues, making regular temperature monitoring a critical component of welfare assessment and clinical health management in rodents.

(B) Comprehensive screening using serology, bacteriology, parasitology, and PCR
(C) Observing coat color
(D) Measuring daily water intake

2018

251. Sentinel animals are used in a rodent facility to:
(A) Protect the colony from external predators
(B) Monitor health via bedding or air exposure
(C) Serve as the primary breeding population
(D) Perform specialized behavioral testing tasks

2018

252. Which species is commonly used as a sentinel animal in mouse colonies because it readily seroconverts when exposed to most murine pathogens?
(A) Rat
(B) Hamster
(C) Outbred mouse (e.g., Swiss Webster or CD-1)
(D) Guinea pig

2008

253. Genetic contamination in an inbred colony occurs when:
(A) A mutation arises spontaneously
(B) An animal from a different strain is accidentally mated with an animal of the inbred colony
(C) The animals are fed an improper diet
(D) The room temperature fluctuates widely

2002

254. A major advantage of using SNPs over microsatellites for genetic monitoring is that SNPs:
(A) Are fewer in number
(B) Can be easily multiplexed and automated for high-throughput analysis using microarrays
(C) Require live tissue grafting
(D) Only occur in mitochondrial DNA

2011

255. Match the genetically modified models in List I with their key characteristics in List II.
List I: (Genetically Modified Model)
P. Transgenic
Q. Knock-out
R. Knock-in
S. Conditional Knock-out
List II: (Key Characteristic)
1. Foreign gene added
2. Endogenous gene disabled
3. Targeted replacement with altered sequence
4. Gene deleted in specific tissue only
(A) P-1, Q-2, R-3, S-4
(B) P-2, Q-1, R-4, S-3
(C) P-3, Q-4, R-1, S-2
(D) P-1, Q-4, R-2, S-3

2018

256. Pronuclear microinjection results in the random integration of the transgene, which can lead to variable expression levels due to:
(A) Position effect of the integration site
(B) Homologous recombination
(C) Complete loss of the transgene
(D) RNA interference

2002

257. Gene targeting in Embryonic Stem (ES) cells relies on which cellular mechanism to ensure precise modification?
(A) Non-homologous end joining
(B) Homologous recombination
(C) Random insertion
(D) Retroviral reverse transcription

2013

258. Chimeric mice are produced during the creation of a knock-out mouse by:
(A) Crossing two entirely different species
(B) Injecting genetically modified ES cells into a wild-type blastocyst
(C) Fusing two separate adult mice
(D) Irradiating a pregnant female

2025

259. A chimeric mouse exhibits physical traits (like mixed coat colors) from both the ES cells and the host blastocyst. To establish a true knock-out line, the chimera must transmit the modified genome through its:
(A) Somatic cells
(B) Germline (sperm or eggs)
(C) Bloodstream
(D) Saliva

2023

260. The leptin protein, deficient in ob/ob mice, is normally secreted by:
(A) Pancreatic beta cells
(B) White adipose tissue (adipocytes)
(C) The anterior pituitary
(D) The adrenal cortex

2008

261. Because db/db mice produce normal or elevated levels of leptin but lack functional receptors, treating them with exogenous leptin will result in:

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(B) Conceive a second litter while simultaneously lactating the first
(C) Produce only male offspring
(D) Avoid the Whitten effect

2004

240. Cross-fostering is a technique used in laboratory animal breeding primarily to:
(A) Create new transgenic models
(B) Rear pups whose biological mother is dead, agalactic, or exhibiting poor maternal care
(C) Increase the mutation rate
(D) Establish a recombinant inbred line

2017

241. A quantitative trait is generally influenced by:
(A) One dominant gene
(B) Multiple genes (polygenic) and environmental factors
(C) Environmental factors exclusively
(D) Mitochondrial DNA only

2013

242. Selection intensity is a measure of:
(A) The physical strength of the animal
(B) How strictly breeders choose the top-performing individuals to become parents of the next generation
(C) The number of spontaneous mutations
(D) The rate of inbreeding depression

2007

243. An inbred strain must be maintained by brother-sister mating. If this is not possible due to reproductive failure, what is the accepted alternative to maintain the inbred status?
(A) Outcrossing to a different strain
(B) Mating offspring to their younger parent
(C) Random mating within the colony
(D) Poiley's rotational mating

2010

244. The phenomenon of "genetic bottleneck" in an outbred colony leads to:
(A) Increased genetic diversity in the population
(B) Reduction in variation due to small population size
(C) Occurrence of heterosis or hybrid vigor
(D) Formation of recombinant inbred populations

2025

245. Given below are two statements: one is labelled as Assertion (A) and the other is labelled as Reason (R).
Assertion (A): Substrains of an inbred mouse line emerge when branches of the colony are separated and bred independently for many generations.
Reason (R): Separated colonies inevitably accumulate distinct spontaneous mutations and undergo independent genetic drift.
(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

2004

246. To establish a new inbred strain from two existing inbred strains (A and B), the first step is to:
(A) Backcross A to B for 10 generations
(B) Cross A and B to produce an F1 generation, then cross F1s to produce F2s, followed by continuous brother-sister mating
(C) Randomly mate A and B indefinitely
(D) Perform a single brother-sister mating and stop

2006

247. The primary goal of creating a segregating inbred strain is to:
(A) Eliminate a specific gene completely
(B) Maintain a lethal or deleterious mutation in a heterozygous state on a uniform genetic background
(C) Maximize outbred diversity
(D) Create a germ-free animal

2007

248. The term "Speed Congenics" refers to a technique that reduces the number of backcross generations needed by utilizing:
(A) Faster reproductive technologies like IVF
(B) Genotyping for high recipient genome percentage
(C) Artificial light cycles to speed up puberty
(D) High-protein diets to accelerate animal growth

NODIA

2018

249. A "closed colony" is one in which:
(A) No new genetic material (animals) is introduced from outside the colony
(B) Animals are kept strictly in darkness
(C) Only inbred animals are maintained
(D) All animals are strictly monogamous

2013

250. The microbiological status of an animal is definitively verified by:
(A) Weighing the animal weekly

(B) The Institutional Head
(C) The Principal Investigator
(D) The Attending Veterinarian

2009

273. The primary ethical justification for using animals in research, provided by regulatory bodies, revolves around the concept that:
(A) Animals have no moral standing
(B) The expected scientific or medical benefits to humans or animals outweigh the potential harm to the research animals
(C) Alternatives are entirely non-existent
(D) Animals do not perceive pain

2015

274. Using the Limulus Amebocyte Lysate (LAL) assay instead of the rabbit pyrogen test is an example of which 3R principle?
(A) Replacement
(B) Reduction
(C) Refinement
(D) Resuscitation

2023

275. Providing complex nesting materials to laboratory mice to allow natural burrowing behavior is a direct application of:
(A) Replacement
(B) Reduction
(C) Refinement
(D) Recycling

2009

276. Euthanasia literally translates from Greek to mean:
(A) Rapid death
(B) Good death
(C) Painless sleep
(D) Final rest

2016

277. The process of cervical dislocation causes death primarily by:
(A) Depressing the respiratory centers in the brain via chemical action
(B) Severing the spinal cord and destroying major neural pathways governing respiration and cardiac function
(C) Exsanguination
(D) Freezing brain tissue

2008

278. To ensure death has occurred following CO2 euthanasia in rodents, a secondary physical method is often recommended, such as:
(A) Decapitation or cervical dislocation
(B) Administration of oxygen
(C) Gentle warming
(D) Injection of normal saline

2017

279. The routine life expectancy of a guinea pig is approximately:
(A) 1-2 years
(B) 4-8 years
(C) 10-12 years
(D) 15-20 years

2022

280. When assessing the welfare of laboratory animals, a hunched posture, piloerection (ruffled fur), and lack of grooming are classic signs of:
(A) Optimal health
(B) Pain, distress, or illness
(C) Impending estrus
(D) Thermal comfort

2022

281. The "Alter-Gnotobiotic" status (e.g., ASF - Altered Schaedler Flora) is primarily used in rodent research to:
(A) Eliminate all bacteria from the gut
(B) Standardize the gut microbiome with a defined set of bacterial species
(C) Increase the susceptibility to viral pathogens
(D) Induce spontaneous mutations for genetic mapping

2001

282. High-Efficiency Particulate Air (HEPA) filters are utilized in barrier facilities. A HEPA filter is designed to remove what percentage of airborne particles 0.3 micrometers in diameter?
(A) 50.0%
(B) 75.5%
(C) 99.97%
(D) 100%

2024

283. The optimal recommended environmental temperature for housing laboratory mice is:
(A) 16 - 18 degrees Celsius
(B) 20 - 24 degrees Celsius
(C) 26 - 28 degrees Celsius
(D) 30 - 32 degrees Celsius

2009

284. Which environmental parameter is most critical to control to prevent thermal stress during the transport of laboratory animals?
(A) Light intensity

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(B) Noise level
(C) Temperature and ventilation
(D) Cage color

2014

285. A mouse strain designated as C3H/HeJ represents a:
(A) Knock-out strain
(B) Substrain of C3H maintained by 'He' and further established by Jackson Laboratory (J)
(C) Congenic strain
(D) Wild-caught outbred stock

2024

286. Recombinant inbred strains are particularly powerful tools for:
(A) Mapping quantitative trait loci using fixed blocks
(B) Analyzing simple monogenic or Mendelian traits
(C) Producing large volumes of high-titer serum
(D) Eliminating all spontaneous genetic mutations

2021

287. Which of the following best describes the "founder effect" in a laboratory colony?
(A) The increase in mutation rate due to radiation
(B) Loss of variation when establishing new colonies
(C) The rapid growth of an established colony
(D) The intentional outcrossing to improve vigor

2004

288. A major disadvantage of using an outbred stock in pharmacological research compared to an inbred strain is:
(A) Reduced hybrid vigor in the population
(B) High variability requiring larger sample sizes
(C) Shorter overall lifespan of the animals
(D) Absolute uniformity of all research results

2016

289. Mice are nocturnal animals, meaning their natural peak period of physical activity and feeding occurs:
(A) During the light phase
(B) Continuously throughout 24 hours
(C) During the dark phase
(D) Only at dawn

2004

290. Environmental enrichment for a laboratory macaque typically includes:
(A) Providing puzzle feeders, climbing structures, and social housing
(B) Keeping the cage completely bare to ensure sterility
(C) Continuous bright lighting
(D) Total isolation from human sight

2003

291. CCSEA regulations strictly require that the primary enclosure (cage) for an animal must provide sufficient space to allow the animal to:
(A) Make normal postural adjustments and behaviors
(B) Run at maximum speed within the enclosure
(C) Avoid all contact with established cage-mates
(D) Hide from the experimenter during observations

2013

292. Assessing the depth of anesthesia in rodents prior to a surgical procedure is reliably performed by testing the:
(A) Ear twitch reflex
(B) Pedal withdrawal (toe-pinch) reflex
(C) Pupillary light reflex only
(D) Tail flick response

2013

293. Analgesia should ideally be administered:
(A) Pre-emptively, before the painful stimulus or surgical incision occurs
(B) Only after the animal shows vocalization of severe pain
(C) Orally in the drinking water 3 days post-surgery
(D) Never, as it always interferes with research data

NODIA

2025

294. According to strict SPF standards, incoming biological materials such as cell lines must be screened for murine viruses (e.g., via MAP or IMPACT testing) before introduction into live mice to prevent:
(A) Spontaneous mutation
(B) Zoonotic infection of personnel
(C) Introduction of adventitious pathogens into the colony
(D) Rejection of the cell line

2025

295. The genetic phenomenon where a single gene affects multiple, seemingly unrelated phenotypic traits is known as:
(A) Epistasis

(B) Codominance
(C) Incomplete dominance
(D) Pleiotropy

2023

296. Epigenetic modifications in laboratory animals, which can alter gene expression without changing the underlying DNA sequence, are most commonly mediated by:
(A) DNA methylation and histone modification
(B) Transgene insertion
(C) Ribosomal RNA degradation
(D) Deletion of entire chromosomes

2013

297. Which type of laboratory diet ensures the highest level of exactness and reproducibility in nutritional studies, as every component is formulated from pure compounds?
(A) Open-formula natural ingredient diet
(B) Closed-formula natural ingredient diet
(C) Chemically defined (purified) diet
(D) Cereal-based extruded diet

2012

298. Overcrowding of mice in a standard cage most commonly leads to which immediate behavioral problem?
(A) Excessive barbering and inter-male aggression
(B) Immediate onset of seasonal hibernation states
(C) Complete cessation of daily water consumption
(D) Refusal to build nests with provided materials

2009

299. In toxicology studies, the concept of a "Maximum Tolerated Dose" (MTD) is defined as the highest dose of a chemical that:
(A) Causes death in 50% of the experimental animals
(B) Produces therapeutic effects without side effects
(C) Causes no excessive toxicity or 10% weight loss
(D) Can be dissolved in standard laboratory water

2016

300. The ultimate ethical goal of the Institutional Animal Ethics Committee (IAEC) is to:
(A) Prohibit all animal research within the institution
(B) Maximize the number of publications produced
(C) Ensure experiments are humane and compliant
(D) Reduce the cost of animal husbandry operations

****

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(A) A cure for their obesity and metabolic syndrome
(B) No effect on weight or food intake
(C) Induction of severe anorexia and weight loss
(D) A cure for their diabetes and insulin resistance

2012

262. The Zucker rat (fa/fa) has a mutation in the gene encoding the:
(A) Leptin receptor
(B) Insulin receptor
(C) Glucagon receptor
(D) Dopamine receptor

2022

263. The primary reason athymic nude mice must be housed under strict SPF or barrier conditions is their high susceptibility to:
(A) Sunburn
(B) Opportunistic infections due to T-cell deficiency
(C) Autoimmune diseases
(D) Metabolic syndrome

2019

264. Human xenograft tumor models are most successfully grown in which of the following host animals?
(A) Wild-type C57BL/6 mice
(B) Outbred Wistar rats
(C) Severely immunodeficient mice (e.g., Nude, SCID, NSG)
(D) Guinea pigs

2023

265. The primary advantage of the NSG mouse over the traditional SCID mouse is:
(A) The presence of normally functioning NK cells
(B) Lack of T, B, and NK cells for engraftment
(C) Its resistance to all pathogenic infections
(D) Its ability to synthesize endogenous vitamin C

2018

266. A substance that causes a rise in body temperature when injected intravenously is known as a:
(A) Teratogen
(B) Carcinogen
(C) Pyrogen
(D) Mitogen

2006

267. The classic rabbit pyrogen test has been largely replaced in modern times by which in vitro alternative assay?
(A) Ames test
(B) Limulus Amebocyte Lysate (LAL) test
(C) ELISA
(D) Western blot

2013

268. Which feature of the guinea pig's reproductive physiology makes it a relevant model for studying human pregnancy?
(A) Very short gestation of 21 days
(B) Hemochorial placentation similar to humans
(C) Egg-laying capability
(D) Avascular placenta

NODIA

2012

269. A non-human primate facility must adhere strictly to occupational health guidelines due to the risk of fatal zoonotic transmission of which agent from Macaques to humans?
(A) Rabies virus
(B) Macacine alphaherpesvirus 1 (B virus)
(C) Canine distemper virus
(D) Feline leukemia virus

2009

270. Safety pharmacology specifically assesses the potential adverse effects of a new drug on vital organ systems. Which three systems are considered the core battery?
(A) Cardiovascular, Respiratory, and Central Nervous System
(B) Hepatic, Renal, and Gastrointestinal
(C) Skeletal, Muscular, and Integumentary
(D) Endocrine, Immune, and Reproductive

2022

271. CCSEA guidelines categorize experiments into different severity levels. Which level involves the least pain or distress?
(A) Procedures causing severe pain without anesthesia
(B) Procedures causing minor to moderate pain treated with analgesics
(C) Non-invasive observational studies
(D) Survival surgeries

2025

272. Who acts as the statutory, external oversight figure ensuring that an IAEC complies with the Prevention of Cruelty to Animals Act during its meetings?
(A) The CCSEA Main Nominee

10. (A) I and II
Laboratory rats exhibit unique physiological characteristics, such as the absence of a gallbladder and a resting heart rate between 330 and 480 beats per minute. While their heart rate is significantly higher than that of larger mammals, their diploid chromosome number is forty-two, not forty. Understanding these species-specific anatomical and physiological details is crucial for laboratory management.

11. (B) Polyestrous continuous
The laboratory mouse is characterized by a continuous polyestrous cycle, meaning it undergoes reproductive cycles throughout the entire year without seasonal interruptions. Each cycle typically lasts four to five days under standard laboratory conditions. This rapid and frequent reproductive capability makes the mouse an exceptionally efficient model for studies involving genetics, embryology, and large-scale colony breeding programs.

12. (B) Whitten effect
The Whitten effect refers to the synchronization of the estrous cycle in a group of female mice following the introduction of a male or his pheromones. This phenomenon is mediated by olfactory cues that stimulate the release of gonadotropins. It is commonly utilized by facility managers to time matings and ensure uniform timing for embryo collection and experiments.

13. (A) Bruce effect
The Bruce effect occurs when a recently mated female mouse fails to implant or terminates her pregnancy after exposure to the odors of an unfamiliar male. This pheromone-mediated response is a form of pregnancy block that typically occurs within the first few days post-mating. It serves as a significant biological factor that influences reproductive success in rodent breeding colonies.

14. (C) Lee-Boot effect
The Lee-Boot effect involves the suppression or prolongation of the estrous cycle in female mice when they are housed together in large groups without exposure to a male. This phenomenon often leads to a state of persistent anestrus or pseudopregnancy. It highlights the profound influence of social environment and pheromonal cues on the reproductive physiology of laboratory rodents.

15. (C) I and II
Reproductive phenomena in rodents include the Bruce effect, which involves a pregnancy block, and the Whitten effect, which facilitates estrus synchronization. Facultative diapause, however, refers to delayed embryonic implantation rather than acceleration. Understanding these biological mechanisms is necessary for effective colony management and for interpreting reproductive data accurately in rodents used for biomedical and genetic research applications.

16. (B) 19 to 21 days
The average gestation period for a laboratory mouse typically ranges from 19 to 21 days. This short duration allows for the rapid production of offspring, making mice highly suitable for multi-generational studies. Factors such as the strain of the mouse and the size of the litter can slightly influence the exact timing of parturition in these animals.

17. (C) 21 days
The standard weaning age for laboratory mice and rats is twenty-one days after birth. At this stage, the pups have developed sufficiently to consume solid food and water independently from the mother. Proper timing of weaning is essential for the health of both the offspring and the dam, and it ensures the correct social development of the rodents.

NODIA

18. (D) Vitamin C
Guinea pigs are unique among common laboratory rodents because they require an external dietary source of Vitamin C. Unlike mice or rats, they cannot synthesize ascorbic acid internally due to a specific genetic deficiency. Providing adequate Vitamin C through fortified feed or water is mandatory to prevent the development of scurvy and ensure the animal's overall health.

19. (A) L-gulonolactone oxidase
Guinea pigs cannot synthesize Vitamin C because they lack the functional enzyme L-gulonolactone oxidase, which is necessary for the final step of ascorbic acid production from glucose. This metabolic deficiency makes them a valuable model for studying Vitamin C metabolism and related disorders. Researchers must ensure that this vitamin is provided daily to maintain the physiological integrity of the animals.

restrictive microbial barrier. They are typically housed in open-top cages or standard rooms where they may be exposed to an undefined mixture of environmental microorganisms. While they are unsuitable for highly sensitive immunological studies, they may still be used for certain types of basic research where a strictly controlled microflora is not required.

57. (D) Skin grafting
Skin grafting is a traditional method used to monitor the genetic purity of inbred mouse strains. Because inbred animals are genetically identical, they should theoretically accept skin grafts from any other member of the same strain. Rejection of a graft indicates genetic variation or contamination within the colony, making this an effective, though time-consuming, immunological assay for maintaining the integrity of inbred lines.

58. (A) Major histocompatibility complex
Immunological assays in genetic monitoring primarily test for variations in the major histocompatibility complex (MHC). These markers are highly polymorphic and are responsible for tissue compatibility. By analyzing MHC antigens through methods such as serology or skin grafting, researchers can detect genetic drift or unintended crossbreeding within inbred colonies, ensuring that the animals remain genetically consistent for use in experimental studies.

59. (B) Isoenzymes
Biochemical genetic monitoring utilizes variations in the electrophoretic mobility of proteins, which are known as isoenzymes. These variations result from different alleles at a single locus producing slightly different forms of the same enzyme. By screening for these biochemical markers, researchers can verify the genetic profile of a strain and detect any contamination that might have occurred during the breeding process.

60. (C) A is true but R is false.
PCR-based microsatellite genotyping is a preferred modern method for genetic monitoring because it is fast, highly sensitive, and only requires a small tissue sample. Unlike skin grafting, it does not involve surgical procedures or long waiting periods for rejection responses. It allows for the precise detection of genetic drift or contamination by analyzing specific DNA markers, making it more efficient and humane.

61. (B) Single base-pair variations in genomic DNA
Single Nucleotide Polymorphism (SNP) genotyping panels detect single base-pair variations at specific locations in the genomic DNA. These variations are the most common form of genetic difference between individuals and strains. SNP arrays provide a high-resolution, automated method for genetic monitoring, allowing researchers to quickly verify the genetic background and purity of laboratory animal colonies with extreme accuracy and throughput.

62. (D) Transgenic animal
A transgenic animal is created by the intentional introduction of foreign DNA into its genome, typically at the embryonic stage. This exogenous DNA, or transgene, is integrated into the host's DNA and can be passed on to future generations. This technology allows researchers to study the effects of overexpressing specific genes or expressing genes from other species within a living vertebrate model.

63. (B) A specific endogenous gene has been intentionally disrupted or deleted
A knock-out (KO) mouse is a genetically engineered model in which a specific endogenous gene has been intentionally disrupted or deleted. This loss of function allows researchers to determine the role of that particular gene in development, physiology, and disease. Knock-out technology has revolutionized biomedical research by providing a systematic way to study the function of thousands of individual genes in a mammalian system.

64. (C) Knock-in (KI) mouse
A knock-in (KI) mouse is created by the targeted replacement of an endogenous gene sequence with a mutated or entirely different sequence at the exact same chromosomal locus. Unlike random transgenic insertion, this method ensures that the new sequence is under the control of the native promoter. This allows for the precise modeling of human genetic mutations and the study of gene function in context.

65. (B) I and II
The Cre-loxP system is a powerful tool for creating inducible or tissue-specific gene knock-outs. It utilizes the Cre recombinase enzyme,

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less traumatic and the tissue heals quickly. Institutional Animal Ethics Committees often require strong scientific justification for this method, as it involves the removal of tissue and can potentially cause pain.

30. (C) Harem breeding system
A harem breeding system consists of housing one male with two or more females continuously for reproductive purposes. This method is highly efficient for maximizing the number of offspring produced per male. It is commonly used in large-scale breeding programs where rapid colony expansion is necessary and where the exact maternal parentage of the pups does not require individual tracking.

31. (D) Harem mating
Harem mating is the most appropriate configuration for maximizing the production of litters per male, as one male is given continuous access to several females. This system reduces the number of males required in a colony and optimizes space within the breeding facility. It is particularly effective for generating large numbers of offspring for diverse experimental and maintenance requirements.

32. (C) Keeping the male continuously with females during parturition
Intensive breeding systems are distinguished from non-intensive systems by keeping the male with the females continuously, including during parturition. This strategy takes advantage of the postpartum estrus, allowing the female to be bred again almost immediately after giving birth. This approach results in higher litter frequency and maximizes the overall reproductive output of the breeding pairs in a colony.

33. (B) 14 to 28 hours
Postpartum estrus in mice occurs approximately 14 to 28 hours after the female gives birth. This fertile period allows for immediate re-mating, which is a key feature utilized in intensive breeding systems to increase productivity. If mating occurs during this time, embryonic implantation may be slightly delayed if the female is also nursing a large litter of pups simultaneously.

34. (D) To select for multiple quantitative traits
A selection index is constructed in quantitative genetics to facilitate the simultaneous selection of multiple quantitative traits in a breeding population. By assigning weight to different characteristics such as growth rate and litter size, breeders can identify individuals with the best overall genetic value. This mathematical approach optimizes genetic progress and ensures that various desirable traits are improved concurrently over successive generations.

35. (B) I, III and IV
Continuous brother-sister mating is the standard method for developing inbred strains, achieving over ninety-eight percent homozygosity after twenty consecutive generations. While it ensures genetic uniformity, it often leads to inbreeding depression, which reduces reproductive vigor. This system is designed to eliminate heterozygosity, making it the opposite of methods used to maintain genetic diversity in outbred stocks for research purposes.

36. (C) 20
An inbred strain of mice is officially defined as a colony produced by a minimum of twenty consecutive generations of brother-sister mating. This extensive inbreeding process ensures that the animals are genetically identical and homozygous at virtually all loci. These strains are essential for research because they minimize genetic variability, allowing for more reproducible and consistent results across different laboratory experiments.

37. (A) Probability that two alleles at a locus are identical by descent
The inbreeding coefficient estimates the probability that two alleles at any given locus in an individual are identical because they were inherited from a common ancestor. As inbreeding progresses over generations, this coefficient increases, leading to higher levels of homozygosity. Calculating this value is essential for managing the genetic health and purity of both inbred strains and outbred laboratory populations.

38. (D) Inbreeding depression
Inbreeding depression refers to the decline in reproductive performance, general health, and vigor that often results from continuous brother-sister mating. This phenomenon is caused by the increased expression of deleterious recessive alleles as homozygosity increases. It is a common challenge when developing new inbred strains

NODIA

20. (A) Both A and R are true and R is the correct explanation of A.
Autoclaved diets for laboratory animals are often formulated with higher concentrations of thermolabile vitamins to compensate for losses during sterilization. Heat-sensitive vitamins, such as Vitamin C and Vitamin A, are significantly degraded by the high temperatures used in the autoclaving process. Therefore, over-fortification ensures that the final sterilized product still meets the nutritional requirements of the research animals.

21. (A) Chemically defined diet
A chemically defined diet is formulated using precise amounts of purified ingredients, including amino acids, specific sugars, and chemically pure vitamins and minerals. This type of diet provides the highest level of nutritional control and consistency. It is primarily used in research where the exact impact of specific nutrients on physiological or pathological processes needs to be evaluated accurately.

22. (C) 10 to 15
The recommended minimum number of air changes per hour for a standard rodent holding room is between ten and fifteen. This ventilation rate is essential for removing heat, moisture, and metabolic gases such as ammonia from the macro-environment. Maintaining proper airflow ensures a healthy living environment for the animals and reduces the risk of respiratory diseases and physiological stress.

23. (C) 45 to 65 percent
The recommended relative humidity range for macro-environmental control in rodent holding rooms is 45 to 65 percent. Maintaining humidity within this range is critical for preventing health issues such as ringtail in suckling rats. Proper moisture levels also ensure the comfort of the animals and minimize the growth of certain environmental pathogens within the facility's air and bedding.

24. (C) 12 hours light, 12 hours dark
Standard light-dark photoperiods for maintaining rodent breeding colonies are typically set to a twelve-hour light and twelve-hour dark cycle. This consistent rhythm helps regulate the animals' circadian patterns and reproductive cycles. Precise control of the lighting schedule is fundamental to ensuring predictable breeding performance and reducing variability in experimental results that are influenced by diurnal biological rhythms.

25. (B) II and III
Optimal environmental parameters for laboratory mice include a temperature range of 20 to 24 degrees Celsius and air changes between 10 and 15 per hour. Humidity should not exceed eighty percent, and excessive lighting intensity should be avoided to prevent retinal damage. Proper control of these factors is essential for maintaining animal welfare and ensuring consistent data in research studies.

26. (A) Low relative humidity
Ringtail is a condition in laboratory rats characterized by circular constrictions on the tail, which can lead to necrosis. It is primarily associated with low relative humidity, often below forty percent, in the holding room. Maintaining adequate moisture levels is essential for preventing this condition, particularly in neonates and suckling rats housed in facilities with high-flow ventilation systems.

27. (B) Coat marking with non-toxic dye
Marking the coat with non-toxic dye is considered a temporary method of animal identification in laboratory settings. This technique is useful for short-term studies but requires regular reapplication as the animal molts or grooms itself. Unlike permanent methods such as tattooing or microchipping, temporary markings allow for quick visual identification without causing long-term physical changes or requiring specialized equipment.

28. (B) Microchipping
Microchipping is a permanent method of animal identification that involves the subcutaneous implantation of a small electronic transponder. Each chip contains a unique identification code that can be read using a specialized scanner. This method is highly reliable, provides lifetime tracking, and causes minimal distress to the animal once the initial injection is completed in a clinical or laboratory setting.

29. (A) 7 days
Toe-clipping for identification purposes in neonatal rodents is generally restricted to animals that are no more than seven days old. At this young age, the procedure is considered

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of a particular allele without interference from other genetic variations within the animal.

48. (C) Spontaneous or induced mutation within an existing inbred strain
Coisogenic strains arise when a spontaneous or induced mutation occurs within an existing, highly inbred strain. Because the mutation happens on a genetically uniform background, the mutant animal and its original strain differ at only that single modified locus. These strains provide a unique opportunity to study gene function without the need for the extensive backcrossing required to create congenic rodent models.

49. (B) Continuous brother-sister mating of individuals from the F2 generation of a cross between two inbred strains
Recombinant inbred (RI) strains are developed by crossing two different inbred progenitor strains to produce an F1 generation, which is then intercrossed to create an F2. From the F2 generation, multiple independent lines are established through at least twenty generations of continuous brother-sister mating. This process fixes unique combinations of the original parental alleles into new, stable, and homozygous genetic backgrounds.

50. (D) Mapping quantitative trait loci
Recombinant inbred strains are exceptionally valuable for mapping quantitative trait loci (QTLs). Because each RI line possesses a fixed, unique mosaic of the progenitor genomes, researchers can correlate phenotypic variations with specific genetic markers across the set of lines. This provides a robust and reproducible framework for identifying the multiple genetic regions that contribute to complex traits such as disease susceptibility or behavior.

51. (A) Mating and selecting for heterozygotes
Segregating inbred strains are maintained such that they remain heterozygous at a specific locus, often because the homozygous state is lethal or infertile. This is achieved through a systematic mating program where individuals are selected for the presence of the desired allele in each generation. This allows researchers to maintain and study deleterious mutations within a uniform and stable inbred genetic background.

52. (C) Axenic
Axenic animals are entirely free of all demonstrable microorganisms, including bacteria, viruses, fungi, and parasites. These animals must be derived via cesarean section and maintained in sterile isolators with sterilized food, water, and air. They are used in specialized research to study the fundamental interactions between a host and its environment in the complete absence of any commensal or pathogenic microflora.

53. (A) Without strangers (germ-free)
The term "axenic" is derived from Greek and literally translates to "without strangers," signifying that the animal is germ-free. This microbiological status is the most restrictive, requiring rigorous sterilization procedures and continuous monitoring. Axenic models are vital for research in immunology and microbiology, as they allow for the introduction of specific, known microbes to study their individual effects on the host.

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54. (D) Harbor only a known, completely defined microflora
Gnotobiotic animals are those that harbor only a known and completely defined microflora. These animals are typically derived from axenic individuals that have been intentionally inoculated with specific, documented microorganisms. This status allows researchers to investigate the complex relationships between the host and particular microbial species under strictly controlled conditions, providing insights into gut health, immunity, and metabolic processes in rodents.

55. (B) Free only of specified pathogenic microorganisms targeted by a testing program
Specific Pathogen-Free (SPF) animals are guaranteed to be free of particular pathogenic microorganisms that are monitored through a rigorous and regular testing program. While they harbor normal commensal microflora, they are protected from common laboratory infections that could interfere with research. This status is the industry standard for most biomedical experiments, ensuring that results are not confounded by underlying subclinical diseases.

56. (C) Absence of a defined, restrictive microbial barrier
Conventional laboratory animals are characterized by the absence of a defined and

essential for studying cancer biology, evaluating the efficacy of new chemotherapeutic agents, and developing personalized medicine strategies for cancer treatment.

75. (A) I, II and IV
SCID mice are characterized by a lack of both functional T and B lymphocytes due to a mutation that impairs the V(D)J recombination process. This defect prevents the proper development of adaptive immunity. Because they cannot mount an effective immune response, they are highly susceptible to infections and are extensively used in studies involving human cell engraftment and the biology of the immune system.

76. (D) Natural killer (NK) cells
The NOD-scid gamma (NSG) mouse is an extremely immunodeficient model because it lacks T and B cells and also possesses a defect in natural killer (NK) cells. This combined deficiency results in one of the most receptive hosts for the engraftment of human cells and tissues. These mice are used in cutting-edge research involving humanized immune systems, hematopoietic stem cell studies, and complex oncology models.

77. (A) NK cells
The NIH-III mouse is an immunodeficient model that combines three different mutations to produce a animal lacking functional T cells, B cells, and natural killer (NK) cells. This triple deficiency provides a very low level of innate and adaptive immunity, making the model exceptionally useful for the long-term survival and study of xenotransplanted human tissues and for researching the role of NK cells in cancer.

78. (C) Rabbit
Polyclonal antibody production is most commonly performed using rabbits because of their relatively large size and the accessibility of their marginal ear veins for blood collection. Rabbits can provide significant volumes of antiserum and generally produce a strong immune response to various antigens. Their manageable temperament and well-documented physiology make them the preferred species for generating high-titer antibodies for research and diagnostic purposes.

79. (A) Body temperature
The classic rabbit pyrogen test evaluates the presence of fever-inducing substances by monitoring changes in the animal's body temperature. Pyrogens, such as bacterial endotoxins, cause a rapid rise in temperature when injected into the rabbit's bloodstream. This test was long the standard for ensuring the safety of parenteral drugs and medical devices, ensuring they are free from contaminants that could cause dangerous fevers in patients.

80. (A) P-4, Q-1, R-3, S-2
Different animal models are utilized for specific research areas based on their unique characteristics. The ob/ob mouse is used for obesity research, while the nude mouse is essential for xenograft tumor studies. The Spontaneously Hypertensive Rat (SHR) is a primary model for hypertension, and the guinea pig is a classic model for studying infectious diseases like tuberculosis, providing critical insights into various human conditions.

81. (A) Acute dermal and ocular irritation
The Draize test is traditionally performed on rabbits to assess the acute dermal and ocular irritation potential of various substances, including cosmetics and chemicals. The test involves applying the material directly to the skin or eyes and observing the physical response over a set period. While increasingly replaced by in vitro methods, it remains a historical reference for evaluating localized toxicity and safety of products.

82. (D) Scorbutus (Scurvy)
Guinea pigs are uniquely susceptible to developing scorbutus, or scurvy, due to their inability to synthesize Vitamin C. Without an adequate dietary supply of ascorbic acid, they cannot produce functional collagen, leading to joint pain, hemorrhages, and weakened tissues. This specific dietary requirement makes the guinea pig an excellent model for studying the physiological roles of Vitamin C and the pathology of its deficiency.

83. (C) Guinea pig
The guinea pig is commonly used in auditory research because it possesses large, accessible middle-ear bullae and exhibits the Preyer reflex, which is a visible ear-flick in response to sound. These anatomical and behavioral features

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which is derived from the P1 bacteriophage. Because loxP sites do not naturally occur in mammalian genomes, they must be intentionally inserted around the target gene. This system allows for precise control over where and when a genetic modification occurs in the animal.

66. (D) loxP sites
In the Cre-loxP recombination system, the Cre recombinase enzyme specifically recognizes 34-base-pair DNA sequences known as loxP sites. When Cre is present, it catalyzes a recombination event between two loxP sites, typically leading to the excision of the intervening DNA sequence. By "floxing" a gene with these sites, researchers can precisely control its deletion in specific cells or at chosen developmental stages.

67. (D) Tissue-specific promoter
To achieve a tissue-specific gene knock-out using the Cre-loxP system, the expression of Cre recombinase must be driven by a tissue-specific promoter. This ensures that the enzyme is only active in a particular organ or cell type, such as the liver or neurons. The target gene remains functional in all other tissues, allowing researchers to study organ-specific gene functions and avoid potential embryonic lethality.

68. (C) Profound obesity and type 2 diabetes
The ob/ob mouse model is primarily characterized by profound early-onset obesity and the development of type 2 diabetes. These animals exhibit extreme hyperphagia, a decreased metabolic rate, and various endocrine abnormalities. Because of these traits, they are widely used in research focused on obesity, insulin resistance, and the metabolic processes that contribute to the development of human metabolic syndrome and related health conditions.

69. (A) Leptin
The genetic defect in the ob/ob mouse is a mutation in the gene encoding the hormone leptin. Normally secreted by adipose tissue, leptin signals the brain to regulate energy balance and suppress appetite. The absence of functional leptin leads to uncontrolled eating and severe obesity. This discovery was a landmark in understanding the biological basis of appetite regulation and the hormonal control of body weight.

70. (D) Leptin receptor
The db/db mouse model is phenotypically similar to the ob/ob mouse, but the mutation occurs in the gene encoding the leptin receptor rather than the hormone itself. These animals produce leptin but cannot respond to its signal, leading to morbid obesity and severe diabetes. Comparing the ob/ob and db/db models has been essential for elucidating the leptin signaling pathway and its role in metabolic health.

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71. (D) Obesity and metabolic syndrome
The Zucker rat (fa/fa) is a widely recognized animal model used primarily to study obesity and metabolic syndrome. These rats possess a mutation in the leptin receptor gene, leading to hyperphagia and the rapid accumulation of adipose tissue. They are essential for researching the physiological consequences of obesity, including insulin resistance, hyperlipidemia, and hypertension, providing insights into human metabolic diseases and potential therapeutic interventions.

72. (A) Cardiovascular disease
The Spontaneously Hypertensive Rat (SHR) is predominantly used as a model for cardiovascular disease, particularly essential hypertension. These rats develop high blood pressure naturally as they age, without the need for external triggers such as high salt intake. This model is vital for testing antihypertensive drugs and for studying the genetic and physiological mechanisms that lead to chronic elevation of blood pressure in humans.

73. (C) T lymphocytes
The athymic nude mouse possesses a genetic mutation that results in the failure of the thymus to develop properly. Since the thymus is essential for the maturation of T lymphocytes, these mice are severely deficient in this cell type. This immune impairment prevents them from rejecting foreign tissues, making them indispensable in research involving immunology, oncology, and the study of human cell transplants.

74. (D) Serving as hosts for human tumor xenografts
Due to their severe T-cell deficiency, athymic nude mice are highly valuable for serving as hosts for human tumor xenografts. They do not mount a cell-mediated immune response against foreign tissue, allowing human cancer cells to grow and form tumors. This model is

and requires careful monitoring to ensure the long-term survival and productivity of the laboratory colony.

39. (B) Poiley's rotational mating
Poiley's rotational mating system is widely used to maintain outbred laboratory animal stocks while minimizing the rate of inbreeding. By systematically rotating breeding pairs across different groups or cages, the system ensures that genetic diversity is preserved over many generations. This method is essential for providing researchers with animals that represent the genetic variability found in natural, non-inbred populations.

40. (A) P-3, Q-4, R-1, S-2
Mating systems are designed to meet specific research and breeding objectives. Monogamous systems pair one male with one female, while harem systems maximize offspring per male. Brother-sister mating is used to maximize homozygosity for inbred strain development. Poiley's rotational system is specifically employed to minimize the inbreeding rate in outbred stocks, ensuring the maintenance of broad genetic variability over time.

41. (D) F
In standardized rodent nomenclature, the symbol "F" is used to denote the generation number of an inbred strain. For example, "F20" indicates that the strain has reached twenty generations of consecutive brother-sister mating. This designation is critical for researchers to verify the genetic stability and level of homozygosity of the animals used in their biomedical or genetic experiments.

42. (A) Congenic backcrossing
In standardized nomenclature, the symbol "N" represents the number of backcross generations used during the development of a congenic strain. This notation tracks how many times a donor allele has been backcrossed onto a specific recipient inbred background. Achieving a high "N" number ensures that the resulting strain is genetically identical to the recipient except for the targeted locus.

43. (B) Slash (/) and institutional code
A substrain of an inbred mouse line is indicated in nomenclature by adding a forward slash followed by a unique institutional code. For example, in the strain C57BL/6J, the "J" represents the Jackson Laboratory. This system allows researchers to identify the origin of the animals and account for potential genetic drift that may have occurred in different breeding facilities over time.

44. (B) Inbred strain C57BL/6 from Jackson Lab
The notation C57BL/6J identifies the specific inbred strain C57BL/6 that is maintained at the Jackson Laboratory. This standardized name provides essential information about the animal's genetic background and source. Using consistent nomenclature is vital for scientific communication, as it ensures that researchers worldwide are using animals with the same defined genetic characteristics for their experimental studies and comparisons.

45. (A) Both A and R are true and R is the correct explanation of A.
Outbred stocks are managed specifically to maintain high genetic variability, simulating the diversity found in natural populations. To achieve this, management practices strictly avoid continuous brother-sister mating, which would otherwise lead to increased homozygosity and reduced diversity. By employing rotational mating schemes, facilities ensure that the stock remains genetically heterogeneous, which is important for certain types of biomedical research.

46. (C) Crl:SD
An outbred stock of Sprague Dawley rats maintained by Charles River Laboratories is correctly designated as Crl:SD. In this nomenclature, the institutional code "Crl" precedes the colon, followed by the stock symbol "SD". This standardized format distinguishes outbred stocks from inbred strains and clearly identifies both the commercial source and the specific genetic background of the laboratory animals provided.

47. (D) Congenic strains
Congenic strains are genetically identical to a recipient inbred strain except for a single defined locus that has been introduced via repeated backcrossing. These strains are powerful tools for studying the specific effects of an individual gene on a standardized genetic background. They allow researchers to isolate the influence

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allow researchers to study hearing loss and ear disorders more easily than in smaller rodents. Their auditory sensitivity and well-defined ear structure provide a robust model for investigating the mechanics of hearing.

84. (C) Guinea pig
Guinea pigs are exceptionally sensitive to histamine, making them a primary model in anaphylaxis and asthma research. Exposure to allergens or histamine triggers severe bronchoconstriction and respiratory distress in these animals, closely mimicking the physiological responses seen in human allergic reactions. This heightened sensitivity allows scientists to test the efficacy of antihistamines and other respiratory treatments in a controlled and predictable laboratory setting.

85. (A) I, II and IV
Non-human primates are valuable research models due to their high phylogenetic proximity to humans and their importance in specialized neurobehavioral studies. However, they are not used for routine acute toxicity tests, which typically employ rodents or dogs first. Their use is subject to very stringent ethical and regulatory oversight, ensuring that they are only utilized when no other suitable alternative models exist for research.

86. (B) Regulatory safety pharmacology and toxicology
Beagle dogs are predominantly utilized in regulatory safety pharmacology and toxicology studies. Their predictable physiology, moderate size, and docile nature make them ideal for evaluating the safety and potential side effects of new drugs before they move into human clinical trials. They are particularly important for assessing cardiovascular and gastrointestinal safety, as their organ systems show significant similarities to those of humans in drug metabolism.

87. (B) 1960
The Prevention of Cruelty to Animals (PCA) Act in India was enacted in 1960. This landmark legislation was established to prevent the infliction of unnecessary pain or suffering on animals and to regulate various activities involving them. It serves as the foundational legal framework for animal welfare in the country, including the rules and guidelines governing the use of animals in scientific and medical research.

88. (A) Animals
Under Indian regulations, CCSEA stands for the Committee for the Control and Supervision of Experiments on Animals. This statutory body is responsible for ensuring that all animal research conducted in India is performed humanely and in accordance with established ethical standards. It oversees the registration of facilities, reviews research protocols, and monitors the welfare of animals used in scientific and educational procedures across the nation.

89. (C) Institutional Animal Ethics Committee
IAEC stands for Institutional Animal Ethics Committee. Every institution in India that conducts research involving animals is mandated by CCSEA to establish this committee. The primary role of the IAEC is to review and approve research protocols, ensuring that they adhere to the principles of the 3Rs and that animal welfare is prioritized throughout every stage of the experimental process within the organization.

90. (C) Only II
The composition of an IAEC must include specific members to ensure balanced ethical review, including a biological scientist, a scientist from another discipline, a CCSEA nominee, and a socially aware member. The requirement for veterinarians is typically one attending veterinarian rather than two. Having the correct committee structure is essential for maintaining regulatory compliance and for conducting thorough and ethical evaluations of all animal research.

91. (B) Russell and Burch
The "3Rs" principle of humane experimental technique—Replacement, Reduction, and Refinement—was first articulated by W.M.S. Russell and R.L. Burch in their 1959 book. This framework has become the global standard for ethical animal research. It encourages scientists to seek alternatives to animal use, minimize the number of animals required, and improve the welfare of those that must be used for scientific advancement.

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92. (C) Replacement
In the context of the 3Rs, replacement refers to the practice of substituting higher animal species with lower species or non-animal models. This can include using cell cultures, organoids, computer simulations, or invertebrates that are less likely to experience pain. Implementing replacement strategies is a primary ethical goal in biomedical research, aiming to reduce the overall reliance on sentient vertebrate animals for scientific discovery.

93. (B) Reduction
Using statistical methods to ensure that experiments are designed with the minimum number of animals necessary to achieve valid results is the essence of "Reduction." This principle focuses on maximizing the information gained from each animal and avoiding the unnecessary use of subjects. Proper experimental design and power analysis are critical tools for researchers to uphold this ethical standard while maintaining scientific rigor.

94. (A) Refinement
Refinement involves implementing any technique that minimizes pain, suffering, or distress and enhances animal welfare throughout their life. This includes providing appropriate analgesia, improving housing conditions with environmental enrichment, and using less invasive procedures. By focusing on refinement, researchers ensure that the welfare of animals used in experiments is maximized, leading to more reliable scientific data and more humane laboratory practices.

95. (A) Both A and R are true and R is the correct explanation of A.
Humane endpoints are established as predefined criteria to determine when an animal should be euthanized before the natural end of an experiment. This practice is essential for preventing unnecessary pain and distress once the scientific objectives have been met or if it becomes clear they cannot be achieved. Implementing these endpoints is a critical component of ethical animal research and upholds the principle of refinement.

96. (C) Carbon dioxide asphyxiation
Carbon dioxide (CO_2) asphyxiation is a conditionally acceptable euthanasia method for rodents when the chamber is gradually filled, allowing a slow displacement of air. A controlled flow rate minimizes pain and distress while ensuring humane death. Rapid filling or improper procedures can increase stress, so established animal welfare guidelines should always be followed.

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97. (A) Barbiturates
An overdose of barbiturates, such as sodium pentobarbital, is an approved pharmacological method of euthanasia for small laboratory animals. These drugs rapidly depress the central nervous system, leading to unconsciousness, respiratory arrest, and cardiac failure with minimal pain or distress. They are widely recommended because they provide a humane and reliable method of euthanasia.

98. (B) Feed and water consumption and behavioral signs of distress
Daily welfare assessment in laboratory animals primarily involves monitoring feed and water intake, body condition, activity, posture, grooming, and behavioral signs of pain or distress. Early detection of abnormal changes enables timely veterinary intervention, ensuring animal welfare, maintaining research quality, and complying with ethical standards for laboratory animal care.

99. (B) 1.5 to 2.5 years
The average life expectancy of a laboratory mouse is approximately 1.5 to 2.5 years, depending on strain, genetics, husbandry, and health status. Although some mice may live longer under ideal conditions, this range is commonly considered normal for research colonies and is important when planning experimental studies.

100. (A) Both A and R are true and R is the correct explanation of A.
Guinea pigs have a relatively long gestation period of about 59–72 days, resulting in the birth of precocial young that are fully furred, have open eyes, and are capable of movement soon after birth. Thus, both the assertion and reason are true, and the reason correctly explains the assertion.

101. (B) Hairless, blind, and dependent
The newborn young of mice and rats are altricial, meaning they are born hairless, blind, deaf, and completely dependent on their mother for warmth, nutrition, and care. Their eyes open and fur develops several days after birth, unlike

precocial species such as guinea pigs, which are relatively mature at birth.

102. (B) 39–49%
The normal hematocrit (packed cell volume) of a healthy laboratory mouse ranges from 39% to 49%. Hematocrit reflects the proportion of red blood cells in blood and is an important indicator of oxygen-carrying capacity, hydration status, anemia, and overall health during laboratory animal monitoring.

103. (C) 80–200 breaths per minute
A healthy laboratory mouse normally has a respiratory rate of approximately 80–200 breaths per minute, varying with age, activity, stress, and environmental temperature. Monitoring respiration is an essential component of health assessment, anesthesia monitoring, and evaluation of physiological status in laboratory animal research.

104. (C) Rabbit
The rabbit is an induced ovulator, meaning ovulation occurs only after mating rather than during a regular estrous cycle. If mating does not occur, rabbits may remain in a prolonged period of estrus. This reproductive characteristic distinguishes them from spontaneous ovulators such as mice, rats, and hamsters.

105. (A) P-1, Q-2, R-3, S-4
The correct diploid chromosome numbers are: Mouse = 40 ($2n = 40$), Rat = 42 ($2n = 42$), Rabbit = 44 ($2n = 44$), and Dog = 78 ($2n = 78$). These chromosome numbers are fundamental cytogenetic characteristics and are widely used in genetics, breeding, and biomedical research involving laboratory animals.

106. (D) Pigment distribution in hair shafts
The dilute (d) locus in mice affects pigment distribution within hair shafts rather than pigment synthesis. Mutations at this locus alter melanosome transport, producing diluted coat colors instead of normal pigmentation. Thus, the gene influences the intensity and appearance of coat color by modifying pigment deposition.

107. (B) H-2
The H-2 complex is the major histocompatibility complex (MHC) of the mouse and is located on chromosome 17. It contains genes involved in antigen presentation and immune responses and plays a crucial role in transplantation studies, disease susceptibility, and immunological research using mouse models.

108. (B) 14–16%
A pelleted maintenance diet for healthy adult laboratory mice generally contains 14–16% crude protein, providing adequate nutrition without promoting excessive growth. Balanced levels of protein, carbohydrates, fats, vitamins, and minerals help maintain normal body weight, reproduction, and physiological function in non-breeding animals.

109. (D) Diet-induced obesity and metabolic syndrome
High-fat diets, often containing up to 60% of calories from fat, are commonly used to create diet-induced obesity and metabolic syndrome models in rodents. These models help researchers investigate obesity, insulin resistance, type 2 diabetes, fatty liver disease, and cardiovascular disorders, as well as evaluate potential therapeutic interventions.

110. (C) Low relative humidity (below 40%)
Ringtail in suckling rats is primarily associated with low relative humidity (below 40%). Dry environmental conditions cause constriction of the tail, leading to swelling, necrosis, and possible tail loss. Maintaining appropriate humidity levels is therefore an important aspect of laboratory animal husbandry and welfare.

111. (A) Primary enclosure or cage
The micro-environment refers to the conditions inside the animal's primary enclosure or cage, including temperature, humidity, airflow, bedding, ammonia concentration, and light exposure. These factors directly affect animal health, behavior, and experimental outcomes, making careful cage management essential in laboratory animal facilities.

112. (B) Within the animal holding room itself
The macro-environment refers to the overall conditions within the animal holding room, including ambient temperature, humidity, ventilation, lighting, and noise. These environmental factors influence the cage micro-environment and are carefully controlled to maintain animal welfare, experimental consistency, and biosecurity in laboratory facilities.

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many times the total volume of air in the room is replaced each hour. High ACH rates are necessary to control odors, regulate temperature and humidity, and ensure the removal of airborne contaminants, which is vital for maintaining a healthy and stable environment.

169. (C) Causes pain; restricted to neonates
A significant disadvantage of toe-clipping for identification is that it involves the removal of tissue and can cause pain to the animal. Consequently, its use is generally restricted to neonatal rodents before seven days of age and requires strong ethical justification. Modern research facilities often prefer less invasive methods, such as ear tagging or microchipping, to minimize distress and uphold animal welfare standards.

170. (B) Stainless steel or special alloys
Ear tags used for rodent identification are typically made of stainless steel or specialized non-corrosive alloys. These tags are durable, permanent, and etched with unique numbers for easy identification. When applied correctly to the pinna, they cause minimal discomfort and stay in place for the life of the animal. They are a reliable and widely used method for individual tracking in research colonies.

171. (A) One male and one female
A monogamous breeding pair is configured with one male and one female housed together. This system allows for the accurate tracking of parentage and is ideal for strains with low fertility or poor maternal care. It is also the standard method for maintaining inbred lines through continuous brother-sister mating, ensuring that every pup can be traced back to its specific biological parents and generation.

172. (B) Successful copulation
The presence of a vaginal plug in a mouse is a definitive indicator of successful copulation. Formed from secretions from the male's coagulating glands, the plug typically remains in the vagina for several hours after mating. Researchers use the detection of a plug, often checked early in the morning, to determine the first day of pregnancy, which is essential for timing developmental and embryological studies.

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173. (B) Removing the male before parturition
A non-intensive breeding scheme is characterized by removing the male before parturition. This prevents the female from being bred during her postpartum estrus, giving her a period of rest between litters. While this system produces fewer offspring over time compared to intensive breeding, it may be preferred for certain strains to ensure the health of the dam or to strictly control the timing of pregnancies.

174. (B) Heterosis (Hybrid vigor)
Heterosis, or hybrid vigor, refers to the superiority in health, growth, and reproductive capacity of outbred hybrid offspring compared to their inbred parents. This phenomenon occurs because the crossing of two different inbred strains masks deleterious recessive alleles and increases overall genetic fitness. Hybrid rodents are frequently used in research because they combine the genetic uniformity of their parents with enhanced robustness and vitality.

175. (B) Inbred A x Inbred B → F1 → F2 → Continuous brother-sister mating
The creation of a recombinant inbred strain follows a specific sequence: crossing two different inbred strains to produce an F1 generation, intercrossing those to produce an F2, and then performing at least twenty generations of continuous brother-sister mating. This process fixes a unique mosaic of the parental genomes into a stable, homozygous line. These strains are indispensable for complex genetic mapping and quantitative trait studies.

176. (C) Selection index
A selection index involves ranking animals based on a mathematical score that incorporates multiple distinct traits. This allows breeders to choose individuals that offer the best overall combination of desirable characteristics, such as high fertility and rapid growth. By weighting traits according to their economic or scientific importance, the selection index provides an objective and efficient method for making genetic progress in a breeding population.

177. (B) The genetically monitored core population used strictly to supply breeding stock
The "foundation colony" refers to the genetically monitored core population that is used strictly to supply breeding stock for an entire facility. These animals are managed with the highest

animals belong to a specific branch or version of the C57BL/6 line. This naming convention is vital for tracking the origin and potential genetic drift of laboratory colonies.

123. (B) BALB strain, substrain c/An, from NIH
The nomenclature BALB/cAnN indicates that the mouse belongs to the BALB strain, specifically the "c" substrain developed by Andervont, and is maintained at the National Institutes of Health. Standardized names like this provide clear information about the animal's genetic history and institutional source. This precision is necessary for researchers to ensure they are using the correct genetic model for their specific experiments.

124. (C) 10
In the creation of a congenic strain, the donor allele is transferred to the genetic background of a recipient strain through a minimum of ten backcross generations. This process ensures that approximately 99.9 percent of the recipient's genome is recovered, with only the targeted locus from the donor remaining. These strains are essential for isolating and studying the effects of individual genes in research.

125. (B) I, II and III
Congenic strains differ from their background strain at a single locus or small chromosomal region, achieved through repeated backcrossing. They are used to study the effect of specific genes on a standardized genetic background, ensuring that observed phenotypic differences are due to the targeted gene. These models are not produced by random mutation but through careful, systematic breeding programs over many generations.

126. (B) BXD
Recombinant inbred strains derived from a cross between C57BL/6J and DBA/2J are commonly designated by the prefix "BXD." This nomenclature identifies the two progenitor strains used to create the lines. The "B" stands for C57BL/6J and the "D" for DBA/2J. These strains are powerful tools for genetic mapping and for studying the inheritance of complex, polygenic traits in laboratory mice.

127. (C) Axenic
Axenic animals require housing within positive-pressure sterile isolators and must be provided with strictly sterilized feed, water, and bedding. This extreme level of isolation is necessary to maintain their germ-free status. These animals are used in specialized studies to understand the fundamental biological processes of a host without any interference from microorganisms, making them essential for certain types of immunology research.

128. (C) Gnotobiotic
If an axenic animal is intentionally inoculated with a known cocktail of specific bacteria, its microbiological status changes to gnotobiotic. This term refers to animals that have a completely defined and known microflora. Gnotobiotic models allow researchers to study the specific effects of individual bacterial species or defined microbial communities on the health, immunity, and development of the host animal in a controlled environment.

129. (C) Specific Pathogen-Free (SPF)
Barrier facilities are primarily designed to maintain the status of Specific Pathogen-Free (SPF) animal colonies. These facilities use physical barriers, specialized ventilation, and strict entry protocols to prevent the introduction of specific microorganisms that could cause disease or interfere with research. Maintaining an SPF environment is essential for ensuring the health of the animals and the reliability of the scientific data produced in experiments.

130. (C) Accumulation of spontaneous random mutations over time
Genetic drift in an isolated inbred colony is primarily driven by the accumulation of spontaneous random mutations over time. Even in a strictly managed colony, small genetic changes occur naturally in each generation. If these mutations become fixed in the population, they can lead to the emergence of new substrains. Regular genetic monitoring is required to detect these changes and maintain the strain's integrity.

131. (C) Permanent acceptance of the graft
In genetic monitoring, orthotopic skin grafting between mice of the same well-established inbred strain should theoretically result in permanent acceptance of the graft. Because the donor and recipient are genetically identical, the recipient's immune system does not recognize the tissue as foreign. This lack of rejection confirms the genetic

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pressure environment and ensure that no external contaminants enter the animal's space. This level of isolation is mandatory for maintaining the germ-free status of axenic colonies and for conducting research that requires complete control over the animal's microbial environment.

187. (C) Autoclaving or gamma irradiation
Sterilization of feed for axenic and gnotobiotic animals is most commonly achieved through autoclaving or gamma irradiation. These processes ensure that all microorganisms, including spores, are eliminated from the diet. Because high heat can damage vitamins, diets for these animals are often over-fortification to compensate for nutritional losses. Maintaining sterile feed is a cornerstone of husbandry for animals housed in isolators or highly controlled barrier environments.

188. (A) Unintentional genetic contamination or drift
Routine genetic monitoring of inbred strains aims to detect unintentional genetic contamination or drift within the colony. Even in well-managed facilities, spontaneous mutations or accidental crossbreeding can occur, potentially compromising the genetic integrity of the strain. By regularly screening for specific genetic markers, researchers can ensure that the animals remain genetically consistent and that experimental data continues to be reliable and comparable over long periods.

189. (D) Single Nucleotide Polymorphism (SNP) array testing
Single Nucleotide Polymorphism array testing is a modern, PCR-based method utilized for high-throughput genetic monitoring in laboratory animal facilities. It allows for the simultaneous analysis of thousands of genetic markers across the genome, providing a detailed and accurate profile of each animal's background. This technology is more efficient and provides higher resolution than traditional biochemical or immunological assays, making it the preferred tool for maintaining strain purity.

190. (D) Ossification increases pain and risk
Tail tip amputation for DNA collection is usually restricted to mice under twenty-one days of age because increasing ossification of the vertebrae makes the procedure more painful and increases the risk of complications as the animal grows. In young pups, the tissue is softer and heals more rapidly. For older animals, less invasive methods such as ear punches or buccal swabs are preferred to minimize distress and comply with welfare standards.

191. (B) Randomly into the genome
A transgenic mouse created via pronuclear injection typically has the transgene integrated randomly into the genome. The location and number of copies can vary between different founder animals, leading to different levels of gene expression. This random integration is a key characteristic of the method and requires researchers to carefully characterize multiple lines to identify the one that best suits their specific experimental needs and scientific objectives.

192. (A) Embryonic stem (ES) cells
Creating a targeted gene knock-out traditionally requires the use of embryonic stem cells. These cells are genetically modified in culture through homologous recombination to disrupt a specific gene. The modified ES cells are then injected into a host blastocyst to create chimeric mice. This sophisticated technology allows for the precise deletion of any gene, providing a powerful way to study gene function and model human genetic disorders.

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193. (A) Highly efficient, targeted double-strand DNA breaks for precise gene editing
The CRISPR/Cas9 system has revolutionized mouse genetics by enabling highly efficient, targeted double-strand DNA breaks that allow for precise gene editing. This technology is faster and more versatile than traditional ES cell methods, making it possible to create knock-outs, knock-ins, and complex genetic modifications directly in the embryo. Its adoption has dramatically accelerated the production of genetically modified animal models for biomedical research worldwide.

194. (D) Transgenic
In the nomenclature of a genetically modified animal, the designation "Tg" indicates that the animal is transgenic. This symbol is followed by information about the promoter and the gene that has been introduced into the genome. Clear nomenclature is vital for distinguishing between different types of genetic modifications, such as knock-outs and transgenics, ensuring that researchers can accurately identify and

141. (A) Foxn1
The genetic mutation causing the athymic nude phenotype in mice is located in the Foxn1 gene. This gene is essential for the proper development of both the hair follicles and the thymus. Consequently, mice with this mutation are hairless and lack a functional thymus, resulting in a severe deficiency of T lymphocytes and making them ideal hosts for xenotransplantation and immunology research.

142. (C) Prkdc
Severe Combined Immunodeficiency (SCID) in the classic SCID mouse model is caused by a spontaneous mutation in the Prkdc gene. This gene encodes a protein kinase essential for the V(D)J recombination process, which is necessary for the maturation of T and B cells. The absence of this enzyme results in a complete lack of functional adaptive immunity, making these mice highly vulnerable to infection.

143. (C) NOD-scid gamma (NSG) mouse
The NOD-scid gamma (NSG) mouse is preferred for the engraftment of human hematopoietic stem cells because of its extreme immunodeficiency. It lacks T, B, and natural killer (NK) cells, and has additional defects in innate immunity. This highly receptive environment allows human cells to survive and proliferate more effectively than in other models, facilitating advanced studies in human immunology and stem cell biology.

144. (C) Lipid metabolism profile resembling humans
Rabbits are excellent models for studying hypercholesterolemia and atherosclerosis because their lipid metabolism profile closely resembles that of humans. When fed a high-cholesterol diet, they rapidly develop arterial lesions and atherosclerotic plaques similar to those seen in human cardiovascular disease. Their size also allows for easier surgical procedures and imaging studies, making them indispensable for research into heart disease and potential treatments.

145. (A) Both A and R are true and R is the correct explanation of A.
The guinea pig is considered a premier model for infectious tuberculosis research because it is highly susceptible to human strains of Mycobacterium tuberculosis. When infected, these animals develop granulomatous lesions that are pathologically similar to those found in human patients. This close similarity allows researchers to study the progression of the disease and test the effectiveness of new vaccines and treatments.

146. (B) Cosmetics and topical chemicals
In the classic Draize test utilizing rabbits, cosmetics and topical chemicals are typically evaluated for their potential to cause irritation or damage to the skin and eyes. The test provides a standardized method for assessing the safety of products before they are released for human use. Although controversial and increasingly replaced by non-animal alternatives, it historically served as a primary safety assessment in toxicology.

147. (B) Beagle dog
Safety pharmacology guidelines often require pre-clinical testing in a non-rodent model, and the Beagle dog is predominantly chosen for this role. Their size allows for sophisticated cardiovascular and respiratory monitoring, providing data that is highly relevant to human safety. Beagles are preferred due to their cooperative nature, consistent health status, and the extensive historical data available on their physiological responses to various compounds.

148. (B) Immune systems highly homologous to humans
Non-human primates, such as Rhesus macaques, are crucial for testing vaccines against human-specific viruses because their immune systems are highly homologous to those of humans. This similarity means they are likely to show comparable responses to vaccines and infections. Their use is particularly important for studying viruses that do not naturally infect other laboratory species, providing critical data for the development of life-saving medical interventions.

149. (A) Institutional Animal Ethics Committee (IAEC)
The Institutional Animal Ethics Committee is the authority responsible for approving and monitoring animal research protocols within an institution in India. The IAEC ensures that all experiments are ethically justified and comply with national guidelines for animal welfare. Their oversight is essential for maintaining high standards of care and for ensuring that the use of animals in research is conducted responsibly.

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113. (B) 99
A standardized ear-punching identification system assigns combinations of holes or notches in the pinna, allowing up to 99 uniquely identifiable animals. This inexpensive and permanent identification method is widely used in laboratory rodents for colony management, breeding records, and accurate tracking of experimental animals.

114. (B) Lineage, generational numbers, and matings
A pedigree chart for an inbred laboratory animal colony records lineage, generations, parentage, and mating history. Accurate pedigree records help maintain genetic integrity, prevent accidental outcrossing, monitor inheritance of traits, and ensure the reliability and reproducibility of research involving genetically defined animal strains.

115. (A) I and II
In polygamous breeding, one male is housed with multiple females, making it more space-efficient than monogamous breeding because fewer cages are required per female. However, unless pregnancies are carefully monitored or females are separated before parturition, determining the exact parentage of every offspring is more difficult.

116. (B) In the continuous presence of the male
Under intensive breeding systems for rodents, parturition typically occurs in the continuous presence of the male. This arrangement allows for mating to take place during the postpartum estrus, which occurs shortly after birth. By maintaining the breeding pair together, the production cycle is maximized, leading to more frequent litters and a higher overall output of offspring within the breeding colony.

117. (B) Continuous variation and polygenic inheritance
Quantitative traits in laboratory animals, such as body weight and litter size, are characterized by continuous variation and polygenic inheritance. These traits are influenced by the combined effects of multiple genes and environmental factors, rather than a single gene. Because they show a range of values rather than distinct categories, they require statistical methods for analysis and are fundamental to studies of genetics.

118. (D) Selection differential
In genetic response estimation, the "response to selection" is mathematically defined as the product of heritability and the selection differential. The selection differential represents the difference between the mean of the selected parents and the mean of the entire population. Understanding this relationship allows breeders to predict the genetic progress that can be achieved in a population over successive generations of targeted breeding.

119. (C) 98.6%
After twenty generations of consecutive brother-sister mating, the theoretical expected percentage of homozygosity in an inbred strain reaches approximately 98.6 percent. This high level of genetic uniformity means that individuals within the strain are virtually identical at all genetic loci. Such strains are essential for biomedical research because they minimize experimental variability and allow for consistent results across different laboratories and studies.

120. (C) Inbreeding depression
Inbreeding depression is a consequence frequently observed during the early generations of creating a new inbred strain. This decline in reproductive performance and general vigor occurs because deleterious recessive alleles become homozygous and are expressed. Not all lines survive this phase, but those that do become stable inbred strains with high genetic uniformity, which are valuable for consistent and reproducible experimental research in various fields.

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121. (A) 1%
To appropriately manage an outbred stock, breeding schemes should ideally keep the coefficient of inbreeding from rising more than one percent per generation. Maintaining a low rate of inbreeding ensures that the genetic variability of the population is preserved over time. This is critical for providing researchers with animals that accurately represent the genetic heterogeneity found in broader, non-inbred natural populations.

122. (C) Forward slash (/)
Under the international standardized nomenclature for mice, a forward slash is the symbol used to separate the main strain name from the substrain designation. For example, in "C57BL/6J," the slash indicates that the

duration results in the birth of precocial young that are fully furred with open eyes and functional teeth. This contrast with the altricial young of mice and rats makes the guinea pig a unique and valuable model for specific developmental and reproductive studies.

160. (B) 30-32 days
The gestation period of a rabbit is typically thirty to thirty-two days. This relatively short pregnancy, combined with their ability to produce large litters, makes them efficient for reproductive and developmental research. Monitoring the pregnancy closely is important, as rabbits are sensitive to environmental stress which can impact the health of the doe and the survival of the kits during the neonatal period.

161. (B) 8-12
A typical litter size for a mature female laboratory rat is eight to twelve pups. This high reproductive output is a significant advantage for large-scale studies and colony maintenance. Rats are attentive mothers, and their ability to successfully rear large litters is essential for providing sufficient numbers of offspring for various research needs, ranging from behavioral studies to complex physiological experiments.

162. (B) 4-5 days
The estrous cycle length in both mice and rats is typically four to five days. This rapid cycle allows for frequent opportunities for mating and is a major factor in the high reproductive efficiency of these rodents. Understanding the stages of the cycle through vaginal cytology is crucial for researchers who need to time matings or study hormone-dependent physiological processes in females.

163. (A) Delayed implantation during lactation
Facultative diapause in mice refers to the phenomenon of delayed embryonic implantation that occurs when a female is mated during her postpartum estrus while still lactating a previous litter. The metabolic demands of nursing stimulate hormones that temporarily pause the development of the new embryos. This mechanism allows the female to balance the energy required for current and future offspring, extending gestation.

164. (C) Carbohydrates
Carbohydrates usually constitute the highest percentage of macro-nutrients in a standard pelleted rodent diet, providing the primary source of energy. These are typically derived from cereal grains such as corn, wheat, and oats. A balanced ratio of carbohydrates, proteins, and fats is essential for maintaining the health, growth, and reproductive performance of laboratory animals throughout their life in a research facility.

165. (B) To prevent degradation of essential thermolabile vitamins
Pelleted diets must be managed strictly regarding shelf-life to prevent the degradation of essential thermolabile vitamins. Over time, vitamins like C and A can lose their potency, leading to nutritional deficiencies in the animals. Proper storage in cool, dry conditions and adhering to manufacturer expiration dates are critical practices for ensuring that the nutritional integrity of the feed is maintained for the animals.

166. (B) Allow personnel to perform duties while preventing phototoxic retinopathy in albino animals
A light level of 325 lux at one meter above the floor is recommended for rodent rooms to provide sufficient visibility for personnel while protecting albino animals from phototoxic retinopathy. Because albino rodents lack pigment in their eyes, they are highly sensitive to bright light, which can cause permanent retinal damage. Maintaining appropriate lighting intensity is therefore essential for both human safety and animal welfare.

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167. (B) Prevent the transmission of airborne particulate matter and microbes
Micro-isolation cages are equipped with a filter top designed to prevent the transmission of airborne particulate matter and microorganisms between the cage and the room environment. This creates a protected micro-environment for the animals, reducing the risk of cross-contamination and the spread of pathogens. These cages are fundamental in barrier facilities for maintaining the health status of SPF or immunocompromised rodent colonies.

168. (B) Air Changes per Hour (ACH)
Air Changes per Hour is a direct measure of macro-environmental ventilation efficiency in an animal holding room. It indicates how

150. (C) Modifying experimental procedures to minimize pain and distress
According to the 3Rs principle, "Refinement" is defined as modifying experimental procedures to minimize pain, suffering, and distress throughout the life of the animal. This includes providing better housing, using analgesia, and employing less invasive techniques. Refinement aims to improve animal welfare and ensure that scientific results are not confounded by the physiological effects of stress or untreated pain in subjects.

151. (A) Humane endpoint
Establishing a humane endpoint involves identifying the earliest clinical signs that predict a severe outcome and euthanizing the animal before significant suffering occurs. This practice is a key component of refinement in animal research. It ensures that the scientific goals are achieved while minimizing the duration and intensity of pain or distress experienced by the animals during the course of an experiment.

152. (C) Exsanguination of conscious animals
Exsanguination of conscious animals is considered an unacceptable method of euthanasia because it causes significant pain and distress. For euthanasia to be humane, the animal must first be rendered unconscious through anesthesia or another approved method. Standard protocols emphasize the rapid loss of consciousness and the prevention of any perception of pain during the final stages of the euthanasia procedure in laboratory animals.

153. (B) Microwave irradiation to the head
Focused microwave irradiation to the head is a specialized physical method of euthanasia used to preserve rodent brain chemistry. By rapidly denaturing enzymes, it prevents the post-mortem degradation of metabolites, allowing for accurate neurochemical analysis. This method requires specific, high-power equipment designed for research and must be performed correctly to ensure immediate loss of consciousness and a rapid, humane death for the animal.

154. (B) 2.5 to 3.5 years
The standard lifespan of a laboratory rat under controlled conditions is approximately 2.5 to 3.5 years. This relatively short life expectancy allows researchers to conduct studies on aging and long-term chronic conditions within a reasonable timeframe. Maintaining rats in a stable, pathogen-free environment with proper nutrition ensures they reach their full biological potential, providing consistent and reliable data for various longitudinal studies.

155. (B) P-3, Q-2, R-1, S-4
Laboratory animals have distinct physiological and reproductive features that define their use in research. Mice form precopulatory plugs, while guinea pigs require dietary Vitamin C. Rabbits are induced ovulators, and dogs possess seventy-eight chromosomes. Recognizing these unique characteristics is essential for proper husbandry, breeding management, and selecting the most appropriate animal model for specific biomedical or genetic experimental investigations.

156. (B) Melanin pigment
An albino coat in rodents is technically defined as the complete lack of melanin pigment throughout the body, including the skin, hair, and eyes. This condition is typically caused by a recessive mutation at the C locus, which prevents the production of the enzyme tyrosinase. Albinism is a common trait in many standardized laboratory strains, such as BALB/c mice and Wistar rats.

157. (C) 12 to 15 years
The life expectancy of a healthy Beagle dog in a laboratory setting can be up to twelve to fifteen years. This long lifespan allows for extensive long-term safety and toxicity studies. Proper veterinary care, socialization, and environmental enrichment are essential for maintaining their health and well-being throughout their life, ensuring they remain robust and reliable models for clinical and pharmacological research programs.

158. (C) 63 days
The gestation period of a Beagle dog is approximately sixty-three days. This duration is consistent across most breeds and allows for predictable timing of litters in a breeding colony. Accurate knowledge of this period is necessary for prenatal care, planning for parturition, and managing the health of both the dam and the puppies in facilities that maintain their own breeding populations.

159. (D) Guinea pig
Among common laboratory species, the guinea pig has the longest gestation period, ranging from fifty-nine to seventy-two days. This extended

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level of scrutiny to ensure genetic purity and health. By maintaining a separate foundation colony, facilities can prevent genetic drift and contamination in their larger production and experimental populations, ensuring long-term consistency in research.

178. (B) It is reduced to near zero
After twenty generations of continuous brother-sister mating, the genetic variance within an inbred strain is reduced to near zero. Because the animals have become homozygous at almost every locus, they are genetically identical. This lack of variation is the primary reason inbred strains are used in research, as it ensures that any observed differences in experimental outcomes are due to the treatment rather than genetic diversity.

179. (C) Outbred stocks
Poiley's system and the Maximum Avoidance of Inbreeding system are designed specifically for the management of outbred stocks. These rotational mating schemes ensure that genetic diversity is maintained and that the rate of inbreeding is kept to a minimum. By systematically avoiding the mating of close relatives, these systems preserve the broad genetic base that is characteristic of outbred populations used in biomedical and toxicological research.

180. (A) SW
The outbred stock of mice commonly referred to as "Swiss Webster" is correctly abbreviated in nomenclature as SW. These animals are widely used in research due to their rapid growth, high fertility, and overall vigor. As an outbred stock, they provide a genetically diverse background that is useful for general toxicity testing and for studies where a representative mammalian response is more important than genetic uniformity.

181. (A) B6D2F1
Standardized nomenclature designates an F1 hybrid of a C57BL/6J mother and a DBA/2J father as B6D2F1. The first part of the name indicates the maternal strain (B6 for C57BL/6), followed by the paternal strain (D2 for DBA/2), and finally the generation (F1). This naming convention is essential for clearly identifying the specific genetic background of hybrid animals used in research and ensuring experimental reproducibility.

182. (B) Coisogenic strain
A coisogenic strain is created when a mutation occurs within an already highly inbred strain, resulting in animals that differ from the parent line at only that single modified locus. Because the background is identical, any phenotypic differences can be directly attributed to the new mutation. Coisogenic strains are extremely valuable for studying gene function and the biological impact of specific mutations without the need for extensive backcrossing.

183. (B) Transfer a gene to a standard background
The primary aim of the backcross breeding technique is to transfer a specific gene or mutation from a donor animal onto a standard inbred background. By repeatedly mating offspring that carry the target gene back to the recipient inbred strain, the researcher eventually creates a congenic strain. This allow for the precise study of a gene's effect within a controlled and uniform genetic environment.

184. (C) Have undefined microflora and no strict barrier
Conventional animals differ from SPF animals because they have an undefined microflora and are housed without a strict microbial barrier. While they are generally healthy, they may carry various environmental microorganisms that could interfere with sensitive experiments. Conventional housing is suitable for basic research and teaching where the high costs and rigorous protocols of a barrier or SPF facility are not necessary for the scientific objectives.

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185. (A) II, IV, III, I
Microbiological statuses are ordered from most to least sterile as: Axenic, Gnotobiotic, SPF, and Conventional. Axenic animals are completely germ-free, while gnotobiotic animals have a defined flora. SPF animals are free of specific pathogens, and conventional animals have an undefined microflora. Understanding these levels is critical for choosing the appropriate animal model based on the requirements of the research and the need for microbial control.

186. (A) Sealed flexible film isolator with half-suits or gloves
A sealed flexible film isolator equipped with half-suits or gloves is used to safely manipulate axenic animals without breaking the sterile barrier. These systems maintain a positive-

uniformity and purity of the inbred colony, making it a classic test for strain consistency.

132. (B) Amplify and analyze specific DNA markers like microsatellites or SNPs
The polymerase chain reaction (PCR) is utilized in genetic monitoring primarily to amplify and analyze specific DNA markers such as microsatellites or single nucleotide polymorphisms. This high-sensitivity technique allows for the rapid detection of genetic variation or contamination within a colony using very small tissue samples. PCR-based methods have largely replaced more traditional immunological assays due to their speed, accuracy, and throughput.

133. (A) Carry integrated foreign germline DNA
Transgenic animals are fundamentally distinct because they carry integrated foreign DNA in their germline, which was introduced through genetic engineering. This modification is present in every cell and can be passed on to offspring. This technology allows scientists to create models that overexpress specific genes or express genes from other species, providing insights into gene function and human diseases in a living system.

134. (B) Pronuclear microinjection of oocytes
Pronuclear microinjection of oocytes is the traditional method used to introduce foreign DNA into a mouse embryo to create a transgenic founder. In this procedure, the DNA is injected directly into one of the pronuclei of a fertilized egg. The integrated DNA then replicates along with the host genome, resulting in a transgenic animal that can be used to establish a new breeding line.

135. (A) I, II and IV
Knock-out mice are created using embryonic stem cell technology or CRISPR/Cas9 to disable a specific target gene. They are a type of genetically modified organism that allows researchers to study the consequences of losing gene function. While some knock-outs may result in embryonic lethality, many do not, and they are essential tools for understanding physiological processes and disease mechanisms in mammals.

136. (C) Bacteriophage P1
The Cre recombinase enzyme is originally derived from the P1 bacteriophage. It is a site-specific recombinase that recognizes loxP DNA sequences. When used in mammalian genetics, Cre allows for the precise manipulation of DNA, such as the deletion or inversion of specific gene segments. This tool has been fundamental in developing sophisticated, conditional genetic models where gene function can be controlled.

137. (B) Inducible Cre model
An inducible Cre model refers to mice genetically engineered to express Cre recombinase only when triggered by a specific drug, such as tamoxifen. This system provides temporal control over gene deletion, allowing researchers to study the effects of a mutation in adult animals while avoiding potential issues with embryonic development. This flexibility is crucial for investigating gene functions that change throughout the lifespan.

138. (A) Hyperphagia resulting from leptin deficiency
The ob/ob mouse develops severe obesity primarily due to hyperphagia caused by a complete deficiency of the hormone leptin. Without leptin's signal to suppress appetite and increase energy expenditure, these mice consume excessive amounts of food. This model has been instrumental in studying the hormonal regulation of hunger and the physiological pathways that lead to obesity and its associated metabolic complications.

139. (C) Zucker (fa/fa)
The Zucker rat (fa/fa) is analogous to the db/db mouse as it exhibits a mutation in the leptin receptor gene, leading to marked obesity. These animals are hyperphagic and develop severe metabolic syndrome, including insulin resistance and hyperlipidemia. The Zucker rat is a classic model in metabolic research, providing a larger vertebrate system for studying the complex pathophysiology of obesity and type 2 diabetes.

140. (D) Spontaneously Hypertensive Rat (SHR)
The Spontaneously Hypertensive Rat (SHR) is the most appropriate model for testing a novel antihypertensive drug. These rats naturally develop high blood pressure that closely mimics human essential hypertension. Their predictable and stable hypertensive phenotype allows researchers to evaluate the efficacy and safety of new medications in reducing blood pressure and preventing the cardiovascular complications associated with chronic hypertension in a living system.

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communicate the specific models used in their studies.

195. (A) Both A and R are true and R is the correct explanation of A.
Inducible gene-targeting systems like Cre-loxP are essential for studying genes whose systemic knock-out would normally result in embryonic lethality. These systems allow researchers to delay the deletion of the target gene until the animal has reached adulthood or to restrict the deletion to a specific tissue. This provides a way to investigate the role of essential genes in mature physiological processes and complex disease states in vivo.

196. (B) Phenotypically lean and healthy
The "ob" mutation in the ob/ob mouse is autosomal recessive, meaning that heterozygous carriers of the mutation are phenotypically lean and healthy. These animals possess one functional copy of the leptin gene, which is sufficient to maintain normal appetite and energy balance. Only homozygous individuals, who lack both functional copies, develop the characteristic profound obesity and metabolic abnormalities that define the ob/ob model used in metabolic research.

197. (A) Wistar Kyoto (WKY)
The Spontaneously Hypertensive Rat (SHR) was selectively bred from the Wistar Kyoto ancestral outbred strain. Researchers identified individuals with naturally higher blood pressure and consistently mated them to fix the hypertensive trait. The resulting SHR line is now a standard model for human essential hypertension, while the WKY strain serves as its genetically related, normotensive control for comparative studies in cardiovascular physiology and pharmacology.

198. (B) Zucker Diabetic Fatty (ZDF) rat
An investigator requiring a rat model that exhibits both massive obesity and insulin resistance should use the Zucker Diabetic Fatty rat. Unlike the standard Zucker rat, which is obese but often remains normoglycemic, the ZDF strain consistently develops type 2 diabetes as it ages, particularly when fed a specialized diet. This makes it a superior model for studying the progression and complications of diabetes in the context of obesity.

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199. (A) Thymic aplasia
The lack of hair in the athymic nude mouse is genetically linked to the mutation that causes thymic aplasia. Both the hair follicles and the thymus require the Foxn1 gene for proper development. This unique combination of traits makes the nude mouse a double-mutant phenotype that is easily identified visually and provides a specialized immunological environment for xenograft studies where cell-mediated immunity must be absent.

200. (D) Cell-mediated immunity
Because athymic nude mice lack functional T cells, they cannot mount a cell-mediated immune response. This type of immunity is essential for rejecting foreign tissue grafts and for defending against certain intracellular pathogens. The absence of cell-mediated responses is the primary reason these mice are used as hosts for human tumor xenografts and for studying the interactions between the immune system and cancer or foreign transplants.

201. (A) SCID
The SCID mouse model lacks both T and B cells and is commonly utilized to study the biology of human tumors. Because their adaptive immune system is completely non-functional, they are excellent hosts for human tissue transplants, including cancer cells and immune system components. Their use has been fundamental in developing humanized mouse models that allow for the study of human diseases and treatments in a living mammalian system.

202. (A) Non-Obese Diabetic
In the name NOD-scid gamma (NSG), "NOD" stands for Non-Obese Diabetic. This background strain possesses unique innate immune characteristics, such as reduced macrophage activity and a lack of hemolytic complement. These traits, when combined with the SCID and gamma chain mutations, make the NSG mouse an exceptionally receptive model for human cell engraftment, leading to higher success rates in creating humanized mice for biomedical research.

203. (D) Guinea pig
The guinea pig has been historically vital for the study of scurvy because of its inability to synthesize Vitamin C. Like humans, they must obtain this vitamin from their diet. This shared metabolic trait allowed early researchers to use

the results of years of research. Facilities use strict breeding protocols and regular genetic monitoring to prevent and detect contamination, ensuring that the animals remain genetically defined and pure.

254. (B) Can be easily multiplexed and automated for high-throughput analysis using microarrays
A major advantage of using SNPs over microsatellites for genetic monitoring is that SNPs can be easily multiplexed and automated for high-throughput analysis. Modern microarray technology allows researchers to screen thousands of SNP markers simultaneously with high accuracy. This efficiency makes SNP genotyping the preferred method for large-scale genetic quality control, providing a rapid and detailed way to verify the background and purity of laboratory animal strains with minimal effort and cost.

255. (A) P-1, Q-2, R-3, S-4
Genetically modified models are defined by their specific alterations: transgenic mice have an added foreign gene, while knock-outs have a disabled endogenous gene. Knock-ins involve the targeted replacement of a sequence, and conditional knock-outs allow for gene deletion in specific tissues. Understanding these differences is essential for choosing the correct model to study gene function and for accurately interpreting experimental data in the context of genetics and human disease research.

256. (A) Position effect of the integration site
Pronuclear microinjection results in random integration of the transgene, which can lead to variable expression levels due to the "position effect" of the integration site. The surrounding chromatin structure and nearby regulatory elements can either enhance or suppress the expression of the transgene. Because of this variability, researchers must characterize several independent lines to find a model that shows the desired level and pattern of gene expression for their scientific studies.

257. (B) Homologous recombination
Gene targeting in embryonic stem cells relies on homologous recombination to ensure precise genetic modification. This cellular mechanism allows a researcher to replace a specific DNA sequence in the genome with a modified version provided in a targeting vector. By utilizing the cell's own DNA repair machinery, targeting ensures that the mutation occurs exactly at the intended locus, making it a highly accurate tool for creating knock-out and knock-in animal models.

258. (B) Injecting genetically modified ES cells into a wild-type blastocyst
Chimeric mice are produced by injecting genetically modified embryonic stem cells into a wild-type host blastocyst. The resulting animal is composed of two distinct cell populations: those derived from the ES cells and those from the host embryo. These chimeras are the first step in creating a new knock-out line. By breeding chimeras that have ES-derived cells in their germline, researchers can eventually obtain offspring that carry the targeted modification in every cell.

259. (B) Germline (sperm or eggs)
To establish a true knock-out line, a chimeric mouse must transmit the modified genome through its germline. This means that the genetically modified ES cells must have contributed to the production of sperm or eggs in the adult chimera. When these germ cells are fertilized, the resulting offspring will carry the genetic modification in all of their cells. Verifying germline transmission is a critical milestone in the creation of any new genetically engineered mouse model.

260. (B) White adipose tissue (adipocytes)
The hormone leptin is normally secreted by white adipose tissue, specifically by adipocytes. Its primary function is to signal the brain about the body's energy stores, helping to regulate appetite and metabolism. In the ob/ob mouse, a mutation prevents the production of functional leptin, leading to the failure of this feedback loop and resulting in hyperphagia and obesity. Understanding this hormonal pathway has been fundamental to research into human obesity and metabolic health.

261. (B) No effect on weight or food intake
Treating db/db mice with exogenous leptin has no effect on their weight or food intake because they lack functional leptin receptors. Even with high levels of the hormone, the brain never receives the signal to stop eating. This contrasts with ob/ob mice, which respond to leptin treatment with significant weight loss. This difference is

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212. (B) Substituting sentient animals with alternatives
The principle of "Replacement" in the 3Rs involves substituting sentient vertebrate animals with non-sentient models or other alternatives whenever possible. This can include using cell cultures, computer simulations, organ-on-a-chip technology, or invertebrates like fruit flies. Replacement is the highest ethical goal in animal research, aiming to advance scientific knowledge while eliminating the need for live animal subjects in experiments that can be successfully performed using alternative methods.

213. (B) Reduction
Designing an experiment with a properly calculated sample size using power analysis directly addresses the principle of "Reduction." This approach ensures that the researcher uses the minimum number of animals required to achieve statistically significant and scientifically valid results. By avoiding both over-utilization and under-utilization of subjects, researchers uphold ethical standards and ensure that animal lives are used as efficiently as possible in the pursuit of scientific discovery.

214. (A) Administering a local anesthetic prior to a painful surgical incision
Administering a local anesthetic prior to a painful surgical incision is a clear example of "Refinement." This action directly reduces the pain and distress experienced by the animal during the procedure, upholding the principle of maximizing welfare for research subjects. Refinement encompasses all such measures that improve the experience of animals in a laboratory setting, from improved analgesia to the provision of better social and physical environments.

215. (C) Refinement
Establishing early humane endpoints is most closely associated with the principle of "Refinement." By identifying clear criteria for when an animal should be humanely euthanized before experiencing severe pain or distress, researchers minimize the overall suffering involved in an experiment. This proactive approach ensures that the welfare of the animal is prioritized without compromising the scientific objectives, and it is a fundamental component of modern ethical research practices.

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216. (C) Consciousness followed by cardiac and respiratory arrest
In terms of humane euthanasia, the method must aim to cause a rapid loss of consciousness followed immediately by cardiac and respiratory arrest. The goal is to ensure that the animal experience no pain or distress during the process. Approved methods, such as anesthetic overdose or controlled CO2 exposure, are designed to be quick and effective, fulfilling the ethical requirement of providing a "good death."

217. (B) 30-70%
When CO2 is used for the euthanasia of rodents, the recommended displacement rate of the chamber air volume is 30 to 70 percent per minute. This flow rate ensures a gradual increase in CO2 concentration, which induces unconsciousness smoothly before death occurs. Using a flow rate that is too high or too low can cause distress, so proper calibration of the gas delivery system is essential for a humane procedure.

218. (B) 70-120 bpm
According to standard physiological references, the normal resting heart rate of an adult Beagle dog typically ranges from 70 to 120 beats per minute. Monitoring heart rate is a fundamental part of veterinary care and safety pharmacology studies, as changes can indicate stress, illness, or the physiological effects of an experimental compound. Maintaining these animals in a stable and healthy state is necessary for ensuring high-quality research data.

219. (B) 38.5 - 39.5 degrees Celsius
The normal resting body temperature of a rabbit is approximately 38.5 to 39.5 degrees Celsius. This core temperature is slightly higher than that of humans and is essential for the animal's metabolic functions. During pyrogen testing, small increases in this baseline temperature are monitored to detect the presence of endotoxins. Consistent environmental conditions are necessary to maintain the rabbit's thermal stability and ensure accurate clinical and experimental results.

220. (B) Cecotropes
Cecotropes are uniquely structured feces produced in the cecum that are consumed directly from the anus by rabbits and rodents. This behavior, known as cecotrophy, allows the animals to

tracking the founder is essential for verifying the genetic consistency and expression patterns of the transgene over generations, ensuring that the resulting line remains a reliable model for scientific research.

238. (B) Removed and housed individually before birth
In a harem mating system for mice, pregnant females are typically removed and housed individually before birth. This prevents the overcrowding of the cage and protects the newborns from potential interference by other adults. Providing the female with a quiet, individual space for parturition and nursing ensures the survival of the pups and allows for more accurate records of litter size and the health of the offspring.

239. (B) Conceive a second litter while simultaneously lactating the first
The occurrence of a postpartum estrus allows mice to conceive a second litter while they are still lactating the first. This biological capability is used in intensive breeding systems to maximize reproductive output. While it can lead to a slight delay in the implantation of the new embryos due to the metabolic demands of nursing, it significantly increases the number of offspring a female can produce over her lifespan.

240. (B) Rear pups whose biological mother is dead, agalactic, or exhibiting poor maternal care
Cross-fostering is a technique used in laboratory breeding to rear pups whose biological mother cannot care for them, such as if she is dead, agalactic, or showing poor maternal behavior. The pups are placed with a different nursing dam of a similar age and litter stage. This practice is essential for saving valuable genetic lines and for ensuring the survival and healthy development of neonatal rodents in a breeding facility.

241. (B) Multiple genes (polygenic) and environmental factors
A quantitative trait is generally influenced by multiple genes and environmental factors, leading to a continuous range of phenotypes in a population. Unlike Mendelian traits, which are determined by a single gene, quantitative traits such as growth rate or blood pressure show a complex pattern of inheritance. Studying these traits requires sophisticated statistical analysis and large sample sizes to identify the various genetic and environmental contributors to the observed variation.

242. (B) How strictly breeders choose the top-performing individuals to become parents of the next generation
Selection intensity is a measure of how strictly breeders choose only the top-performing individuals to become the parents of the next generation. A higher selection intensity means that only a small, elite percentage of the population is allowed to breed, which can lead to faster genetic progress. However, it also increases the risk of reducing genetic diversity and must be managed carefully in outbred stocks to prevent excessive inbreeding.

243. (B) Mating offspring to their younger parent
If brother-sister mating is not possible in an inbred strain, the accepted alternative to maintain the inbred status is mating an offspring to its younger parent. This backcrossing approach maintains the high level of homozygosity while helping to overcome temporary reproductive failures. It is a critical management strategy for preserving the genetic integrity of valuable inbred lines when standard mating pairs fail to produce viable offspring.

244. (B) Reduction in variation due to small population size
A genetic bottleneck in an outbred colony leads to a significant reduction in genetic variation due to a small population size. When only a few individuals contribute to the next generation, many alleles are lost by chance. This can increase the level of inbreeding and change the genetic characteristics of the stock. Maintaining a large, diverse breeding population is essential for preventing bottlenecks and ensuring the long-term genetic health of outbred colonies.

245. (A) Both A and R are true and R is the correct explanation of A.
Substrains of an inbred mouse line emerge when different branches of the colony are separated and bred independently for many generations. Because each group will inevitably accumulate different spontaneous mutations and undergo independent genetic drift, they eventually become genetically distinct from one another. Standardized nomenclature tracks these branches, allowing researchers to identify the specific substrain and account for any genetic

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229. (B) 4-6%
A typical laboratory rat diet consists of approximately 4 to 6 percent crude fat. This level provides sufficient essential fatty acids and energy while preventing the development of obesity and related metabolic issues in maintenance populations. Precise control of the fat content in animal feed is necessary to ensure the health of the colony and to minimize variability in research results that could be influenced by nutritional status.

230. (B) The precise effect of a single trace mineral or specific amino acid omission
A chemically defined diet is often necessary when studying the precise effect of a single trace mineral or specific amino acid omission. Because these diets are made from purified components, researchers can exactly control every nutrient. This allows for highly accurate studies of metabolic pathways and nutritional requirements that would be impossible with natural ingredient diets, where the exact composition of components like grain can vary slightly between batches.

231. (A) 16 to 22 degrees Celsius
The standard temperature range for a guinea pig housing room is typically 16 to 22 degrees Celsius, which is lower than the range for mice and rats. Guinea pigs are more comfortable in cooler environments and are highly susceptible to overheating. Maintaining the temperature within this specific range is a critical part of their husbandry to ensure they remain healthy and to prevent the physiological stress of heat exhaustion.

232. (A) Have very thick fur and lack functional sweat glands
Guinea pigs are extremely susceptible to heat stress primarily because they have very thick fur and lack functional sweat glands. They are unable to dissipate heat efficiently through evaporation, making them highly vulnerable to high ambient temperatures. Facility managers must ensure that their environment is kept cool and well-ventilated to prevent heatstroke, which can occur rapidly and is often fatal for these animals in a laboratory setting.

233. (B) Poor ventilation or infrequent bedding changes
In macro-environmental monitoring, high levels of ammonia in an animal room usually indicate poor ventilation or infrequent bedding changes. Ammonia is produced by the breakdown of urea in animal waste and can reach toxic levels if not effectively removed. Monitoring this gas is essential because elevated concentrations can cause respiratory irritation and increase susceptibility to disease, directly impacting the health and welfare of the laboratory animals and staff.

234. (B) Respiratory infections (e.g., Mycoplasma)
Prolonged exposure to high intracage ammonia levels in rats strongly predisposes them to respiratory infections, such as those caused by Mycoplasma pulmonis. Ammonia irritates the mucous membranes and impairs the ciliary clearance mechanisms of the respiratory tract, making it easier for pathogens to colonize the lungs. Maintaining low ammonia levels through proper cage hygiene and room ventilation is therefore vital for preventing chronic respiratory diseases in rodent colonies.

235. (A) II, IV, I, III
Breeding systems are ordered from lowest to highest homozygosity as: outbred rotational mating, monogamous mating within an outbred stock, congenic backcrossing at generation ten, and continuous brother-sister mating at generation twenty. Outbred systems maximize genetic diversity, while inbred systems aim for complete genetic uniformity. Understanding these levels is essential for selecting the correct genetic model for research and for managing the genetic health of laboratory animal populations.

236. (B) Radio Frequency Identification (RFID)
The microchip used for permanent animal identification operates on the principle of Radio Frequency Identification. Each chip contains a passive transponder that is activated by the radio frequency signal from a scanner, transmitting a unique identification code. This technology allows for the rapid and error-free identification of animals without the need for physical handling or visible markings, making it an efficient and humane tool for large-scale research studies.

237. (B) Founder
In a pedigree chart for a transgenic mouse line, the original animal that first integrated the engineered DNA into its germline is termed the "founder." All subsequent animals in the line are descendants of this individual. Identifying and

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guinea pigs to identify the cause of scurvy and to test the effectiveness of various treatments. They continue to be important models for studying the physiological roles of ascorbic acid.

204. (B) Marginal ear vein or central ear artery
Polyclonal antibodies are typically harvested from rabbits by collecting blood from the marginal ear vein or the central ear artery. These vessels are easily accessible and allow for the collection of large volumes of blood without causing significant distress to the animal. The rabbit's size and well-developed ear vasculature make it the most efficient species for regular antibody production in many laboratory and commercial facilities.

205. (A) P-1, Q-2, R-3, S-4
Laboratory animals are matched to specific research areas based on their unique biological characteristics. Rabbits are used for pyrogen testing, guinea pigs for tuberculosis models, and dogs for safety pharmacology. Macaques are vital for testing vaccine efficacy against human viruses. This specialization ensures that the most appropriate and relevant animal models are used to address specific scientific questions and to ensure the safety of medical treatments.

206. (C) Histamine
Guinea pigs used in anaphylaxis research exhibit severe respiratory distress due to the rapid release of histamine, which causes intense constriction of the bronchioles. This reaction closely parallels the physiological events of human allergic asthma and anaphylactic shock. Their extreme sensitivity to histamine makes them an invaluable model for studying the mechanisms of allergic reactions and for developing new pharmacological treatments to manage respiratory and immune-mediated disorders.

207. (A) Less than 1%
Non-human primates account for less than one percent of the total number of animals used in biomedical research. Despite their small numbers, they play an outsized role in critical areas such as neuroscience, infectious disease research, and vaccine development, where their close physiological and genetic similarity to humans is essential. Their use is reserved for studies where no other suitable animal or non-animal models can provide the necessary scientific insights.

208. (C) Docile nature, moderate size, and robust health
The Beagle is the preferred breed of dog in laboratory research due to its docile nature, moderate size, and generally robust health. These characteristics make them easy to handle, house, and care for within a research facility. Their consistent physiological responses and the large amount of background data available on the breed ensure that they provide reliable and reproducible results for safety pharmacology and toxicology studies.

209. (A) CCSEA
Under the PCA Act in India, the CCSEA is the statutory body responsible for ensuring that animal experiments are performed humanely and avoid unnecessary suffering. They provide the regulatory framework for the use of animals in research and education, oversee the registration of facilities, and ensure that all institutional ethics committees are operating correctly. Their oversight is essential for maintaining high ethical standards in animal research across the country.

210. (B) Small laboratory animals up to the size of rodents and rabbits
An Institutional Animal Ethics Committee is mandated to review and approve research protocols involving small laboratory animals, such as mice, rats, and rabbits. Their role is to ensure that the proposed experiments are ethically sound, scientifically justified, and follow the principles of the 3Rs. For research involving larger animals like dogs or primates, the IAEC's recommendation must be further reviewed and approved by the central CCSEA authority.

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211. (A) The IAEC, and subsequently forwarded to the main CCSEA for final approval
According to CCSEA guidelines, experiments on large animals such as dogs and non-human primates must first be approved by the local IAEC and then forwarded to the main CCSEA for final national-level approval. This two-tier review process provides an extra layer of ethical oversight for studies involving more sentient and higher-order species, ensuring that their use is strictly necessary and that welfare standards are fully met.

differences that may impact their research results.

246. (B) Cross A and B to produce an F1 generation, then cross F1s to produce F2s, followed by continuous brother-sister mating
To establish a new inbred strain from two existing inbred strains, the process begins by crossing them to produce an F1 generation. The F1 animals are then intercrossed to create an F2 generation, which provides a pool of genetic diversity. From this point, continuous brother-sister mating is performed for at least twenty generations to fix a new, unique combination of alleles into a stable and homozygous inbred genetic background.

247. (B) Maintain a lethal or deleterious mutation in a heterozygous state on a uniform genetic background
The primary goal of creating a segregating inbred strain is to maintain a lethal or deleterious mutation in a heterozygous state within a uniform inbred background. Because the homozygous mutant may be non-viable or infertile, the strain must be kept by mating heterozygotes in each generation. This allows researchers to study the biological effects of the mutation without the confounding factor of genetic variation from the animal's background.

248. (B) Genotyping for high recipient genome percentage
"Speed congenics" is a technique that reduces the number of backcross generations needed by using genotyping to identify offspring with the highest percentage of the recipient strain's genome. By selecting these "best" individuals for further breeding, researchers can achieve a genetically uniform background in fewer generations than traditional backcrossing. This approach saves time and resources while maintaining the precision of the resulting congenic model for genetic and biomedical research.

249. (A) No new genetic material (animals) is introduced from outside the colony
A "closed colony" is one in which no new genetic material is introduced from outside sources. All breeding occurs among the animals already within the colony. This practice is used to maintain the genetic consistency of a stock and to protect the colony from the introduction of new pathogens. Over time, closed colonies may develop unique genetic characteristics due to drift, making them distinct from the original population from which they were derived.

250. (B) Comprehensive screening using serology, bacteriology, parasitology, and PCR
The microbiological status of an animal is definitively verified through comprehensive screening using serology, bacteriology, parasitology, and PCR. This regular health monitoring program identifies the presence of any pathogens or commensal organisms that could affect the animal's health or the validity of research data. Maintaining a documented microbial status is a fundamental requirement for the use of animals in standardized biomedical research, ensuring results are reproducible and welfare is protected.

251. (B) Monitor health via bedding or air exposure
Sentinel animals are used in rodent facilities to monitor the health of the colony by exposing them to soiled bedding or air from the main population. Because they are regularly tested for various pathogens, they act as an early warning system for any infections that may be present. Using sentinels allows for effective health monitoring without the need to sample every animal in the colony, making it a practical and efficient management strategy.

252. (C) Outbred mouse (e.g., Swiss Webster or CD-1)
Outbred mice are commonly used as sentinels because they readily produce detectable antibodies (seroconvert) when exposed to most murine pathogens. Their genetic diversity often makes them more robust and representative of a broad immune response. By regularly testing these sentinel mice, facilities can gain an accurate picture of the microbial health of the entire colony, ensuring that any introduction of disease is quickly identified and managed to protect research integrity.

253. (B) An animal from a different strain is accidentally mated with an animal of the inbred colony
Genetic contamination occurs when an animal from a different strain is accidentally mated with an individual from an inbred colony. This introduces new alleles and destroys the genetic uniformity that is the hallmark of an inbred strain. Even a single such event can compromise

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are essential for protecting personnel who work with these animals in research.

270. (A) Cardiovascular, Respiratory, and Central Nervous System
Safety pharmacology specifically assesses the potential adverse effects of new drugs on the cardiovascular, respiratory, and central nervous systems. These three areas constitute the "core battery" of systems that must be evaluated before a compound can proceed to human clinical trials. By testing for changes in heart rate, breathing, and behavioral responses in animal models, researchers can identify potential life-threatening side effects and ensure the safety of new medical interventions for patients.

271. (C) Non-invasive observational studies
CCSEA guidelines categorize experiments into different severity levels, with non-invasive observational studies representing the level involving the least pain or distress. These studies might include behavioral monitoring or routine weighing, which do not cause significant physical or psychological harm. Categorizing procedures by severity is a fundamental part of the ethical review process, ensuring that researchers always seek the least invasive methods and provide appropriate care for the animals involved in their work.

272. (A) The CCSEA Main Nominee
The CCSEA Main Nominee acts as the external oversight figure on an Institutional Animal Ethics Committee. Their role is to ensure that the committee's decisions and the research protocols it approves comply with the Prevention of Cruelty to Animals Act and national guidelines. By providing independent review, the nominee helps maintain high ethical standards and ensures that the institution remains accountable to the national regulatory body for all activities involving animals.

273. (B) The expected scientific or medical benefits to humans or animals outweigh the potential harm to the research animals
The primary ethical justification for using animals in research is the principle that the expected scientific or medical benefits to humans or other animals outweigh the potential harm to the research subjects. Regulatory bodies require this "harm-benefit analysis" to ensure that animal use is only permitted when the potential outcomes are of significant value. This ethical framework guides researchers and ethics committees in making responsible decisions about the use of animals in biomedical discovery.

274. (A) Replacement
Using the Limulus Amebocyte Lysate (LAL) assay instead of the rabbit pyrogen test is a direct application of the principle of "Replacement." This transition substitutes a live animal procedure with an in vitro biochemical test, achieving the same safety goal without the use of vertebrate subjects. Implementing such alternatives whenever they are scientifically valid is a primary goal of ethical animal research and reflects a commitment to the 3Rs throughout the pharmaceutical industry.

275. (C) Refinement
Providing nesting materials to laboratory mice to allow for natural burrowing and nesting behavior is a clear application of "Refinement." This enrichment enhances the psychological and physical well-being of the animals by allowing them to express natural behaviors and better regulate their micro-environment. Refinement strategies focus on improving the quality of life for laboratory animals, which leads to reduced stress and more reliable scientific data by providing a more stable and humane environment.

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276. (B) Good death
The term "euthanasia" is derived from Greek and literally translates to "good death." In the context of laboratory animal science, it refers to the practice of ending an animal's life in a way that minimizes pain, distress, and anxiety. A humane euthanasia must cause a rapid loss of consciousness followed by cardiac and respiratory arrest, ensuring that the process is quick, effective, and ethically sound for the welfare of the research subject.

277. (B) Severing the spinal cord and destroying major neural pathways governing respiration and cardiac function
Cervical dislocation causes death by severing the spinal cord and destroying the major neural pathways that govern respiration and heart function. This physical method results in an immediate loss of consciousness when performed correctly by trained personnel. It is commonly used for rodents as it avoids the introduction of pharmacological agents into the body, which

key to understanding the distinction between hormone deficiency and hormone resistance in the development of obesity and related metabolic disorders.

262. (A) Leptin receptor
The Zucker rat (fa/fa) carries a mutation in the gene encoding the leptin receptor. This defect prevents the animal from responding to leptin's satiety signals, leading to hyperphagia and the rapid development of morbid obesity. Because it accurately models leptin resistance, the Zucker rat is a vital tool for studying the pathophysiology of obesity, insulin resistance, and the metabolic consequences that follow when the body's primary energy-regulation system is disrupted.

263. (B) Opportunistic infections due to T-cell deficiency
Athymic nude mice must be housed under strict SPF or barrier conditions because they are highly susceptible to opportunistic infections due to their severe T-cell deficiency. Without functional T cells, their immune system cannot mount an effective cell-mediated defense against common environmental bacteria, fungi, or viruses. Maintaining a protected environment is essential for their survival and for ensuring that they remain healthy enough to be used in long-term experimental studies, particularly in oncology.

264. (C) Severely immunodeficient mice (e.g., Nude, SCID, NSG)
Human xenograft tumor models are most successfully grown in severely immunodeficient mice such as the Nude, SCID, or NSG models. Because these animals lack various components of the adaptive and innate immune systems, they do not reject the human cells. This allows for the study of human cancer growth and its response to treatments in a living system. These models are fundamental to modern oncology research and the development of new anti-cancer medications.

265. (B) Lack of T, B, and NK cells for engraftment
The primary advantage of the NSG mouse over the traditional SCID model is its complete lack of functional T, B, and natural killer (NK) cells. The additional loss of NK cells removes a major barrier to the survival of foreign tissues, making the NSG mouse the most receptive host for the engraftment of human cells and tissues. This enhanced immunodeficiency allows for more successful and complex humanized mouse models in immunology and oncology research.

266. (C) Pyrogen
A substance that causes a rise in body temperature when injected intravenously is known as a pyrogen. Pyrogens are often derived from bacterial endotoxins and can cause dangerous fevers in humans and animals. Testing for pyrogenicity is a critical safety requirement for all parenteral drugs and medical devices. The identification and removal of these contaminants are essential for ensuring that medical treatments do not cause life-threatening immune reactions or febrile responses in patients.

267. (B) Limulus Amebocyte Lysate (LAL) test
The classic rabbit pyrogen test has been largely replaced by the Limulus Amebocyte Lysate (LAL) test, which is a modern in vitro alternative. The LAL assay uses the blood of horseshoe crabs to detect bacterial endotoxins with high sensitivity and specificity. By replacing live animal tests with this biochemical assay, researchers fulfill the principle of Replacement while maintaining a rigorous safety standard for ensuring that pharmaceutical products are free from dangerous fever-inducing contaminants.

268. (B) Hemochorial placentation similar to humans
The guinea pig's reproductive physiology is a relevant model for human pregnancy because it possesses hemochorial placentation, which is similar to the placental structure in humans. This allows for studies of nutrient transfer and placental function that are more representative of human biology than those in other rodents. Combined with their long gestation period, these features make the guinea pig an excellent model for studying fetal development, pregnancy complications, and maternal-fetal interactions.

269. (B) Macacine alphaherpesvirus 1 (B virus)
Non-human primate facilities must adhere to strict occupational health guidelines due to the risk of zoonotic transmission of the Macacine alphaherpesvirus 1, also known as B virus. While the virus is common and relatively harmless in Macaques, it can cause fatal encephalitis in humans if transmitted through bites, scratches, or mucous membrane exposure. Rigorous safety protocols, training, and rapid response measures

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recover essential nutrients, such as B vitamins and proteins, that were synthesized by their gut bacteria. Differentiating cecotropes from regular hard feces is important for understanding the specialized digestive physiology and nutritional requirements of these laboratory species.

221. (B) B-complex vitamins and proteins synthesized by hindgut bacteria
Coprophagy, specifically the consumption of cecotropes, is essential for rodents and rabbits to adequately absorb B-complex vitamins and proteins synthesized by their hindgut bacteria. These nutrients are produced after the main site of absorption has passed, so re-ingestion is the only way for the animal to utilize them. This process is a vital part of their metabolic health and ensures they meet their daily nutritional requirements efficiently.

222. (B) Red, blood-like crusts
The Harderian gland in rodents secretes porphyrin, which, during times of stress or illness, can accumulate around the eyes and nose and appear as red, blood-like crusts. This phenomenon, often mistaken for bleeding, is a clear clinical sign of distress in rats and mice. Observing these secretions is a standard part of welfare monitoring, helping facility staff identify animals that may require veterinary attention or environmental adjustments.

223. (A) Chromodacryorrhea
The excessive accumulation of red porphyrin staining around a rat's eyes and nose is a condition known as chromodacryorrhea. This "bloody tear" response is typically triggered by stress, respiratory infection, or poor environmental conditions. It serves as an important visual indicator of the animal's overall health and well-being. Facility managers use the presence of chromodacryorrhea to identify underlying issues within the colony that need to be addressed.

224. (B) Grow continuously throughout the animal's life
Rodent incisors are hypsodont, meaning they grow continuously throughout the animal's life. This constant growth is balanced by the natural wearing down of the teeth as the animal gnaws on hard food or nesting materials. If this wear is interrupted, the teeth can overgrow, leading to serious health issues. Providing appropriate materials for chewing is a necessary part of rodent husbandry to maintain their dental health.

225. (A) Sentinel exposure to soiled bedding → Blood collection → Serum separation → ELISA / MFI testing
To obtain a definitive microbiological diagnosis using sentinels, the animals are first exposed to soiled bedding from the colony. After a sufficient exposure period, blood is collected and serum is separated. This serum is then tested using assays like ELISA or MFI to detect antibodies against murine pathogens. This sequence is a standard health monitoring protocol, providing a reliable way to screen the main colony indirectly.

226. (B) Develop malocclusion and tissue damage
If a rodent's continuously growing incisors do not wear down properly due to misalignment, the animal will develop malocclusion. This can cause the teeth to pierce the soft tissues of the mouth or grow into the skull, leading to pain, inability to eat, and severe injury. Regular dental checks and the provision of gnawing materials are essential practices to prevent this condition and ensure the long-term health of laboratory rodents.

227. (B) Providing hard pelleted diets or wooden chew blocks
The most effective method to prevent malocclusion in laboratory rodents is providing hard pelleted diets or wooden chew blocks. These materials encourage natural gnawing behavior, which naturally wears down the continuously growing incisors. This simple husbandry practice is essential for maintaining the animal's ability to eat and for preventing the painful and potentially fatal consequences of overgrown teeth, ensuring their well-being and productivity in a research setting.

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228. (C) Premolars
Guinea pigs differ from mice and rats in their dental formula because they possess premolars. Like their incisors and molars, these teeth grow continuously and must be worn down through the mastication of fibrous plant material. Understanding the unique dental structure of the guinea pig is important for providing proper nutrition and for diagnosing dental problems that can occur when their specialized dietary and environmental needs are not met.

could interfere with certain types of scientific analysis, such as those involving brain chemistry or drug metabolism.

278. (A) Decapitation or cervical dislocation
To ensure that death has occurred following CO2 euthanasia in rodents, a secondary physical method, such as decapitation or cervical dislocation, is often recommended. This "death-check" is a mandatory step in many welfare protocols to prevent the possibility of an animal recovering after being removed from the CO2 chamber. Confirming death through a secondary means is a final, essential component of a humane euthanasia process in a research or breeding facility.

279. (B) 4-8 years
The routine life expectancy of a guinea pig is approximately four to eight years. Their relatively long lifespan compared to smaller rodents like mice and rats makes them suitable for certain chronic studies and longitudinal research. Providing proper nutrition, particularly Vitamin C, and a stable environment is essential for their long-term health. Understanding their lifespan is important for planning research studies and for managing the ongoing care and housing of these animals in a facility.

280. (B) Pain, distress, or illness
In assessing animal welfare, clinical signs such as a hunched posture, piloerection (ruffled fur), and a lack of grooming are classic indicators of pain, distress, or illness. These subtle behavioral and physical changes are often the first signs that an animal is unwell. Daily observation by trained staff is essential for identifying these markers early, allowing for timely veterinary intervention or the application of humane endpoints to prevent unnecessary suffering in research subjects.

281. (B) Standardize the gut microbiome with a defined set of bacterial species
The "alter-gnotobiotic" status, such as Altered Schaedler Flora, is used in rodent research to standardize the gut microbiome with a specific, defined set of bacterial species. By providing a consistent microbial background, researchers can eliminate the variability that comes with undefined environmental microflora. This standardization is critical for studies involving immunology, metabolism, and nutrition, where the composition of gut bacteria is known to significantly influence the animal's physiological responses and experimental outcomes.

282. (C) 99.97%
High-Efficiency Particulate Air (HEPA) filters are designed to remove 99.97 percent of airborne particles that are 0.3 micrometers in diameter. These filters are essential in barrier facilities to ensure that air entering or leaving animal rooms is free from pathogens and particulate contaminants. The use of HEPA filtration is a cornerstone of maintaining the health status of SPF, gnotobiotic, and axenic animal colonies, providing a highly controlled and clean environment for sensitive biomedical research.

283. (B) 20 - 24 degrees Celsius
The optimal recommended environmental temperature for housing laboratory mice is between 20 and 24 degrees Celsius. This range supports their metabolic health and ensures they can maintain homeothermy without excessive stress. Maintaining a stable temperature is essential for minimizing experimental variability, as fluctuations can affect rodent behavior, physiology, and the outcomes of scientific studies. Facility HVAC systems must be precisely controlled to keep the macro-environment within this specific, comfortable range for the animals.

284. (C) Temperature and ventilation
Temperature and ventilation are the most critical environmental parameters to control during the transport of laboratory animals to prevent thermal stress. Animals in transit are highly vulnerable to overheating or chilling if air circulation is inadequate or ambient temperatures are extreme. Proper shipping containers and climate-controlled transport vehicles are necessary to ensure that animals arrive at their destination healthy and without the physiological confounding factors that result from transport-related stress and discomfort.

285. (B) Substrain of C3H maintained by 'He' and further established by Jackson Laboratory (J)
A mouse strain designated as C3H/HeJ represents a specific substrain of the C3H line that was maintained by Heston (He) and later established at the Jackson Laboratory (J). The slash separates the original strain from the substrain designation. Standardized nomenclature like this is essential for tracking the unique genetic history and potential phenotypic differences of

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amount of pain management required after the procedure. By managing pain effectively from the start, researchers uphold the principle of refinement, improve the recovery time of the animals, and minimize the physiological impacts of untreated pain on scientific data.

294. (C) Introduction of adventitious pathogens into the colony
Biological materials like cell lines must be screened for murine viruses before being introduced into live mice to prevent the introduction of adventitious pathogens into a clean colony. Many cell lines can carry latent viruses that, once injected, can spread rapidly through a research facility, compromising the health of the animals and the validity of experimental results. Rigorous testing protocols are essential for maintaining the high health status of barrier and SPF animal facilities.

295. (D) Pleiotropy
Pleiotropy is the genetic phenomenon where a single gene affects multiple, seemingly unrelated phenotypic traits. For example, a mutation in a gene essential for pigment production might also cause defects in the immune system or internal organs. Understanding pleiotropy is important in laboratory animal science because it helps explain the diverse symptoms seen in certain genetic models and reminds researchers that a single targeted genetic change can have widespread biological consequences throughout the animal.

296. (A) DNA methylation and histone modification
Epigenetic modifications alter gene expression without changing the underlying DNA sequence and are most commonly mediated by DNA methylation and histone modification. These changes can be influenced by environmental factors such as diet, stress, and housing conditions. Understanding epigenetics is increasingly important in research because these modifications can be passed on to offspring and can significantly impact the phenotype and experimental responses of laboratory animals, adding another layer of complexity to genetic studies.

297. (C) Chemically defined (purified) diet
A chemically defined diet ensures the highest level of exactness and reproducibility in nutritional studies because every component is formulated from pure chemical compounds. This eliminates the natural variability found in cereal-based diets, where nutrient levels can fluctuate between batches. These purified diets allow researchers to precisely manipulate individual nutrients to study their specific biological effects, providing a powerful tool for investigating metabolic pathways and the foundational principles of mammalian nutrition and health.

298. (A) Excessive barbering and inter-male aggression
Overcrowding of mice in a standard cage commonly leads to behavioral problems such as excessive barbering and inter-male aggression. Barbering is the removal of fur from cage-mates, which is a sign of social stress and hierarchy disruption. Aggressive encounters can lead to serious injury or death. Maintaining appropriate social group sizes and providing sufficient space and enrichment are essential for preventing these issues and ensuring a stable and humane environment for laboratory rodents.

299. (C) Causes no excessive toxicity or 10% weight loss
In toxicology, the Maximum Tolerated Dose (MTD) is defined as the highest dose of a chemical that causes no excessive toxicity or more than a ten percent loss in body weight over a specified period. The MTD is used in long-term carcinogenicity and safety studies to ensure that the animals are exposed to the maximum possible dose without compromising their survival or general health. Identifying this dose is essential for accurately assessing the potential risks of a compound.

300. (C) Ensure experiments are humane and compliant
The ultimate ethical goal of the Institutional Animal Ethics Committee (IAEC) is to ensure that all animal experiments are conducted humanely and in full compliance with established laws and guidelines. By reviewing research protocols and monitoring facility operations, the IAEC protects animal welfare and ensures that the use of animals in science is justified, responsible, and meets the highest ethical standards, maintaining public trust and the integrity of the biomedical research enterprise.

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laboratory animals, ensuring that researchers can select the most appropriate model and accurately report their findings.

286. (A) Mapping quantitative trait loci using fixed blocks
Recombinant inbred strains are powerful tools for mapping quantitative trait loci because each line possesses fixed, unique blocks of the progenitor genomes. By correlating the phenotypic traits of multiple RI lines with their known genetic markers, researchers can pinpoint the chromosomal regions responsible for complex traits. This method provides a stable and reproducible genetic framework that is invaluable for identifying the multiple genes that contribute to health, disease, and behavioral characteristics in rodents.

287. (B) Loss of variation when establishing new colonies
The "founder effect" refers to the significant loss of genetic variation that occurs when a new laboratory colony is established by a very small number of individuals from a larger population. This reduction in diversity can lead to the fixation of specific alleles and the emergence of unique traits within the new stock. Understanding this effect is critical for managing the genetic health of colonies and for interpreting phenotypic differences that arise between geographically separated laboratory populations.

288. (B) High variability requiring larger sample sizes
A major disadvantage of using an outbred stock in pharmacological research is the high phenotypic variability, which often requires larger sample sizes to achieve statistical significance. Because each animal is genetically unique, they respond differently to treatments, mimicking the diversity of human populations. While this variability is useful for broad safety testing, it makes it more difficult to identify subtle therapeutic effects compared to the highly uniform responses seen in inbred rodent strains.

289. (C) During the dark phase
Mice are nocturnal animals, meaning their natural peak period of physical activity, social interaction, and feeding occurs during the dark phase of the photoperiod. In a laboratory setting, this cycle is typically regulated by a twelve-hour light and twelve-hour dark schedule. Understanding this circadian rhythm is essential for timing behavioral observations, conducting physiological measurements, and ensuring that researchers work within the animal's natural periods of activity to obtain more accurate and representative data.

290. (A) Providing puzzle feeders, climbing structures, and social housing
Environmental enrichment for laboratory macaques typically includes providing puzzle feeders, climbing structures, and social housing with compatible cage-mates. These enhancements are necessary to meet the complex cognitive and physical needs of non-human primates. By promoting natural behaviors and reducing stress-related stereotypical behaviors, enrichment improves animal welfare and ensures that the animals are better suited for neurobehavioral and biomedical research, leading to more valid and reliable scientific conclusions and results.

291. (A) Make normal postural adjustments and behaviors
CCSEA regulations require that the primary enclosure for a laboratory animal must provide sufficient space to allow the animal to make normal postural adjustments and express natural behaviors. This includes the ability to stand, turn around, and rest comfortably. Proper cage sizing is a fundamental requirement for animal welfare, preventing the physical and psychological stress associated with confinement in overly restricted spaces and ensuring the overall health and well-being of the research subjects.

292. (B) Pedal withdrawal (toe-pinch) reflex
Assessing the depth of anesthesia in rodents is most reliably performed by testing the pedal withdrawal (toe-pinch) reflex. A firm pinch to the foot or toe should result in no movement if the animal is in a deep plane of surgical anesthesia. Monitoring this reflex, along with respiratory rate and mucous membrane color, is essential for ensuring that the animal remains unconscious and perceives no pain during invasive experimental or surgical procedures.

293. (A) Pre-emptively, before the painful stimulus or surgical incision occurs
Analgesia should ideally be administered pre-emptively, before a painful stimulus or surgical incision occurs. This practice, known as pre-emptive analgesia, helps prevent the sensitization of the nervous system and reduces the overall

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